

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 135509

TO: James Schultz

Location: REM/2D18/2C18

Art Unit: 1635

Tuesday, October 19, 2004

Case Serial Number: 09/695451

From: David Schreiber

Location: Biotech-Chem Library

Remsen E01A61 Phone: 272-2526

david.schreiber@uspto.gov

Search Notes		Harman Control of the		
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Access	DR#	
Access	UD#	

SEARCH REQUEST FORM

Scientific and Technical Information Center

Lequester's Full Name:			Date:
			(circle): PAPER DISK E-MAI
Tail Box and Bldg/Room Loca	tion:	Results Format Preferred	(circle): PAPER DISK E-MAII
f more than one search is su	ibmitted, please pr	ioritize searches in orde	r of need.
******************	******	********	the subject matter to be searched.
******************************* Please provide a detailed statement of nelude the elected species or structure tility of the invention. Define any to known. Please attach a copy of the co	the search topic, and decess, keywords, synonyms	escribe as specifically as possible s. acronyms, and registry number scial meaning. Give examples of	ers, and combine with the concept or
Fitle of Invention:			
Inventors (please provide full name	es):		
Earliest i riority Filing Date: _			
Earliest r Hority r Hing Date	include all pertinent infor	mation (parent, child, divisional, o	or issued patent numbers) along with the
*For Sequence Searches Only - Fleuse appropriate serial number.	menae an personal y		
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	*****	********	*******
STAFF USE ONLY	Type of Searc	···	and cost where applicable
Scarcher: 0, Schre, ber	NA Sequence (#)		
Searcher Phone #: 2-72 - 25	AA Sequence (#)		
Searcher Location: Remsey EOI A	Structure (#)		
Date Searcher Picked Up:	Bibliographic		
Date Completed: 10 19	Litigation		
Searcher Prep & Review Time:	Fulltext _	Sequence Systems	ompugen
C-erical Pron Time:	Patent Family		
Colline Time: 183	Other	Other (specify)	

PTO-1590 (3-01)

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SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 65%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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source
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Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
Expressed sequence tags from soybean root hair subtractive cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION: CF921494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      October 18, 2004, 14:17:38; Search time 0.001 Seconds (without alignments) 0.352 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Unpublished (2003)
Unpublished (2003)
Unpublished (2003)
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0586
Email: stacepy@missouri.edu
Single pass sequence
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 1 summaries
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Glycine max
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KEYWORDS
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ORGANISM
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AUTHORS
TITLE
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FEATURES

Location/Qualifiers

1..8

source

/organism="Glycine max"
/organism="Glycine max"
/wol type="mRNA"
/db xxef="texxon:3847"
/fiscue type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
gmrhkwwa!
/note="Organ: root hairs; Vector: pGR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradythizobium japonicum for 3 hours."

Query Match

Query Match

Query Match

29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 734 AGAAACAG 741

Db 8 AAAACAG 1

Search completed: October 18, 2004, 14:17:39
Job time: 0.001 secs
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2390, Ap
6036, Ap
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5182195
                          ; Search time 0.001 Seconds (without alignments) 135.608 Million cell updates/sec
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                                                                                                                                                                                                                            Sequence 6036,
Sequence 2873,
Patent No. 5182
Sequence 10, A
Sequence 12, A
                                                                                                                                                                       Sequence 45,
Sequence 45,
Sequence 45,
Sequence 67,
Sequence 6, A
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    GenCore version 5.1.6
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US-08-488-242A-45
US-08-488-211A-45
US-08-488-211A-45
US-08-438-4211A-45
US-08-438-421A-45
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US-08-21-632A-11
US-08-21-632A-11
US-08-21-32A-11
US-08-231-232A-11
US-08-231-232A-11
US-08-231-232A-11
US-08-231-232A-11
US-08-231-232A-11
US-08-231-232A-11
US-08-231-240-125
US-08-231-232A-11
US-08-231-246-654
US-08-231-246-654
                                                                            of hits satisfying chosen parameters:
                                                                                                                                     SUMMARIES
                                                                                               Minimum Match 0%
Maximum Match 100%
Listing first 276 summaries
                   nucleic search, using sw model
                                                  tgccaggagaaacagaacacg 22
                           2004, 14:09:43
                                                         IDENTITY NUC Gapoxt 0.5
                                                                    276 segs, 3082 residues
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                                          US-09-695-451-1
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                           October 18,
                                                                                    length: 8
length: 30
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Query
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Perfect score:
                                                         Scoring table:
                                                                                                                                                                                                                                        Score
                    ı
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                                                                                    DB
                   nucleic
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                                                  Sequence:
                                                                     Searched:
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Maximum I
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Result No.

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US-09-513-783A-65 US-09-475-947A-329 US-09-475-947A-329 US-08-687-916-11 US-08-687-916-11 US-08-138-614-11D-5 US-08-388-333-477 US-08-388-333-477 US-08-388-333-477 US-08-388-333-477 US-08-388-333-32 US-08-522-384-33 US-08-522-384-33 US-08-522-384-33 US-08-522-384-33 US-08-522-384-33 US-08-522-384-33 US-08-522-384-33 US-08-522-384-31 US-08-522-384-31 US-08-523-33-32 US-08-523-33-32 US-08-523-53-33 US-08-523-53-481 US-08-523-53-481 US-08-523-53-481 US-08-523-53-481 US-08-523-53-481 US-08-523-53-481 US-08-523-53-481 US-08-523-33-481 US-08-523-33-481 US-08-528-53-481 US-08-528-53-481 US-08-528-53-481 US-08-528-53-481 US-09-508-753-482-23 US-09-508-	7.864984040809090909090909090909090909090909
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US-08-485-942A-45/c

US-08-485-942A-45/c

Sequence 45, Application US/08485942A

Sequence 45, Application US/08485942A

Sequence 45, Application

Patent No. 6048837

APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,

APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE:

TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS TITLE OF INVENTION: AMBNDED)

NUMBER OF SEQUENCES: 99

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: DEADER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,942A
FILING DATE: UNDE 7, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6048837cmber 30, 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: AUGUST 17, 1994
CLASSIFICATION SEGGEN S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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732 GGAGAAACAGAACACCG 748
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TELERAX: 201
TELERA: 133521
INFORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 18 base pairs
TVPE: nucleic acid
                                                                    18 GGAGAACAGAACACCG 2
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US-09-106-038A-47/C

Sequence 47.0 Application US/09106038A

Sequence 17.0 Application US/09106038A

Sequence 17.0 Application US/09106038A

SETEMBRAL INFORMATION:

APPLICANT: Branda F. Baker and Lex M. Cowsert

TITLE OF INVENTION: EXPRESSION

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Isis Pharmaceuticals, Inc.

STREET: 292 Faraday Avenue

CITY: Carlsbad

STREET: 292 Faraday Avenue

COUNTYR: US.A.

ZIP: 9200.0 S.A.

COUNTYR: IBM PC compatible

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

COMPUTER: IBM PC compatible

CONSTANTION OF THE STATEM WINGOWS NT

SOFTHARE: Joint SOFTEM: Windows NT

SOFTHARE: June 26, 1998

CLASSIFICATION NUMBER: 37,280

REFERENCE/DOCKET NUMBER: 37,280

REFERENCE/DOCKET NUMBER: 37,280

REFERENCE/DOCKET NUMBER: 37,280

TELEPHONE: (760) 931-9200

INPORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 18
                                                                                                    US-08-678-117

US-08-465-590-126

US-08-465-590-126

US-08-605-163-7

US-08-605-163-7

US-08-605-163-7

US-08-605-163-7

US-08-41-607-21

US-08-41-607-21

US-08-71-78-21

US-09-363-600-21

US-09-363-600-21

US-09-363-600-21

US-09-363-600-21

US-09-369-789-2401

US-09-989-789-2401

US-09-989-789-2401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-106-038A-47
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GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: WICLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (primer)
DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.0%; Score 15.4; DB 1; Length 18; 94.1%; Pred. No. 6.6; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,208A
FILING DATE: Unne 7, 1995
APPLICATION NUMBER: 08/486,943
FILING DATE: Unne 7, 1995
CLASSIFICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION NUMBER: 08/436,431
FILING DATE: More 10, 1995
CLASSIFICATION S14
PRIOR APPLICATION S14
PRIOR APPLICATION NUMBER: 08/347,563
APPLICATION NUMBER: 08/2448ember 30, 1994
CLASSIFICATION S14
PRIOR APPLICATION NUMBER: 08/222,345
FILING DATE: Adquet 17, 1994
CLASSIFICATION NUMBER: AGUST 17, 1994
CLASSIFICATION NUMBER: AGUST 17, 1994
CLASSIFICATION NUMBER: AGUST 17, 1994
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US-08-483-211A-45/c
Sequence 45, Application US/08483211A
Patent No. 6309853
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                730 CAGGAGAACAGAACAC 746
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                  ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                   STREET: 411 Hackens
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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ORIGINAL SOURCE:
ORGANISM: HUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-488-208A-45
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                     US-08-488-214A-45/C
US-08-488-214A-45/C
Sequence 45, Application US/08488214A
Patent No. 6124439
GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
APPLICANT: MARCHERITA MAFFELY, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE
TITLE OF INVENTION: (AS AMENDED)
TITLE OF INVENTION: (AS AMENDED)
TITLE OF INVENTION: (AS AMENDED)
CORRESPONDENCES: 99
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
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                                                                                                                                                                                                                                                                                                                                                                                                                 CALF: 0.004
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,214A
FILING DATE: JUNE 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: AUGUST 17, 1994
CLASSIFICATION:
NAME: JGKENT INFORMATION:
NAME: JGKENT ENCYPACTION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 187-5800
TELEFAX: 201,343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: JUNE 7, 1995
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: 00, 1994
CLASSIFICATION:
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US-08-488-208A-45/c
; Sequence 45, Application US/09488208A
                                                                                                                                                                                                                                                                           ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  730 CAGGAGAACAGAACAC 746
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.19
Matches 16; Conservative
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ORGANISM: Human
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ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEN
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) Sequence 45, Application US/08438431A
) Sequence 46, Application US/08438431A
) Sequence 47, Application US/08438431A
) Patent No. 6429290
) GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIXING ZHANG, RICARDO PROBNCA, MARGHERITA MAFFEI,
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR
) NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/488,223A
FLING DATE: O7-JUN-1995
CLASSIFICATION NUMBER: 08/485,943
PRIOR APPLICATION NUMBER: 08/485,943
APPLICATION NUMBER: 08/485,943
APPLICATION NUMBER: 08/347,563
FLING DATE: AUGUST 17, 1994
ATTORING POR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 45:
CHARACTER 18 base pairs
TUDEST 1804
ATTORING CHARACTERISTICS:
AUGUST 1804
AUGUST 18
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                                             NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Human
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-08-488-223A-45
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STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              730 CAGGAGAACACACAC 746
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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RESULT 6
US-08-488-223A-45/c
US-08-488-223A
Sequence 45, Application US/08488223A
Setent No. 6350730
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (primer)
DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.0%; Score 15.4; DB 1; Length 18; 94.1%; Pred. No. 6.6; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                730 CAGGAGAACAGAACAC 746
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Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Human
US-08-483-211A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359 Gaps

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Sequence 67, Application US/08577081A
Sequence 67, Application US/08577081A
Seturice 67, Application US/08577081A
SENERAL INFORMATION:
APPLICANT: Careb, Nazh
ITILE OF INVENTION: Methods and Reagents for Typing HLA
ITILE OF INVENTION: Methods and Reagents for Typing HLA
ITILE OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedall & Larson
STREET: 1992 Commerce Street Suite 309
CONTY: Yorktown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 70.0%; Score 15.4; DB 1; Length 18; Best Local Similarity 94.1%; Pred. No. 6.6; Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear Molacule Molacule TYPE: DNA (primer)
DESCRIPTION: sequence tagged-site specific PCR primer
DESCRIPTION: sWSS2359
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Diskette - 3.5 inch, 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS DOS SOFTWARE: Word Dark
                    FILING DATE: June 7, 1995
CLASSIFICCATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION SATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6471956ember 30, 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 26,742
FILING DATE: August 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERBURE/DOCKET NUMBER: 600-1-087 CIP2J
TELECOMMUNICATION NUMBER: 26,742
REPERBURE/SOCKET NUMBER: 26,742
FELEFRAN: 201,487-5800
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APPLICATION NUMBER: US/08/577,081A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    730 CAGGAGAACAGAACAC 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10598
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Hum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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Sequence 45, Application US/08488225A

Sequence 45, Application US/08488225A

Patent No-Faralon

Patent No-Faralon

APPLICANT: THE ROCKEFELLER UNIVERSITY

TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

TITLE OF INVENTION: MOLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 98

CORRESSONDENCE ADDRESS:

ADDRESSES: Klauber & Jackson

STREET: 411 Hackensack

CITY: Hackensack

COUNTRY: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (primer)
DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 70.0%; Score 15.4; DB 1; Length 18; Best Local Similarity 94.1%; Pred. No. 6.6; Matches 16; Conservative 0; Mismatches 1; Indels
                    COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOUTWARE: Patentin Release #1.0, Version #1.25
SOUTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,431A
FILING DATE: May 10, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6429290ember 30, 1994
CLASSIFICATION S14
PRIOR APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION NUMBER: 08/292,345
FILING SAPELICATION NUMBER: 26,742
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/OPERATION:
TELECHOME: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CARRENT APPLICATION NATM:

APPLICATION NUMBER: US/08/488,225A

FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    730 CAGGAGAACAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 CAGGAGAACACACACAC 2
  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: June 7,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE
  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-438-431A-45
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Query Match 56.4%; Score 12.4; DB 1; Length 18; Best Local Similarity 92.9%; Pred. No. 23; Matches 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-179-656A-6/c

Sequence 6, Application US/08179656A

Sequence 6, Application US/08179656A

Patent No. 6673893

GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Grotendorst, Buscoyte Derived GROWTH FACTORS
TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
NUMBER OF SEQUENCES: 18
NUMBER OF SEQUENCES: 18
STREET: 60 State Street, Suite 510
    TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 227-7400
TELEPRX: (617) 227-5441
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTER.STICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                              732 GGAGAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             732 GGAGAACAGAACA 745
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                                                                                                                                                                                                                                                                                                                                                                                                                          16 GCAGAACAGAACA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 60 State Stree CITY: Boston STATE Massachusetts COUNTRY: USA ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hybridization probe GE2-183 for typing of
HLA Class I genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.7%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 13; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-08-465-095-6/c
; Sequence 6, Application US/08465095
; Patent No. 5849534
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
APPLICANT: Ilda, Naoka
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKPIELD
; STREET: 60 State Street, Suite 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT, NAME:
ARTORNEY/AGENT, NAME:
REGISTRATION NUMBER: 32,038
REPRENCE/POCKET NUMBER: MSK.P-001-US
TELECOMMUNICATION INFORMATION:
TELEPAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AGOII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,095
PILING DATE: 07-JAN-1994
APPLICATION NUMBER: 08/101,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 08/001,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/472,377
FILING DATE: 07-DAN-1993
APPLICATION NUMBER: 07/472,377
FILING DATE: 01-F2B-1990
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GZI-003C2
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731 AGGAGAAACAGAACACC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AGGAGACACGGAACACC 18
                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
CTHER INFORMATION:
CTHER INFORMATION:
US-08-577-081A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: human
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Pred. No. 23;
0; Mismatches 1; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,656A
FILING DATE: 07-JAN-1994
CLIASSIFRICATION DATA:
APPLICATION NUMBER: 08/001,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/172,377
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/172,377
FILING DATE: 01-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRALION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GZI-003C2
TELECOMMUNICATION INFORMATION:
TELEPXX: (617) 227-7400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTER/STICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative
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STRANDEDNESS: single
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Sequence 42, Application US/08912129A;
Sequence 42, Application US/08912129A;
Patent No. 5922533;
GENERAL INFORMATION:
APPLICANT: VALLARI, ANADRUZELA S.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: HICKMAN, ROBERT K.
APPLICANT: MARTINE, VINCENT A. JR.
APPLICANT: GOLDEN, ALAN M.
APPLICANT: ALAN M.
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4649, Application US/09422978

Sequence 4649, Application US/09422978

Parent No. 6537751

GENERAL INFORMATION:
PAPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TILE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION WUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER RILING DATE: 1998-11-23
EARLIER RILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-04-21

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NOS: 11796
                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                         DB 1; Length 19;
                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                         Query Match 56.4%; Score 12.4; Di
Best Local Similarity 92.9%; Pred. No. 25;
Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 731 AGGAGAAACAGAACACC 747
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                                                                                                                                                                                                                                                                                                                     727 TGCCAGGAGAACA 740
                                                                                                                                                                                                                                                                                                                                                                                 16 TGCCAGGACAACA 3
                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-268-140-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: primer_bind LOCATION: 1..18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Abbott Park
STATE: IL
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-422-978-4649/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-912-129A-42
LENGTH: 19
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APPLICANT: Gemmill, Robert M.
APPLICANT: Gemmill, Harry A.
TITLE OF INVENTION: TRG8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED FILE REFERENCE: 93445-00004
CURRENT APPLICATION NUMBER: US/09/268,140
CURRENT FILING DATE: 10990-03-12
PRIOR FILING DATE: 19990-03-12
NUMBER: OF SEQ ID NOS: 46
SOFTWARE: PATCHIN Ver. 2.0
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 18;
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                                                                                                                                CT-US94-00300-6/c
Sequence 6, Application PC/TUS9400300
SEGNEAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Idad, Naoka
TITLE OF INVENTION: LEUKCCYTE DERIVED GROWTH FACTORS
NUMBER OF SEQUENCES: 13
CORRESSONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.4%; Score 12.4; C 92.9%; Pred. No. 23; vative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GZI-003C2
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-7401
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00300
FILING DATE: 07-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JAN-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/001,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/472,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-268-140-28/c
; Sequence 28, Application US/09268140
; Patent No. 6268176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  732 GGAGAAACAGAACA 745
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16 GCAGAACAGAACA 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US.08-584-040-5499
US.08-584-040-5499
Sequence 5499, Application US/08584040
Fatent No. 6346398
GENERAL INPORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Scinchcomb, Dan T.
APPLICANT: U.S.A.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
AZIP: 90071-2066
COMPUTER: READABLE FORM:
MEDIUM TYPE: Scinchcomb, Dan D. Doc E.
COMPUTER: IBM Compatible COMB
APPLICATION NUMBER: US 08/841,636
FILING DATE: 30-AFR-1997
APPLICATION DATA:
APPLICATION NUMBER: US 60/005,335
FILING DATE: 17-CCT-1995
FILING DATE: 17-CCT-1995
FILING DATE: 04-DEC-1995
FILING DATE: 04-DEC-1995
FILING DATE: 04-DEC-1995
FILING DATE: 04-DEC-1995
FILING DATE: 08-UNN-1996
FILING DATE: 10-CCT-1996
FILING DATE: 10-CCT-1996
FILING DATE: 10-CCT-1996
FILING DATE: 10-CCT-1996
FILING DATE: 17-CCT-1996
FILING DATE: 1906
FILING DATE: 1906
FILING DATE: 1906
FILING DATE: 1906
FILING DATE: 
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-329-350-40
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APPLICANT: Londesborough, John
APPLICANT: Londesborough, John
APPLICANT: Londesborough, John
APPLICANT: Haakana, Heli
APPLICANT: Hathan, Heli
APPLICANT: Elantto, Minna
APPLICANT: Elovainio, Minna
APPLICANT: Blovainio, Minna
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Mashington
STATE: D.C.
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,350
FILING DATE: Herewith
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
COMPOTER: 1EM COMPATIBLE
OPERATIOS SYSTEM: MS-DOS (Windows 95)
SOFTWARE: Microsoft Word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,129A
FILING DATE: 15-AUG-1997
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 32,622
ATPORNEY/AGENT INFORMATION:
NAME: DALOCKET NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 86.7%; Pred. No. 29;
Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40, Application US/09329350 Patent No. 6184019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 847-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA
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US-08-912-129A-42
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APPLICANT: Pavco, Pam
APPLICANT: Backsigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stochedo, Jaime
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00,876-J (237/198)
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US (60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR APPLICATION NUMBER: US 08/584,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                              APPLICANT: ESCOBEDO, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: A LYON
ADDRESSEE: LYON & LYON
STREET: 613 West Fifth Street
STREET: 633 West Fifth Street
STREET: Galifornia
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTEN READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.9%; Score 11.2; D
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: STORMS SOUR COMPUTER: STORMS SOUR COMPUTER: IBM COMPATION COMPUTER: STORMS SOUR COMPUTER: STORMS SOUR COMPUTER: STORMS SOUR COMPUTER: STORMS SOUR COMPUTER: US/08/584,040 FILLING DATE: January 11, 1996 CLASSIFFCATION: S14 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION UNDER: S0, 1995 ATTORNEY/AGENT INFORMATION: NAME: WATDLEY RECISTANTION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-371-772B-2873/c
; Sequence 2873, Application US/09371772B
; Patent No. 6566127
APPLICANT: Stinchcomb, Dan T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       728 GCCAGGAGAAACAGAA 743
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 base pairs
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STRANDEDNESS: single
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Rabozyme Pharmaceuticals, Inc.
APPLICANT: Pavoc, Pam
APPLICANT: Bacobed, Jaim
APPLICANT: Stinchcomb, Dan
APPLICANT: Sconded, Jaim
APPLICANT: Sconded, Jaim
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE REPERENCE: MBHB00,871,772B
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR PELLING DATE: 1995-10-26
PRIOR PELLING DATE: 1995-10-26
PRIOR PELLING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOCTIMARE: PARCENTED APPLICATION OF PARCENTED APPLICATION OF PARCENTED APPLICATION OF PARCENTED APPLICATION OF PARCENTED APPLICATION NUMBER: US OF PAR
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Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches
                                                                                                                         PATOR AFFLACTION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEFONMUNICATION INFORMATION:
TELEFONE: (213) 955-0440
TELEFAK: (213) 955-0440
INFORMATION: SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-371-772B-2390
; Sequence 2390, Application US/09371772B
; Patent No. 6566127
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Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
     January 11, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          733 GAGAACAGAACA 745
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Best Local Similarity 92.3
Matches 12; Conservative
                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus sp. US-09-371-772B-2390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.1%; Score 10.8; DB 1;
85.7%; Pred. No. 35;
tive 0; Mismatches 2;
           described below:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 1012
ZIP: 1012
ZIP: TOWN TYPE: J.S. TOWN: WEDIUM TYPE: J.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: J.S. TICH 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,664
FILING DATE: May 12, 1994
CLASSIFICATION: S14
ATTOCNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA: described bel APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LIENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                     TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731 AGGAGAAACAGAAC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AGGGGAACAGATC 1
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Matches 12; Conservative
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; Pacent No. Makhawa, Kazuo; Kaisho, Yoshihiko; Yoshimura, Koji
; Title Of Invention: Method For Increasing Using Protease
; Deficient Yeachs
NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
                                                                                                                                                                               DB 1; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 11; DB 1; Length 15; 100.0%; Pred. No. 32; 1. ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08291932A

Sequence 10, Application US/08291932A

Patent No. 56587B0.

GENERAL INFORMATION.

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Daper, Kenneth G.

APPLICANT: Daper, Kenneth G.

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: NP-KB

NUMBER OF SEQUENCES: 830

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: Suite 4700

CITY: Los Angeles

STREET: Suite 4700

STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
                                                                                                                                                                           50.9%; Score 11.2; D
81.2%; Pred. No. 35;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: AUGUST 15, 1994
                                                                                                                                                                                                                                                              728 GCCAGGAGAACAGAA 743
      NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2873
                                                                                                                                                                                                                                                                                                      16 GCCAGGAGACACGTAA 1
                                                                                                                                                                           Query Match
Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 50.0
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           732 GGAGAAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGAGAACAGA 12
                                                                                          ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;SEQ ID NO:60:
;
;ENGTH: 15
5182195~60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: ...
CONDUTRY: USA
ZITP: 92037

ZITP: 92037

COMPUTER READABLE FORM:
RUBLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Batentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,080
FILING DATE: April 24, 1996
CILASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: HARTIS, SCOLT C.
RESTREATION NUMBER: 32,030
REFERENCE/DOCKET NUMBER: 32,030
REPERENCE/DOCKET NUMBER: 36618/129001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
COUNTRY:

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM FC-
OPERATING SYSTEM: Enchology
OPERATING SYSTEM: FC-
STILING DATE: May 13, 1994

CLASSIFICATION NUMBER: PCT/US95/06379

FILING DATE: May 13, 1994

CLASSIFICATION NUMBER: 28,678

REFERENCE, John P.
REFERENCE, JOCKET NUMBER: 44683-PCT
FELEPRAY: 212-39-0526

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: LENGTH: 12 base pairs

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US95-06379-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 AGGAGAAACAGA 742
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SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGGAGAAAGAGA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 26
US-08-639-080-4
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                                  Gaps
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47.3%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 31;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                 RESULT 24
US-08-484-138-12
IS-08-484-138-12
Sequence 12, Application US/08484138
Fatent No. 5652350
Fatent Natural Natural
Fatent Natura
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GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Ren, Wu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
COAPERSEE: COAPERSS:
ADDRESSEE: COAPER & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IEM FC
COMPUTER: IEM FC
COMPUTER: DESCRIPTIONS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
FILING DATE: June 7, 1995
CLASSIFTCATION: 435
ATORNEY MAICH INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
TELEPHONE: 212-977-9550
TELEPHONE: 212-64-0525
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
   Pred. No. 31;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
US-08-484-138-12
Best Local Similarity 91.7%;
Matches 11; Conservative C
                                                                                               731 AGGAGAAACAGA 742
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                               1 AGGAGAAAGAGA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGAGAAAGAGA 12
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 25
PCT-US95-06379-12
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Gaps

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KESULT 28
US-09-874-601-18/C
Sequence 18, Application US/09874601
Sequence 18, Application US/09874601
Sequence 18, Application US/09874601
Sequence 18, Application
GENERAL INFORMATION:
APPLICANT: ERMIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
TITLE OF INVENTION UNMERS: US/09/874,601
CURRENT APPLICATION NUMBER: 00/045,147
PRIOR PLING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR PLING DATE: 1997-04-21
PRIOR FILING DATE: 1997-04-21
PRIOR APPLICATION NUMBER: 60/044,492
PRIOR FILING DATE: 1997-04-21
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 14
TWOEL DATE: 140-140
TWOELDATE: 140-140
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47.3%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCOUNT 23

Sequence 11, Application US/08291932A

Sequence 11, Application US/08291932A

Parent No. 5658700

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: RIBGINER TREATMENT OF
TITLE OF INVENTION: RIBGINER CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NF-KB

NUMBER OF SEQUENCES: 830

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: misc feature

LOCATION: ()..()

TOTER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-18
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STATE: Callfornia
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/08/291,932A
August 15, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           731 AGGAGAAACAGA 742
          1 AGGAGAAGCAGA 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Raimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bodelann, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Ctore
CTTW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
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47.3%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 37;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10577/P58418
STRANDEDNESS: double TOPOLOGY: linear MODECULE TYPE: other nucleic acid DESCRIPTION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-535-249-125
; Sequence 125, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REPERBUCE DOCKET NUMBER: 106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELERAX: (202) 393-5550
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                         2 GAÁACAGTACAC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE:
; ANTI-SENSE: YE
US-08-535-249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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US-08-639-080-4
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Gaps

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Sequence 132, Application US/09081646

Sequence 132, Application US/09081646

Batent No. 6333152

GENERAL INFORMATION:

APPLICANT: Kinzler, Kenneth

APPLICANT: Zhang, Lin

APPLICANT: Zhang, Lin

APPLICANT: Zhang, Lin

TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

TITLE OF INVENTION: Cancer Cells

TITLE OF INVENTION: Cancer Cells

TITLE OF INVENTION: Cancer Cells

TITLE OF INVENTION: 1998-05-20

CURRENT APPLICATION NUMBER: 05/047,352

EARLIER APPLICATION NUMBER: 05/047,352

SAPRIER FILING DATE: 1997-05-21

NUMBER OF SEQ ID NOS: 871

NUMBER OF SEQ ID NOS: 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNER PERIOR OF A PAPLICATION US/09081646

Sequence 867 Application US/09081646

Patent No. 6333152

GENERAL INFORMATION:

APPLICANT: Kinzler, Kenneth

APPLICANT: Zhang, Lin

APPLICANT: Zhang, Lin

APPLICANT: Concertin, Bert

APPLICANT: Concertin, Bert

TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

TITLE OF INVENTION: Cancer Cells

TITLE OF INVENTION: Cancer Cells

TITLE OF INVENTION: Cancer Cells

CURRENT APPLICATION NUMBER: US/09/081,646

CURRENT FILING DATE: 1998-05-20

EARLIER PILING DATE: 1997-05-21

NUMBER OF SEQ ID NOS: 871

NUMBER OF SEQ ID NOS: 871

NUMBER OF SEQ ID NOS: 871
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                                                                                                                                                                                                                                 DB 1; Length 15;
                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                 Score 10.4; Di
Pred. No. 41;
0; Mismatches
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                      TELEX: 67.3510
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDENESS: single
1 TOPOLOGY: linear
US-08-363-240A-654
  (213) 955-0440
                                                                                                                                                                                                                                                                                                                            732 GGAGAAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91...
Thes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   727 TGCCAGGAGAAA 738
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                                                                                                                                                                                                                                                                                                                                                                        12 ggagaaccagaa 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 31
US-09-081-646-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-081-646-132
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LENGTH: 15
       TELEFAX:
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Coulure, Larry
APPLICANT: Coulure, James
APPLICANT: Bisgaier, Charles
APPLICANT: Bisgaier, Charles
APPLICANT: Bagaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PREVENTION, INHIBITION OF
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGRAT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELECONWUNICATION INFORMATION:
TELECONWUNICATION INFORMATION:
TELECONG (213) 955-0440
TELECONG (213) 955-0440
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10.4; DB
Pred. No. 41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIE: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
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CURRENT ARE.

APPLICATION DATA:

APPLICATION NUMBER: US/08/363,240A
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-363-240A-654/c
; Sequence 654, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             731 AGGAGAAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AGGGGAAACAGA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
US-08-291-932A-11
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Gaps

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Gaps
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VENDUT: RESULT SORE, JOHN K.

PATENT NO. 616894

GENERAL INFORMATION:

APPLICANT: ROSE, JOHN K.

TITLE OF INVENTION: USES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas

CITY: New York

CITY: New York

CONDUTRY: USA

INFORTING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Blopy disk

COMPUTER: BADABLE FORM:

MEDIUM TYPE: Plopy disk

COMPUTER: BADABLE FORM:

MEDIUM TYPE: PLOPY disk

COMPUTER: BADABLE FORM:

MADIUM TYPE: PLOPY DATA:

COMPUTER: BADABLE FORM:

MADIUM TYPE: PLOPY DATA:

COMPUTER: BADABLE FORM:

MATCREET APPLICATION DATA:

APPLICATION NUMBER: US/08/64,595

ATTORNEY/AGENT INFORMATION:

MADE: MISTORY, S. Leslie

MATCREET MASSERICATION: 435

ATTORNEY/AGENT INFORMATION:

MADE: MADABLE TO ME PENNIE

MATCREET MASSERICATION NUMBER: 6223-008

TELEFRAX: (212) 780-9090

TELEFRAX: (212) 780-9090

TELEFRAX: (212) 780-9090

TELEFRAX: (212) 780-9015

TELEFRAX: (212) 780-9015

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ DAIRS

TYPE: MADICANORM: ASSENTINGES:

MADE: MADICAL STANDER: ASSENTINGES:

MADE: MADICAL STANDER: ASSENTINGES:

MADE: MADE: MADICAL STANDER: ASSENTINGES:

MATCREET MADE: MADE:
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Sequence 15, Application PC/TUS9606053

Sequence 15, Application PC/TUS9606053

GENERAL INFORMATION: RECOMBINANT VESICULOVIRUSES AND THEIR
TITLE OF INVENTION: USES
TITLE OF SEQUENCES: 41

CORRESPONDENCE 41

CORRESPONDENCE 4DRESS:
ADDRESSE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.5%; Score 10; DB 1; Length 11; 100.0%; Pred. No. 32;
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Matches 10; Conservative
731 AGGAGAAACAGA 742
                                                     4 AGGAGAAAAAGA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   730 CAGGAGAAAC 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
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                                                                                     Score 10.4; DB 1; Length 15;
Pred. No. 41;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                        RESULT 33
US-08-137-024-4
| US-08-137-024-4
| Sequence 4, Application US/08137024
| Patent No. 6005167
| GENERAL INFORMATION:
| APPLICANT: VAN TUNEN, Adriamus, J. APPLICANT: VAN DER MEER, Ingrid M. APPLICANT: WAN TUNEN, Josephus N.M. TITLE OF INVENTION: POR OBTAINING MALE STERILE TITLE OF INVENTION: PLANTS AND RECOMBINANT DNA FOR TITLE OF INVENTION: USE THEREIN
| TITLE OF INVENTION: USE THEREIN NUMBER OF SEQUENCES: 7
| CORRESPONDENCE ADDRESS: 7
| STREET: 26 West 61st Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10023
ZIP: 10023
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette 3.50 inch, DS, DD 720
MEDIUM TYPE: KD/720K0
COMPUTER: ISA PC Compatible 286 SX 12 Mhz
COMPUTER: ISA PC Compatible 286 SX 12 Mhz
OCHRANT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14-0CT-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: BP 91200910
FILING DATE: 16-APR-1991
ATTORNEY/AGST INFORMATION:
NAME: MASS. Clifford, J.
REGISTRATION NUMBER: 09918
FELEPHONE: (212) 708-1800
TELEPHONE: (212) 708-1800
TELEPHONE: (212) 708-1800
TELEPHONE: (212) 246-8959
TELES: 23328
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: NUCleic acid
STRANDEDNESS: double
TOPOLOGY: Innear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 47.3%; Score 10.4; D
Best Local Similarity 91.7%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches
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HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Petunia hybrida
US-08-137-024-4
                                                                                              Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                727 TGCCAGGAGAAA 738
                                                                                                                                                                                                                                                                      3 TGCCAGGAGGAA 14
   ; ORGANISM: Homo sapiens
US-09-081-646-867
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STATE: New York
COUNTRY: USA
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phic Loci in an ADN Sequence, Nucleotide Sequences Forming Hybridisation Probes and Their Biological Applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Defoung, Mary Beth
APPLICANT: Siwkowski, Andrew M.
APPLICANT: Siwkowski, Andrew M.
APPLICANT: Hampel, Arnold E.
TITLE OF INVENTION: WICHOUTE SEQUENCES AND RIBOZYMES DERIVED THEREOF
TITLE OF INVENTION: UUCLEOTIDE SEQUENCES AND RIBOZYMES DERIVED THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 9.8; DB 1; Length 14;
Pred. No. 48;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Michigan

COUNTRY: US
                                                                                                                                                                                                                                                                                          OPERATION SYSTEM: C-LUGS/MS-LUGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,004
FILING DATE: US/08/303,004
FILING DATE: US/08/303,004
FILING DATE: US/09/31,311B
FILING DATE: 19920818
ATTOREY/AGENT INFORMATION:
NAME: BERTICATION NUMBER: 30,024
REGISTRATION NUMBER: 30,024
REGISTRATION NUMBER: 30,024
REGISTRATION NUMBER: 30,024
REGISTRATION NUMBER: 30,024
TELEFRAX: (703) 836-6400
TELEFRAX: (703) 836-6400
TELEFRAX: (703) 836-2787
TELER: 90-1799 PTO ALEX
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                             ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 38
US-08-442-513A-11/C
; Sequence 11, Application US/08442513A
; Satch No. 5646031
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: phic Loci : TITLE OF INVENTION: Hybridisatic NUMBER OF SEQUENCES: 38 CORRESPONDENCE ADDRESS: ADDRESSE: Oliff & Berridge STREET: P.O. Box 19928 CITY: Alexandria STATE: Virginia COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               733 GAGAAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACAAACAGAGCA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-303-004-13
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| Sequence 456, Application US/09081646
| Patent No. 63313152
| GENERAL INFORMATION:
| APPLICANT: Kinzler, Kenneth
| APPLICANT: Zhou, Wei
| TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
| TITLE OF INVENTION: Cancer Cells
| TITLE OF INVENTION: Cancer Cells
| FILE REFERENCE: 0107.74664
| CURRENT APPLICATION NUMBER: 05/9/081,646
| CURRENT FILING DATE: 1998-05-20
| EARLIER FILING DATE: 1998-05-21
| NUMBER OF SEQ ID NOS: 871
| NUMBER OF SEQ ID NOS: 871
| NUMBER OF SEC ID NOS: 871
| NUMBER OF SEC ID NOS: 871
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Sequence 13, Application US/08303004
Patent No. SSSSSS;
GENERAL INFORMATION:
APPLICANT: Vergnaud, Gilles
TITLE OF INVENTION: Process for Detection of New Polymor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10; DB 1; Length 11;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06053
FILING DATE: 01-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%; Score 10; DB 1;
100.0%; Pred. No. 48;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.5%; Scc. No. ... 100.0%; Pred. No. ...
                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Masrock, S. Leslie
REGISTRATION NUMBER: 18,32
REFERENCE/DOCKET NUMBER: 6523-009-228
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            732 GGAGAAACAG 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-081-646-456
                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: RNA PCT-US96-06053-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                      FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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LENGTH: 15
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Gaps

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RESULT 40
US-08-173-489C-186/C
; Sequence 186, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
    APPLICANT: WANG, C. -G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
    NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
    STREET: 510 EAST 73RD STREET,
    CITY: NEW YORK

STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 186 ;FROM 1 TO 14
US-08-173-489C-186
                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER NEADABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 18M PC/XT/AT

OPERATING SYSTEM: MS-DOS version 6.2

SOFTWARE: Wordeperfect Version 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2 DEC 1993

CLASSIFCATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08,436

FILING DATE: 29 OCT 1992

ATTORNEY/AGENT INFORMATION:

NAMM: Handelman, OSeeph H.

REDISTRAVION NUMBER: 26,179

REFERENCE/DOCKET NUMBER: 26,179

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                        Score 9.8; DB Pred. No. 48; 0; Mismatches
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US-08-173-489C-198/c
; Sequence 198, Application US/08173489C
                           Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6%;
Matches 11; Conservative
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                                                                                                                                                             736 AAACAGAACACCG 748
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US-08-442-513A-16/c
US-08-442-513A-16/c
US-08-646031
; Patent No. 5646031
; APPLICANT: DeYoung, Mary Beth
APPLICANT: Siwkowski, Andrew M.
APPLICANT: Hampel, Arnold E.
TITLE OF INVENTION: METHOD FOR DERIVING RIBOZYMES FROM
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND RIBOZYMES DERIVED THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5646031thwestern Hwy., Suite 410
CITY: Farmington Hills
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,513A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Ribozyme substrate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Ribozyme substrate" US-08-442-513A-11
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APPLICATION.

FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 2384.00014
TELEPHONE: (810) 539-5050
TELEPHONE: (810) 539-5055
TELEPHONE: (810) 539-5055
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear

'Aasc = "Ribozyme sub
                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROAD, Kenneth.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 2384.00014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: NUCleic acid
TYPE: NUCleic acid
STRANDEDNESS: single
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,513A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   736 AAACAGAACACCG 748
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MOLECULE TYPE: other nucleic acid DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: isolate adw2 sequence region in Seq ID No. 5861244185 Score 9.8; DB 1; Length 14; Pred. No. 48; 0; Mismatches 2; Indels

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& No. 6190866ris LLP
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                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
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Patent No. 6190866
GENERAL INFORMATION:
APPLICANT: Alelsen et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having
TITLE OF INVENTION: Antibacterial Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz STRET; One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-AMY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31 409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHANE: (202) 638-666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
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APPLICATION NUMBER: US/09/049,190
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202)638-6666
TELEPAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   728 GCCAGGAGAACA 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 14 base pairs
nucleic acid
EDNESS: unknown
Washington D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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US-09-049-190-11/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price Transforming-growth-factor Appressive effect of transforming-growth-factor Appressive ADDRESSEE: Jacobson, Price Transforming-growth-factor ADDRESSEE Transforming-growth-factor ADDRESSE Transforming-growth-factor ADDRESSE Transforming-growth-factor ADDRESSE Transforming-growth-factor ADDRESSE Transforming-growth-factor ADDRESSE Transfo
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DESCRIPTION: third strand derived from Hepatitis B
DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels
                        GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, C. -G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:

RELEVANT RESIDUES IN SEQ ID NO: 198 :FROM 1 TO 14
US-08-173-489C-198
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400 Seventh St. N:W.
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUM TYPER: 3.5 inch, 1.44Mb storage COMPUTER: TEB PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/08/173,489C
FILING DATE: 2.2 DEC 1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 2.9 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: US/179
REFERENCE/DOCKET NUMBER: US/179
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: CALTORNEY) (212) 246-8959
SECURACE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 126, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingenslepen, Georg-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731 AGGAGAAACAGAA 743
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NEW YORK
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US-08-535-249-126
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGIGSTRATION NUMBER: 28,937
REFRENCE/DOCKET NUMBER: ISIS-2560
TELECOMMUNICATION INFORMATION:
TELEPRONE: 215-568-310
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 bases

TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear

); OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-lysine-glycine); OTHER INFORMATION: backbone US-09-049-190-11 Query Match
44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 2; Indels RESULT 44
US-08-932-140C-11/C
| Sequence 11, Application US/08932140C
| Sequence 11, Application US/08932140C
| SEQUENCE 11, Application US/08932140C
| SERERAL INFORMATION:
| TITLE OF INVENTION: Peptide Nucleic Acids Having
| TITLE OF INVENTION: Antibacterial Activity
| NUMBER OF SEQUENCES: 23
| CORRESPONDENCE ADDRESS: 3
| ADDRESSE: No. 630318 fis LLP
| STREET: One Liberty Place - 46th Floor
| CITY: Philadelphia NAME/KRY: Modified-site
LOCATION: 13
COTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KRY: Modified-site
LOCATION: 14
COTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine OTHER INFORMATION: backbone COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMBUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Mcrosoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,140C
FILING DATE: Septemeber 16, 1997
CLASSIFICATION NUMBER:
FILING DATE:
ATTORIEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER:
FLEIDHOME: 15.5-568-3409
TELEDEMONE: 215-568-3100
TELEMONETH: 15 bases
TYPE: nucleic acid
STRANDEDMESS: single US/08/932,140C ISIS-2560 FEATURE:
NAME/KEY: Modified-site
LOCATION: 15 NAME/KEY: Modified-site 731 AGGAGAAACAGAA 743 15 AGGAGAAAGAGTA 3 à FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: Dackbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: Dackbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: Dackbone
FEATURE:
FEATURE: NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: Dackbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: Dackbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: Dackbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: Dackbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
LOCATION: 9 NAME/KEY: Modified-site
LOCATION: 1
COTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone FRATURE:
NAME/KEY: Modified-site
LOCATION:
OTHER INFORMATION: N-acetyl (2-aminoethyl) glycine
OTHER INFORMATION: backbone TRATURE:
NAME/KEY:
MODIFIED-SITE
LOCATION: 10
COTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone LOCATION: 11
OTHER INFORMATION: N-acetyl (2-aminoethyl)glycine
OTHER INFORMATION: backbone LOCATION: 9
OTHER INFORMATION: N-acetyl (2-aminoethyl)glycine
OTHER INFORMATION: backbone N-acetyl (2-aminoethyl)glycine backbone

'RATURE: NAME/KEY: Modified-site

'EATURE: NAME/KEY: Modified-site

LOCATION: 12 OTHER INFORMATION: OTHER INFORMATION:

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44.5%; Score 9.8; DB 1; Length 15;

Query Match

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LENGTH:
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backbone
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COTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-
COTHER INFORMATION: lysine-glycine backbone
15-08-932-140C-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME, NATION: 8
LOCATION: 8
OTHER INFORMATION: backbond FEATURE:
NAME/KEY: Modified-site
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LOCATION: 6
OTHER INFORMATION: N-acety
OTHER INFORMATION: backbor
FEATURE:
NAME/KEY: Modified-site
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NAME/KEY: Modified-site
LOCATION: 10
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NAME/KEY: Modified-site
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    NAME/KEY: Modified-site
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LOCATION: 13
OTHER INFORMATION: N-ace
OTHER INFORMATION: back
               Modified-site
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OTHER INFORMATION:
                            LOCATION: 2
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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NAME/KEY:
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is Squence 460, Application US/09081646

is SPELICANT: Kenneth

is APPLICANT: Zhou, Wei

is APPLICANT: Zhou, Wei

is APPLICANT: Zhou, Wei

is TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

is TITLE OF INVENTION: Cancer Cells

is TITLE OF INVENTION: 1998-05-20

is EARLIER APPLICATION NUMBER: 60/047,352

is EARLIER PLING DATE: 1997-05-21

is NUMBER OF SEQ ID NOS: 871

is NUMBER OF SEQ ID NOS: 871

is LENGTH: 15
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84.6%; Pred. No. 52;
tive 0; Mismatches 2; Indels
                           Indels
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Description of Artificial Sequence:
TOTHER INFORMATION: Sequences
US-09-531-000-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60, Application US/09531000
; Requence 60, Application US/09531000
; Ratent No. 6464810
GENERAL INFORMATION:
; APPLICAMT: JOHNSON, Marion D.
; APPLICAMT: TRESCO, Jacques R.
; TITLE OF INVENTION: TR.PLEX IN-SITU HYBRIDIZATION
; FILE REPERENCE: 2448-103
; CURRENT APPLICATION NUMBER: US/09/531,000
; CURRENT FILING DATE: 2000-09-08
; CURRENT FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 60/064,997
; PRIOR FILING DATE: 1997-11-10
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 60
                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

44.5%; Score 9.8; DB 1;
Best Local Similarity 84.6%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 2
Best Local Similarity 84.6%; Pred. No. 52; Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             728 GCCAGGAGAACA 740
                                                                             731 AGGAGAAACAGAA 743
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Best Local Similarity 84.65
Matches 11; Conservative
                                                                                                                              15 AGGAGAAAGAGTA 3
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US-09-531-000-60
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US-08-916-120A-15/C

Sequence 15, Application US/08916120A

Fatent No. 596228

FARERAL INFORMATION:
APPLICANT: Sydney Brenner

TITLE OF INVENTION:
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSED: Stephen C. Macevicz, Lynx Therapeutics, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.7%; Score 9.4; DB 1; Length 12; Best Local Similarity 90.9%; Pred. No. 46; Matches 10; Conservative 0; Mismatches 1; Indels
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ZIP: 94545
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word, vers. 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/916,120A
FILING DATE: 22-AUG-97
CLASSIFTATION NATA:
APPLICATION NUMBER: 08/611,155
FILING DATE: 05-YAR-96
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (510) 670-9365
TELEREAX: (510) 670-9365
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/611,155B
FILING DATE: 05-MAR-96
CLASSIFICATION 1435
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/560,313
APPLICATION NUMBER: 08/560,313
FILING DATE: 17-NOV-95
ATTORNEY AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 31,285
FILEDRAMICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-08-611-155B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-916-120A-15
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                                                                                                                                                                                                                                                                                  Patent No. 57/8713.

APPLICANT: Sydney Brenner
TITLE OF INVENTION: Simultaneous Sequencing of Tagged Polymucleotides
NUMBER OF SEQUENCES: 9
CORRESSEN: Stephen C. Abcevicz, Lynx Therapeutics, Inc.
STREET: 3332 Bay Center Place
CITY: Hayward C.
CITY: Hayward C.
CITY: Hayward C.
CITY: Hayward C.
CITY: Stephen C.
STREET: Sast Bay Center Place
CITY: Hayward C.
COMPUTER: California
COMPUTER READMALE FORM:
MEDIUM TYPE: J. Sinch diskette
COMPUTER: Power Machintosh
OPERATING SYSTEM: Machintosh
OPERATING SYSTEM: Machintosh
OPERATING SYSTEM: Walnincosh
OPERATING STEMER: Solus
FILING DATE: NOWER: Solus
FILECOMMUNICATION NUMBER: Setlus
FILECOMMUNICATION NUMBER: Setlus
FILECOMMUNICATION NUMBER: Solus
FELECOMMUNICATION NUMBER: Solus
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US-08-611-155B-13/C

Sequent No. 5/80231

Sequent No. 5/80231

GENERAL INFORMATION:

APPLICANT: Sydney Brenner

TITLE OF INVENTION: DNA Extension and Analysis with Rolling Primers

NUMBER OF SEQUENCES: 13

CORESSPONDENCE ADDRESS:

ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
STREET: 3832 Bay Center Place

CITY: Hayward

STATE: California

COUNTRY: USA

COMPUTER: 3.5 inch diskette

COMPUTER: IBM compatible

COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 12;
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                                                                                                                               RESULT 47
US-08-560-313A-9/c
; Sequence 9, Application US/08560313A
; Partent No. 5763175
2 AGGTGAAAAAGAA 14
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TOPOLOGY:
US-08-560-313A-9
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TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Microtron Internation: nisms and Method of Assaying Contaminant
FILE REFERENCE: 9982-7
CURRENT APPLICATION NUMBER: US/09/281,418
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: UP/1998/87651
EARLIER APPLICATION NUMBER: UP/1999/69694
EARLIER APPLICATION NUMBER: 1999-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lerd; Neumann, Gabriele; Menke, Annette
An Attenuated Vaccination and Gene-Transfer Virus, a
Method
to Make the Virus and a Pharmaceutical Composition Comprising t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Pred. No. 46;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 9.4; DB 1; Length 12;
Pred. No. 46;
0; Mismatches 1; Indels
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US-09-513-783A-73
Sequence 73, Application US/09513783A
Sequence 73, Application US/09513783A
Sequence 73, Galliano Galliano, Renneth A.
GENERAL INFORMATION:
APPLICANT: Galliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Screening
TITLE OF INVENTION: A System for Cell Based Screening;
FILE REFERENCE: 97-022-11
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 180
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US-08-809-513A-9/c
US-08-809-513A-9/c
; Sequence 9, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
    TITLE OF INVENTION: An Attenuated Vaccinat:
    TITLE OF INVENTION: Method
    TITLE OF INVENTION: to Make the Virus and invention of the Companies of SEQUENCES:
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: NORRIS MCLAUGHLIN & MARCUS
    STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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90.9%;
                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.9
Matches 10, Conservative
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Best Local Similarity 90.9
Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Primer US-09-281-418-162
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STREET: 600
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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; Patent No. 6287769
; GENERAL INFORMATION: ApPLICATE TRACK TRACK
; APPLICATE INOUE, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA
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                                           Score 9.4; DB 1; Length 12;
Pred. No. 46;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/228,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION TO THE TELLING DATE:
APPLICATION NUMBER: US 07/749,385
FILING DATE: 22-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 5490A-
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-326-2400
TELEFAX: 415-326-2400
TELEFAX: 415-326-2420
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/749,385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.7%;
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                                                Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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US-09-281-418-162
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US-08-507-032-14
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPPLICANT: EHWIN, ALFRED S.
FAPPLICANT: SHAW, LYRIN G.
APPLICANT: SHAW, LYRIN G.
TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
FILE REFERENCE: 4300.014100
CURRENT APPLICATION NUMBER: 09/08/874,601
CURRENT FILING DATE: 1996.04.21
FRIOR FULING DATE: 1996.04.21
FRIOR FILING DATE: 1997-06-21
FRIOR FILING DATE: 1997-06-21
FRIOR PELING DATE: 1997-04-21
FRIOR PELING DATE: 1997-04-21
FRIOR FILING DATE: 1997-04-21
FRIOR FILING DATE: 1997-04-21
FRIOR FILING DATE: 1997-06-31
FRIOR FILING DATE: 1997-06-31
FRIOR FILING DATE: 1997-06-31
FRIOR FILING DATE: PALON NUMBER: 60/044,492
FRIOR FILING DATE: PALON NUMBER: 60/044,492
FRIOR FILING DATE: PALON STANDARD STANDA
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Pred. No. 51;
0; Mismatches 1; Indels
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Pred, No. 51;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Influenza virus, vRNA 3' sequence
INDIVIDUAL ISOLATE: pHL1104 vRNA Promoter Element
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03663
FILING DATE: 18-5EP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94115505.3
FILING DATE: 30-5EP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: Hobom 9832-KGB
REGISTRATION NUMBER: 33-141
REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
TELECOMMUNICATION INFORMATION:
TELEBATA: (914) 332-1844
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE GRARACTERISTICS:
LEMENTH: 13 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TYPE: NOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
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| LOCATION: ()...()

| THER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE

US-09-874-601-59
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90.9%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Matches 10; Conservative
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US-08-809-513A-4/C
Squence 4, Application US/08809513A
Squence 4, Application US/08809513A
Squence 4, Application US/08809513A
Satisfies 1 Mobow, Gerd, Neumann, Gabriele; Menke, Annette
APPLICANT: Hobow, An Attenuated Vaccination and Gene-Transfer Virus, a
ITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
ITLE OF INVENTION: Machod
ITLE OF INVENTION: To Make the Virus and a Pharmaceutical Composition Comprising
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRIS MCLAUGHLIN & MARCUS
STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                        ALE TOWARDER READBLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage COMPUTER: Gateway Pentium II OPERATING SYSTEM: Windows 98

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,513A
FILING DATE: 24 MAR-1997
CLASSIFICATION: 424
FILING DATE: 24 MAR-1997
FILING DATE: 18-SEP-1995
FILING DATE: 18-SEP-1995
FILING DATE: 30-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: KALE G. BEISCOE
REGISTRATION NUMBER: BP 94115505.3
FILING DATE: 33,141
REFERENCE/CACT NUMBER: 4 bbcom 9832-KGB
TELECOMMUNICATION INFORMATION:
NAME: KALE G. BEISCOE
REGISTRATION NUMBER: 33,141
REFERENCE/CORT NUMBER: 4 bbcom 9832-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
FIELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY. USA

ZIP: 10591-5144

COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Gateway Pentium II
OPERATING SYSTEM: Windows 98
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,513A
FILING DATE: 24-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Influenza virus, vRNA 3' sequence
INDIVIDUAL ISOLATE: pHL1104 vRNA Promoter Element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NATI-SENSE: NO ORIGINAL SOURCE
          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-809-513A-9
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Gaps
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Sequence 30. Application US/09508753B

Patent No. 6544736

GENERAL INFORMATION:

APPLICANT: Akira MinAMOTO

APPLICANT: Yasuhiro FURUICHI

APPLICANT: Wick SHIBATA

APPLICANT: Hiroko FUNAKI

APPLICANT: Hiroko FUNAKI

APPLICANT: MASANOTI WATAHIKI

APPLICANT: MASANOTI WATAHIKI

APPLICANT: MASANOTI WATAHIKI

CURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

NUMBER OF SEQ ID NOS: 472

LENGTH: 10
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US-09-508-753B-64/c
; Sequence 64, Application US/09508753B
; Parent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Yasua SHIMAMOTO
; APPLICANT: Yasua SHIMAMOTO
; APPLICANT: Yasua SHIMAMOTO
; APPLICANT: Yasua SHIMAMOTO
; APPLICANT: Hiroko FUNAITA
; APPLICANT: Eiji OHARA
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIXI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
APPLICANT: Eiji OHARA
APPLICANT: MATAHIKI
TITLE OF INVENTION: MACHOO for Synthesizing CDNA from mRNA sample
FILE REFERENCE: 00162/HG
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILIAD DATE: 2000-06-16
PRIOR APPLICATION NUMBER: UP 9/270324
PRIOR APPLICATION NUMBER: UP 9/270324
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 21
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-7538-30
                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-21
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9, Conservative
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US-09-508-753B-30
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                                                                                                                                                                                         APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Rail-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION 514
PRICAR APPLICATION 514
PRICAR APPLICATION DATE:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 13-ANY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
RESPERANCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.8%; Score 9.2; DE 78.6%; Pred. No. 61; Itive 0; Mismatches
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; Sequence 21, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yashliro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                              Sequence 35, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 393-5350
TELEFAX: RCA 24859 IDBA UR
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
3: DNA (genomic)
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Best Local Similarity 78.6
Matches 11; Conservative
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ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
            11 AGCAGAAACAG 1
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US-08-535-249-35
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; OTHER INFORMATION: substrate recognition sequence US-09-513-783A-75
                                                       Query Match
40.9%; Score 9; DB 1;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches
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; Sequence 6, Application US/09332319
; Patent No. 6171821
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; Sequence 5, Application US/09332319
; Patent No. 6171821
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100.0%;
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 100.
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CORGANISM: Homo sapiens
US-09-332-319-5
                                                                                                                                                                    3 AGAAACAGA 11
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                                                                                                                                                                                                                            RESULT 62
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OTHER INFORMATION: Description of Artificial Sequence: proCaspase-3
TOTHER INFORMATION: substrate recognition sequence
US-09-513-783A-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: proCaspase-8
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US-99-513-783A-75
; Sequence 75, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.; APPLICANT: Giuliano, Kenneth A.; TITLE OF INVENTION: A System for Cell Based Screening; FILE REPRENCE: 97-022-11; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT APPLICATION PROFE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SEQ ID NO 75
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                 Length 10;
                                                                                                                                                                                                                                                               Query Match 40.9%; Score 9; DB 1;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches
                          CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 64
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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             FILE REFERENCE: 00162/HG
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LENGTH: 12
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Matches
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539527-3
; Patent No. 5395927
; APELICANT: BOCK, AUGUST; BINDER, FLORIAN; MULLER, FRANK
APPLICANT: BOCK, AUGUST; BINDER, FLORIAN; MULLER, FRANK
; TILLE OF INVENTION: DNA-FRAGMENT HAVING THE CYCLODEXTRIN
; GLYCOSYLTRANFERASE GENE
; WUMBER OF SEQUENCES: 4
; CURRENY APPLICATION DATA:
; APPLICATION NUMBER: US/07/450,126
; FILING DATE: 27-NOV-1989
; FILING DATE: 24-OCT-1986
; FILING DATE: 24-OCT-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 8.8; DB 1; Length 12;
Pred. No. 59;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                     0; Indels
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Length 12;
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APPLICANT: Holcik, Martin
APPLICANT: Liston, Peter
TITLE OF INVENTION: XIAP IRES AND USES THEREOF
FILE REFERENCE: 07891/01002
CURRENT APPLICATION NUMBER: US/09/332,319
CURRENT PILING DATE: 1999-06-14
EARLIER FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 9; DB 1;
Pred. No. 60;
0; Mismatches
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IMMOBILIZED OLIGONUCLEOTIDE
                            FILE REFERENCE: 03804.0138-01
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: 08/860,038
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/FR95/01468
PRIOR APPLICATION NUMBER: PCT/FR95/01468
PRIOR APPLICATION NUMBER: PCT/FR95/01468
SOFTWARE: PALENT NOS: 36
SOFTWARE: PALENT NOS: 36
SOFTWARE: PALENT NOS: 36
                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 857-7887
TELEFAX: (202) 857-7929
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            731 AGGAGAACAGA 742
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STRANDEDNESS: single
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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
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              TITLE OF INVENTION:
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Cameron, Beatrice
Blanche, Francis
VVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: variation

LOCATION: (1)...(1)

OTHER INFORMATION: Wild-type polypyrimidine tract.
US-09-332-319-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-33-119-10/C
Sequence 10, Application US/09332319
Sequence 10, Application US/09332319
PREMENT NO. 6171821
APPLICANT: MOTORY MATTION:
APPLICANT: Holoth, Martin
APPLICANT: Liston, Peter
TITLE OF INVENTION: XIAP IRES AND USES THEREOF
FILE REFREENCE: 07891/021002
CURRENT APPLICATION NUMBER: US/09/332,319
CURRENT FILING DATE: 1999-06-14
BARLIER FILING DATE: 1999-06-14
BARLIER FILING DATE: 1999-07-24
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 10
SEQ ID NO 10
SEQ ID NO 10
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Holcik, Martin
APPLICANT: Liston, Peter
TITLE COF INVENTION: XIAP IRES AND USES THEREOF;
FILE REFERENCE: 07891/021002
CURRENT APPLICATION NUMBER: 05/9/332,319
CURRENT FILING DATE: 1999-06-14
EARLIER FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 12
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108-09-580-923-28/c
'Sequence 28, Application US/09580923
'Parent No. 6319672
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Scherman, Daniel
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                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CNGANISM: Homo sapiens
US-09-332-319-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Crouset,
APPLICANT: Scherman,
APPLICANT: Wils, Pie
APPLICANT: Cameron,
APPLICANT: Blanche,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca.
Matches
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RESULT 67
US-08-465-293A-8/C
i Sequence 8. Application US/08465293A
i Patent No. 5789651
j Patent No. 5789651
j Patent No. 5789651
j Patent No. 5789651
j TILE OF INVENTION:
i TITLE OF INVENTION:
i TORRESPONDENCES:
i ADDRESSEE:
ADDRESSEE: Morgan & Finnegan
STREE: 555 13th Street, N.W., Suite #480 West
CITY: Washington
I STATE: District of Columbia
I STATE: STATE: DISTRICT ON THE STATE
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0
                                                                                                                                                                                                                                 Query Match 40.0%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 59; Matches 10; Conservative 0; Mismatches 2; Indels
) OTHER INFORMATION: Description of Artificial Sequence: , OTHER INFORMATION: oligonucleotide US-09-580-923-28
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ioD: Experimental In addition to hair color in mice, the addition to hair color in mice, the Agouti gene is responsible for embryonic lethality, obesity, and the development of tumor in a wide variety of tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                      transition point of exon 1 from exon 2 in Agouti locus of mouse chromosome 2.
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Patent No. 6080550

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF AGOUTI
TITLE OF INVENTION: A DIABETES/OBESITY RELATED GENE
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 13;
                                                                                                                                                                                                                                                                                                                                                                Score 8.8; DB 1; Length 13;
Pred. No. 65;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: C-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,977
FILING DATE: 2-JUN-1998
CLASSIFICATION ATA:
APPLICATION NUMBER: US 08/899,134
FILING DATE: 23-JUL-1997
PRIOR APPLICATION DATE: US-0462,732
APPLICATION NUMBER: US 08/462,732
APPLICATION NUMBER: US 08/462,732
ATONEX/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 31,014--1
TELEPHONE: (112)418-3000
TELEPHONE: (112)418-3000
TELEPHONE: (12)414-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.0%; Score 8.8; Disect Local Similarity 83.3%; Pred. No. 65; Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                           40.0%;
                                                                                               FEATURE:

NAME/KEY: Agout locus

DENUIFICATION METHOD: E>

OTHER INFORMATION: In add

THER INFORMATION: Agout;

OTHER INFORMATION: and the US-08-463-387A-8
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Arnold, Wh:
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 AGAAGCAGCACA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AGAAGCAGCACA 2
                             CHROMOSOME/SEGMENT:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-09-102-977-9
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 69
US-09-102-977-9/c
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                                                                                                                                                                                                                                                                 NAME/KEY: Agouti locus
DENTIFICATION METHOD: Experimental
OTHER INFORMATION: In addition to hair color in mice, the
OTHER INFORMATION: Agouti gene is responsible for embryonic lethality, obesity,
OTHER INFORMATION: and the development of tumor in a wide variety of tissues.
US-08-465-293A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                 TISSUE TYPE: Adult kidney and testis
IMMEDIATE SOURCE:
CLONE: Wild-type CDNA clones
POSTION IN GLA-type CDNA:
CHROMOSOME/SEGMENT: transition point of exon 1 from exon 2 in
CHROMOSOME/SEGMENT: Agouti locus of mouse chromosome 2.
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US-08-463-387A-8/C
US-08-463-387A-8/C
Sequence 8, Application US/08463387A
Patent No. 843662
GENERAL INFORMATION:
APPLICANT: Woychik, Richard P.
TITLE OF INVENTION: Isolation and Characterization of
TITLE OF INVENTION: Agouti A Diabetes/Obesity Related Gene.
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 555 13th Street, N.W., Suite #480 West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20015 CONTROLLE OF COLUMNIA STATES AND STATES AND STATES OF S
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MULCULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: SOURCE:
CRAMISM: Wild
TISSUE TYPE: Adult kidney and trasue Type: CLONE: Wild-type CDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
STATE: District of Columbia
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 AGAAACAGAACA 745
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STRANDEDNESS: single
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       Wild
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ZIP: 75201-6776
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                            13 AGAAGCAGCACA 2
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CITY: Dallas
STATE: Texas
COUNTRY: USA
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US-09-781-811-23/c
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US-08-808-474A-2
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; Sequence 23, Application US/0903408BA
; Patent No. 6310034
; GENERAL INFORMATION;
; APPLICANT: WOYCHIK, RICHARD P.
; APPLICANT: WOYCHIKAN, SCOTT J.
; APPLICANT: MICHAUD, EDWARD D.
; TITLE OF INVENTION: METHODS AND POLYPEPTIDES ENCODED BY AGOUTI GENE
; FILE REFERENCE: 4310-001600
; CURRENT APPLICATION NUMBER: 1998-03-03
; PRIOR APPLICATION NUMBER: 08/09/034,088A
; CURRENT FILING DATE: 1998-03-03
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
NGS-09-102-977-14/c

Sequence 14, Application US/09102977

Sequence 14, Application US/09102977

Father No. 6080550:

APPLICANT: MOYCHIK, Richard P.

TITLE OF INVENTION: A DIABETES/OBESITY RELATED GENE
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred, No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,977
FILING DATE: 22-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/899,134
FILING DATE: 23-JUL-1997
PRIOR APPLICATION NUMBER: US 08/462,732
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,732
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITCHEL, 05-JUN-1995
REFERENCE/DOCKET NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ORNL:014-1
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENT NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ORNL:014-1
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (512)418-3000
TELEFAX: (512)44-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         734 AGAAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 AGAAGCAGCACA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Sequence 23, Application US/09781811
Fatent No. 6514747
GREBEAL INFORMATION:
APPLICANT: WOYCHIK, RICHARD P.
APPLICANT: WOYCHIK, RICHARD P.
APPLICANT: BULTMAN, SCOTT J.
TITLE OF INVENTION: AGOUTH DOLYNUCLEOTIDE COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4310.001682
CURRENT APPLICATION NUMBER: 08/03/781,811
CURRENT FILING DATE: 12998-03-03
FRIOR APPLICATION NUMBER: 09/034,088
FRIOR APPLICATION NUMBER: 09/034,088
FRIOR APPLICATION NUMBER: 09/034,088
FRIOR APPLICATION NUMBER: 09/034,088
FRIOR FILING DATE: 11998-03-03
FRIOR FILING DATE: 11998-03-03
FRIOR FILING DATE: 11998-03-03
FRIOR FILING DATE: 11908-03-05-11
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; SEQ ID NO 23
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: OLIGONUCLEOTIDE
US-09-034-088A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC OTHER INFORMATION: OLIGONUCLEOTIDE
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Patent No. 5856103
GENERAL INFORMATION:
APPLICANT: Gray, Donald M.
APPLICANT: Clark, Chris L.
TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES TITLE OF INVENTION: FOR ANTISENSE TARGETING NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Locke Purnell Rain Harrell
                                                                                                                                                                                                                                                                                                                                                       Query Match
40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 10; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Locke Purnell Rain Harrell
2200 Ross Avenue, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             734 AGAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                734 AGAAACAGAACA 745
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Gaps

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                                                                                                  DB 1; Length 10;
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                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Nicholas J Deacon
APPLICANT: Nicholas J Deacon
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STRATE: 400 GANDEN CITY PLAZA
CITY: GARDEN CITY
COMPUTER: ISO-0299
COMPUTER: IBM PC Compatible
COMPUTER: DAPE: TOPPY disk
COMPUTER: DAPE: TOPPY disk
COMPUTER: PRADABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: PROPER: PC-009/MS-DOS
SOFTWARE: PRADABLE FORM:
MEDIUM TYPE: PROPER: DC-009/MS-DOS
SOFTWARE: PRADABLE FORM:
MEDIUM TYPE: PROPER: DS-009/MS-DOS
SOFTWARE: PRADABLE FORM:
MEDIUM TYPE: PROPER: DS-009/MS-DOS
SOFTWARE: PRADABLE FORM:
MEDIUM TYPE: PROPER: DS-009/MS-DOS
SOFTWARE: PRADABLE FORM:
MEDIUM TYPE: DS-009/MS-DOS
SOFTWARE: PRADABLE FORM:
PILING DATE: US-009/MS-DOS
APPLICATION NUMBER: PM402 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: PN301/95
ATTORIEY/AGENT INPORMATION:
TELEFRAK: SD-001 TOPORMATION:
TELEFRAK: SD-001 
                                                                                              Query Match
38.2%; Score 8.4; DB
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.2%; Score 8.4; DB 90.0%; Pred. No. 54; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-488-551B-478
; Sequence 478, Application US/08488551B
; Patent No. 6015661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                           738 ACAGAACACC 747
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            738 ACAGAACACC 747
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                   US-08-388-353-478
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US-09-508-753B-19
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Pred. No. 54;
0; Mismatches 1; Indels
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Sequence 478, Application US/0838353

Patent No. 6010895

PAPLICANT: Deacon Nicholas J.

APPLICANT: Learmont, Jennifer C.

APPLICANT: Cooper, David

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 800

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City Plaza

STREET: 400 Garden City Plaza

COUNTRY: United States

ZIP: 11530

COMPUTER: EADABLE FORM:

MEDIUM TYPE: Floppy disk

COUNTRY: United States

ZIP: 11530

COMPUTER: IDM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Facture Release #1.0, Version #1.25

CURRENT APPLICATION DATA: 9606

FILING DATE: 14-FEB-1995

CLASSIFICATION HUMBER: 31,346

REGISTRAINON NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 31,346

TELEFAX: (316) 742-433

TELEFAX: (316) 742-433

TELEFAX: (316) 742-436

TELEFAX: (316) 74
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
COTRACTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,474A
FILING DATE: 03-MR-1997
ATTORNEY FAGENT INFORMATION:
NAME: Mayfield Denise L.
REGISTRATION NUMBER: UTDAL:001
FELEPAN: (214) 740-8000
TELEPAN: (214) DAO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
STRANDEDISS: single
STRANDEDISS: single
STRANDEDISS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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GENERAL INFORMATION:
APPLICANT: SRIVASTATA, SHIV
APPLICANT: MOUL, JUDD W.
APPLICANT: XU, LINDA L.
APPLICANT: SEGAMA, TAKEHIKO
TITLE OF INVENTION: PROTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: PROTATE-SPECIFIC ANDROGEN-SIGNALING-CURENT FILLS REFRENCE: 04995.0657-00000
CURRENT APPLICATION NUMBER: US/09/769,482
CURRENT FILLING DATE: 2001-01-26
                                            APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
FROM CONTROL OF SEQ ID NOS: 472
FROM CONTROL OF SEQ ID NOS: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.2%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 54; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION WUNBER: 60/178,772
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTLY OF. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-769-482-47/c
; Sequence 47, Application US/09769482
; Patent No. 6566130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
               Yasuhiro FURUICHI
Yuko SHIBATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          731 AGGAGAAACA 740
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 10
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APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: MASANOTI MATAHIKI
TILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 41
LENGTH: 10
               Patent No. 6544736

GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Akira SHIMAMOTO
APPLICANT: Akira SHIMAMOTO
APPLICANT: VAKO SHIBATA
APPLICANT: HINCKO FUNAKI
APPLICANT: HIJ OHARA
APPLICANT: HIJ OHARA
APPLICANT: Bij OHARBE: US/09/508,753B
CUTRENT APPLICATION NUMBER: US/09/508,753B
CUTRENT PILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence; Primer US-09-508-753B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8.4; DB 1; Length 10;
Pred. No. 54;
0; Mismatches 1; Indels
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Sequence 19, Application US/09508753B
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Best Local Similarity 90.0%;
Matches 9; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 9; Conserv
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
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Sequence 18, Application US/09332319

Partent No. 6771821

GENERAL INFORMATION:
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US-09-508-753B-127/c , Sequence 127, Application US/09508753B . Patent No. 6544736 , GENERAL INFORMATION:

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Gaps

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                                                                                  Length 10;
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                                                                                      36.4%; Score 8; DB 1; 100.0%; Pred. No. 64;
                                                                                                                                                              0; Mismatches
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; Sequence 479, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) US-08-388-353-480
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Best Local Similarity 100.
                                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                             740 AGAACACC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    740 AGAACACC 747
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                  US-08-388-353-479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VESULE AND SECTION OF 
APPLICANT: Korneluk, Robert G.
APPLICANT: Holcik, Martin
APPLICANT: Liston, Peter
TITLE OF INVENTION: XLAP IRES AND USES THEREOF
FILE REFERENCE: 07891/021002
CURRENT APPLICATION NUMBER: US/09/332,319
CURRENT FILING DATE: 1999-06-14
BARLIER APPLICATION NUMBER: 09/121,979
EARLIER PILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: variation
LOCATION: (11)...(12)
COTATION: (11)...(12)
US-09-332-319-18
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Homo sapiens
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Gaps

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US-09-229-151C-15/C

i Sequence 15, Application US/09229151C

i Sequence 15, Application US/09229151C

i Patent No. 6537784

i Patent No. 6537784

i Patent No. 6537784

i APPLICANT: Tatake, Revati J.

APPLICANT: Marlin, Steven D.

APPLICANT: Marlin, Steven D.

APPLICANT: Marlin, Steven D.

TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy

TITLE OF INVENTION: 1999-01-12

CURRENT FILING DATE: 1999-01-12

CURRENT FILING DATE: 1998-02-7

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 2.0

SEQ ID NO 15

LENGTH: 10
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PatentIn Release #1.0, Version #1.25
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100.0%; Pred. No. 64;
tive 0; Mismatches
                                                                                                         APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM028 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAX-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGILO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
                                      APPLICATION NUMBER: US/08/488,5518
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: KappaB3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 480:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.4
Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10;
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Sequence 480, Application US/08488551B

Patent No. 6015661

GENERAL INFORMATION:

APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: GARDEN CITY

CITY: GARDEN CITY

CITY: GARDEN CITY
                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FLING APPLICATION DATA:
APPLICATION NUMBER: PM364 (AU)
FLING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FLING DATE: 21-FEB-1994
APPLICATION NUMBER: PM30284 (AU)
FLING DATE: 22-DEC-1994
APPLICATION NUMBER: US 08/388,353
FLING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
APPLICATION NUMBER: PM3021/95
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1 NUMBER OF SEQUENCES: 841 CORRESPONDENCE ADDRESS: ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
           STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STABLE: NEW YOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.4%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-MAY-1995
ATTONEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4346
INFORMATION FOR ENQ ID NO: 479:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          740 AGAACACC 747
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                                                                                                                                        NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-488-551B-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-488-551B-480
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FEATURE:
NAME/KEY: A
LOCATION: 7
OTHER INFORMATION: /label= variable
OTHER INFORMATION: /note= an intervening sequence Nx of any length
OTHER INFORMATION: may be inserted between nucleotides 7 and 8
US-08-231-227-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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US-08-173-489C-10/C

Sequence 10, Application US/08173489C

Sequence 10, Application US/08173489C

Sequence 10, Application US/08173489C

Sequence 10. Sef61244

TITLE NOTE NEWRATION:
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.

CORRESPONDENCES: 365

ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,

STREET: 510 BAST 73RD STREET,

COTRIES PROFILE DIAGNOSTIC SCIENCES, INC.,

STREET: 10021.

COMPUTER: NEW YORK

COMPUTER: NEW YORK

COMPUTER: STREET AND STREET,

COMPUTER: STREET AND STREET,

COMPUTER: STREET AND STREET,

COMPUTER: STREET AND STREET

APPLICATION NUMBER: US/08/173,489C

FILING DATE: 22 DEC 1993

CLASSIFICATION NUMBER: US 07/968,436

FILING DATE: 29 OCT 1992

ATTORNEY/GENT INFORMATION:

MAME: Handelman, JOSEPH H.

REGISTRATION NUMBER: US-0179

RESERVENCE/DOCKET NUMBER: US-0179

RESECOMMUNICATION INFORMATION:

REGISTRATION NUMBER: US-0179

RESECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.4%; Score 8; DB 1; Length 12; 88.9%; Pred. No. 80; tive 0; Mismatches 1; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,227
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth M.
REFERENCE/DOCKET NUMBER: 0973.001
TELEPHONE: G100 655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
FTYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           731 AGGAGAAAC 739
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; Sequence 5, Application US/08231227
; Patent No. 5631148
; GENERAL INFORMATION:
    TITLE OF INVENTION: RIBOZYMES WITH PRODUCT EJECTION BY TITLE OF INVENTION: STRAND DISPLACEMENT
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Chiron Corporation
    STREET: 4560 Horton Street
    CITY: Emeryville
    STATE: California
    COUNTRY: U.S.A.
    ZIP: 94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                                       Sequence 12, Application US/08671824

Patent No. 6025167

GENERAL INFORMATION:
APPLICANT: Cach, Thomas R.
APPLICANT: Cach, Thomas R.
APPLICANT: Been, Michael D.
ITILE OF INVENTION:
TITLE OF INVENTION: BERHOSPHORYLASES, RESTRICTION
TITLE OF INVENTION: BUDGE SOURCEASES AND METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
TITLE OF INVENTION: BUDGE SOURCEASES AND METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
CONTRY: US.A.
ZIP: 90071-2066
COUNTRY: US.A.
ZIP: 90071-2066
CONTRY: US.A.
ZIP: 90071-2066
CONTRY: US.A.
ZIP: Word Perfect 5.1
CONTRY: US.A.
ZIP: Word Perfect 5.1
CONTRY: US.A.
SOFTWARE: Word Perfect 5.1
CONTRY: US.A.
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION NUMBER: US/08/671,824
FILING DATE: June 5, 1996
CLASSIFICATION NUMBER: 220/166
TELECOMMUNICATION NUMBER: 220/160
TELECOMMUNICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.4%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches
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US-08-671-824-12
                                     US-08-671-824-12/c
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8; Conservative
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JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                              STATE:
  Matches
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/note= an intervening sequence Nx of any length
may be inserted between nucleotides 7 and 8
                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                            Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 5, Application PC/TUS9504632
GENERAL INFORMATION:
APPLICANT: CHIRON CORPORATION
TITLE OF INVENTION: RIBOZYMES WITH PRODUCT EJECTION BY
TITLE OF INVENTION: STRAND DISPLACEMENT
NUMBER OF SEQUENCES:
ADDRESSEE: Chiron Corporation
                                                                                                                                                   MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from c-myc
DESCRIPTION: sequence region in Seq ID No. 58612449
HYPOTHETICAL: Yes
                                                                                                                                                                                                                               ANTI-SENSE: NO
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 10 :FROM 1 TO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLOATION NUMBER: PCT/US95/04632
FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                          Query Match 36.4%; Score 8; DB 1; Best Local Similarity 100.0%; Pred. No. 80; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Goldman, Kenneth M.
REFERNEC/DOCKET NUMBER: 0973.100
TELEPHONE: (510) 601-2719
TELEPHONE: (510) 662-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
  (attorney) (212) 708-1880 (ttorney) (212) 246-8959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    JOURNAL
TYPE: Nucleic Acid
STRANDEDNESS: single stranded
STRANDEDNESS: lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.4%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4560 Horton Street
                      TELEFAX: (attorney) (2:
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 7
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AGGAGAAA 1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: A
                                                                                                                                                                                                                                                                                          US-08-173-489C-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-04632-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-04632-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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Gaps
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                                                                                                                                                                                            US-08-173-489C-89
Sequence 89, Application US/08173489C
Sequence 89, Application US/08173489C
Sequence 89, Application US/08173489C
SEREMAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECTLE TYPE: genomic DNA
DESCRIPTION: superoxide dismutase gene (accession #
DESCRIPTION: J02947) nucleotides 21 to 31
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 : FROM 1 TO 11
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superoxide dismutase
Proceedings of the National Academy
Sciences, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER TYPE: 3.5 inch, 1.44Mb storage COMPUTER: 1BM PC/XI/AT OPERATING SYSTEM: MS-DOS version 6.2 SOFTWARE: WORDERED SOFTWARE: WORDERED 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/173,489C FILING DATE: 22 DEC 1993 CLASSIFICATION A35 PRIOR APPLICATION A35 PRIOR APPLICATION DATA: APPLICATION A185 APPLICATION DATA: APPLICATION NUMBER: US 07/968,436 FILING DATE: 29 OCT 1992 ATTORNEY/AGENT INFORMATION:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REGISTRATION NUMBER: 09518-6
TELECOMMUNICATION INFORMATION:
TELEPRAN: (attorney) (212) 708-1880
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 21
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US-08-173-489C-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROWGSOME/SEGMENT: chro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                   731 AGGAGAAAC 739
                                                                                                4 ANGAGAAAC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEW YORK
: NEW YORK
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6340-6344
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schultz1-727

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Gaps ; 0

Score 7.8; DB 1; Length 11; Pred. No. 78; 0; Mismatches 2; Indels

35.5%;

Query Match 35.5 Best Local Similarity 81.8 Matches 9; Conservative

731 AGGAGAAACAG 741

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1 AGGAGAGAAAG 11

RESULT 91
US-08-681-916-14/C
US-08-681-914
Sequence 14, Application US/08687916
Patent No. 5908972
GENERAL INFORMATION:

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Won Oct 18 14:40:09 2004
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

SUBUNIT N. METHYLFRANSFERASE AND METHOD OF INACTIVATING

TITLE OF INVENTION:

TITLE OF INVENTION:

SUBUNIT N. METHYLFRANSFERASE AND METHOD OF INACTIVATING

TITLE OF INVENTION:

NUMBER OF SUGURIES:

ADDRESSEE:

ADDRES MOLECULE TYPE: DNA (genomic) TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: US-08-687-916-14

35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 78; tive 0; Mismatches 2; Indels Query Match
Best Local Similarity 81.6

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GENE EXPRESSION SYSTEM COMPRISING THE PROMOTER REGION OF THE ALPHA-AMYLASE GENES ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive/6300 Sears Tower CITY: Chicago CONTRY: United States
ZIP: 60606
COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/072,435
FILING DATE: US 09/072,435
FILING DATE: US 08/639,792
FILING DATE: US 08/639,792
FILING DATE: US 07/973,324
APPLICATION NUMBER: US 07/973,324
FILING DATE: US 07/973,324
FILING D CITY: Chicago STATE: Illinois COUNTRY: United States of America TITLE OF INVENTION: GEN TITLE OF INVENTION: PRO NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS: MOLECULE TYPE: CDNA US-09-072-435-8

. 0 35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 78; cive 0; Mismatches 2; Indels Query Match Best Local Similarity #1.8 Matches 9; Conservative

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734 AGAAACAGAAC 744 11 AGAAACGCAAC 1 à

Sequence 14, Application US/09138614

Sequence 14, Application US/09138614

Patent No. 6245541

GENERAL INFORMATION:
TITLE OF INVENTION: SOLATED SPINACH

TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING

TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING

TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 2213-1404 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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Parent No. 6288302
GENERAL INFORMATION:
PAPLICANT: Yu. Su.May
APPLICANT: Liu, Li-Fei
APPLICANT: Liu, Liu, Li-Fei
APPLICANT: Liu, Liu-Fei
APPLICANT: Liu,
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                                                                                                                                                     DB 1; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                               Indels
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                                                                                                                                 uery Match
35.5%; Score 7.8; DE
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIPRICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-A04-1995
ATTORNEY AGENT INFORMATION:
NAME: Gass, David A.
REGISTATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28123/34257
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; Sequence 10, Application US/09072917A
; Patent No. 6288302
                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (312) 474-043
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: single
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Best Local Similarity
Matches 9; Conserva
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STREET: 200
TTV: Chicago
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STRANDEDNESS
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                                                                       ; MCLECULE 11:
US-08-083-945C-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08083945C
Patent No. 6274134
GENERAL INFORMATION:
APPLICANT: Liotta, Lance A.
APPLICANT: Liotta, Lance A.
APPLICANT: Liotta, Lance A.
TITLE OF INVENTION: AAMP-1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,945C
FILING DATE: 25-UN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,043
FILING DATE: 29-UN-1992
ATTORNEY/AGENT INFORMATION:
SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,614
                                                                                     FILING DATE:
PRIOR PAPLICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/687,916
FILING DATE:
ATTONENY FAGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 028750-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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REGISTATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-156-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEG ID NO: 8:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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US-08-083-945C-8
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Gaps

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ratent No. 5837832
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chee, Mark
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Loban, Peter E.
APPLICANT: Sheldon, Peter E.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew LIP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                     DB 1; Length 11;
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CID: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-MAY-1995
ATING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT 1993
ATING DATE: 26-OCT 1993
ATING DATE: 25-JUN-1993
ATING DATE: 25-JUN-1
                                                                                                                                                 Query Match 35.5%; Score 7.8; DE
Best Local Similarity 81.8%; Pred. No. 78;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-441-887A-271/c
; Sequence 271, Application US/08441887A
; Patent No. 5837832
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INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-07107A-8
                                                                                                                                                                                                                                                                                                   731 AGGAGAAACAG 741
                                                                                                                                                                                                                                                                                                                                                                        1 AGGAGGAAGAG 11
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US-09-249-155A-73/C

Sequence 73, Application US/09249155A
Fatent No. 6538173
SENERAL INFORMATION:
FATEL NO. FUNCEMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: Healing
FILE REFERENCE: 00486,78503
CURRENT APPLICATION UNMER: 1999-02-12
FRIOR APPLICATION NUMBER: US 60/074,737
FRIOR APPLICATION NUMBER: US 60/097,937
FRIOR APPLICATION NUMBER: US 60/097,937
FRIOR APPLICATION NUMBER: US 60/097,937
FRIOR FILING DATE: 1998-02-13
FRIOR FILING DATE: 1998-02-13
FRIOR FILING DATE: 1998-09-8
SECTIOR APPLICATION NUMBER: US 60/102,051
FRIOR FILING DATE: 1998-09-8
SOFTWARE: FastSEQ for Windows Version 4.0
SECTIOR OF THE NOTE THE NUMBER OF SEQ ID NOS: 346
SECTIOR APPLICATION NUMBER: US 60/102,051
FRIOR FILING DATE: 1998-09-8
SECTIOR APPLICATION NUMBER: US 60/102,051
FRIOR FILING DATE: 1998-09-8
SOFTWARE: LEASTED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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PCT-US94-07107A-8
; Sequence 8. Application PC/TUS9407107A
; Sequence 8. Application PC/TUS9407107A
; SENDEAL INFORMATION:
    APPLICANT: The Government of the United States of APPLICANT: America, as represented by the Secretary, APPLICANT: Department of Health and Human Services TITLE OF INVENTION: AAMP-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
; TITLE OF LAIL OF ALLO
STREET: JO ALLO
; STATE: Callifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Fish PC Compatible

OPERATING SYSTEM: PC-DCS/MS-DCS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PC-JUN-1993

CLASSIPICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,043

FILING DATE: 25-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Karen B.

REGISTRATION NUMBER: 15280-156-1

TELEPHONE: (415) 326-2400

TELEPHONE: (415) 326-2400

TELEPHONE: (415) 326-2422

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7.8; DE
Pred. No. 78;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732 GGAGAACAGA 742
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; ORGANISM: Mus musculus
US-09-249-155A-73
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Gaps

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MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s rRNA gene from Escherichia coli
DESCRIPTION: (Accession # M25458) nucleotides 212 to 223
HYPOTHETICAL: no
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Edwards, K, Koessel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         returner of contacts only MRE 600 23S ribosomal RNA Comparison with models of secondary structure for maize chloroplast 23S RNA and for large portions of mouse and human 16S mitochondrial rRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 :FROM 1 TO 12
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                          SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08 0,173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
OPERATING SYSTEM: MS-DOS version 6.2 SOFTWARE: Wordperfect Version 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krol, A,
Ebel, J P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES IN SEQ ID NO: US-08-173-489C-215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS; double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primary and secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: no ANTI-SENSE: no ORIGINAL SOURCE: ORGANISM: Escherichia cc STRAIN: NESCOO PUBLICATION INFORMATION: AUTHORS: Pouyet, J, ER AUTHORS: Pouyet, J, ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 81.8
Matches 9; Conservative
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US-08-173-489C-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL:
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                                                                                                                                                                                                                                        Sequence 3, Application US/08494301A

| Batent No. 5856461
| Patent No. 5856461
| ProtzAnT: Protzky, Eduardo
| TITLE OF INVENTION: Oligonucleotides to Inhibit the
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| CORRESPONDENCES: 36
| CORRESPONDENCE ADDRESSE: Actas & Just
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
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| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
| TITLE OF INVENTION: Bxpression of Isoprenyl Protein Transferases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET: 510 EAST 73RD STREET, CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XI/AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: 184 MB compatible
COMPUTER: 187 WAS COMPATIBLE
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
FILING DATE: 23.01WB-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB 9413035.8
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity Bl..
Best Local 9; Conservative
   732 GGAGAAACAGA 742
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APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AGGAGTAGCAG 12
                                                                       12 GGGGAAGCAGA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: line;
ANTI-SENSE: Yes
US-08-494-301A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-173-489C-215
                                                                                                                                                                                RESULT 99
US-08-494-301A-3
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Length 12;
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ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Home sapiens
PUBLICATION INFORMATION:
AUTHORS: Harlow, E, williamson, N M, Ralston, R, AUTHORS: Harlow, D M, Adams T E.
TITLE: Molecular cloning and in
TITLE: vitro expression of a cDNA for human cellular TITLE: thunor antigen p53
JOURNAL: Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) DATE: 1985
; RELEVANT RESIDUES IN SEQ ID NO: 351 :FROM 1 TO 12
US-08-173-489C-351
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM FC/XI/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordberfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 29 OCT 1992
ATTORNEY AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: US-179
REFERENCE/DOCKET NUMBER: US-180
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 351:
SEQUENCE CHRAPATERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
UNDOWENTER: US
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Pred. No. 87;
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US-08-779-355-19
; Sequence 19, Application US/08779355
; Patent No. 6017701
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.5%;
81.8%;
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Best Local Similarity 81.8
...hes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: 233 FRNA gene from Halococcus morrhuae
DESCRIPTION: (Accession # X05481) nucleotides 1628 to 1639
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE: Evolutionary Relationship
TITLE: Amongst Archaebacteria: A Comparative Study of
TITLE: 23 Ribosomal RNAs of a Sulphur-dependent
TITLE: Extreme Thermophile, an Extreme Halophile and a
TITLE: Thermophilic Methanogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 351, Application US/08173489C
| Patent No. 5861244
| GENERAL INFORMATION:
| APPLICANT: HEPBURN, C. -G. |
| APPLICANT: HEPBURN, A. G. |
| TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA |
| TITLE OF INVENTION: TELPLE-STRAND FORMATION. |
| NUMBER OF SEQUENCES: 365 |
| CORRESPONDENCE ADDRESS: 365 |
| ADDRESSEE: FROFTLE DIAGNOSTIC SCIENCES, INC., STREET: 510 EAST 73RD STREET, CITY: NEW YORK STATE: NEW YORK STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) DATE: 1987 -- ; BALEVANT RESIDUES IN SEQ ID NO: 229 :FROM 1 TO 12 US-08-173-489C-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kjems, J, Ostergaard, L, Garrett, R A.
CCMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM FC/XT/AT
CORREATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436
FILING DATE: 29 DCT 1992
FILING DATE: 29 OCT 1993
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISCHARTION NUMBER: US/199
REFERENCE/DOCKET NUMBER: US/199
REFERENCE/DOCKET NUMBER: US/199
REFERENCE/DOCKET NUMBER: US/199
REFERENCE/DOCKET NUMBER: US/199
REFERENCE/COCKET NUMBER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Halococcus morrhuae
PUBLICATION INFORMATION:
WITHOURS: Leffers, H, Kjems, J
AUTHORS: Larsen, N, Garrett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             733 GAGAAACAGAA 743
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US-08-173-489C-351
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GENERAL INFORMATION:
APPLICANT: Sorge, Joseph A.
APPLICANT: MILLIAAX, REDECAL L.
APPLICANT: MILLIAAX, REDECAL L.
TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING
TITLE OF INVENTION: SPECIFIC NUCLEIC ACID POPULATIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA E: Evenson, McKeown, Edwards & Lenahan P.L.L.C. 1200 G Street N.W., Suite 700

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Gaps ; ;

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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 87; cive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98-962-431-24
9 Sequence 24, Application US/08862431
9 Patent No. 6120994
9 Patent No. 6120994
9 PATENT NO. 6120994
1 TITLE OF INVENTION: ANTIOXIDANT RESPONSIVE ELEMENT
1 NUMBER OF SEQUENCES: 51
1 CORRESPONDENCE ADDRESS: 51
1 CORRESPONDENCE ADDRESS: 51
2 ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
5 TREET: 1100 New YORK AVENUE, SUITE 600
1 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: DC
COUNTRY: US
ZIP: 20005-3334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEMIN FOLDOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,431
FILING DATE: 23-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                           Pred. No. 87;
0; Mismatches
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US-09-043-149-33/c
; Sequence 33, Application US/09043149
; Patent No. 6355418
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Gunter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Kim, Judith U.
RECISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 166
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                  TOPOLOGY: linear // MOLECULE TYPE: DNA (genomic) US-08-938-835A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
   202-408-4400
                                                                                              : 12 base pairs
nucleic acid
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                727 TGCCAGGAGAA 737
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                        TYPE: nucleic
STRANDEDNESS:
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   TELEFAX:
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Sequence 19, Application US/08938835A

Patent No. 6060245

GENERAL INFORMATION:

APPLICANT: SORGE, Joseph A.

APPLICANT: SORGE, Joseph A.

APPLICANT: SORGE, Joseph A.

APPLICANT: MULLINAX, Rebecca L.

ITILE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING

TITLE OF INVENTION: SPECIFIC NUCLEIC ACID POPULATIONS

NUMBER OF SEQUENCES: 69

CORRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner, L.L.P.

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COMPUTER: BDC COMPUTER: ISONE: MEDIC COMPUTER: ISONE COMPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 12;
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                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Barker, M. Paul
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 04121.0044-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Pred. No. 8
                                                                              APPLICATION NUMBER: US/08/779,355
FILING DATE: 06-JAN-1997
CLASS/FICATION 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/775,993
FILING DATE: 03-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/775,993
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/779,335
FILING DATE: 06-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        43092CP
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 12 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    NAME: Kulik, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 430
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-779-355-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.5%;
Best Local Similarity 81.8%;
Matches 9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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                     ; SEQ ID NO 59
; IENGTH: 12
; TYPE: DNA
; ORCANISM: human
US-09-475-947A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: human
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                                                                                                                                                                                                                                                                        Query Match
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TITLE OF INVENTION: Chimeric Oligonucleotides and Uses Thereof in the TITLE OF INVENTION: Identification of Antisense Binding Sites FILE REFERENCE: 020600-272
CURRENT APPLICATION NUMBER: US/09/043,149
CURRENT FILING DATE: 1996-03-13
PRIOR APPLICATION NUMBER: PCT/GB96/02275
PRIOR APPLICATION NUMBER: ED 996-09-13
PRIOR FILING DATE: 1996-09-13
PRIOR FILING DATE: 1995-09-14
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 33
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 87;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7.8; DB 1; Length 12;
Pred. No. 87;
0; Mismatches 2; Indels
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; Sequence 59, Application US/09475947A
; Patent No. 6471154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: POLYMOTPHIC Repeats in Human Genes
; TITLE OF INVENTION: POLYMOTPHIC REPEATED:
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL MINORMATION:
GENERAL MINORMATION:
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Giuliano, Kenneth A.
AITLE OF INVENTION: A System for Cell Based Screening;
FILE REFERENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT APPLICATION DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SSOFWARE: Patentin Ver. 2.0
SSOFWARE: Laboration of Street Control of Street
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US-09-513-783A-65
'Sequence 65, Application US/09513783A,
'Patent No. 6416959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: oligonucleotide US-09-043-149-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.5%;
Best Local Similarity 81.8%;
Matches 9; Conservative
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APPLICANT: HOUTZ, Robert L.
TITLE OF INVENTION: ISOLATED SPINACH
TITLE OF INVENTION: ISOLATED SPINACH
TITLE OF INVENTION: RIBULOSE-1,5-BISPHOSTHATE CARBOXYLASE/OXYGENASE LARGE
TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE AND METHOD OF INACTIVATING
TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE ACTIVITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
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                                          Gaps
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0
  DB 1; Length 12;
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                                          Indels
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US-09-475-947A-329/C
Sequence 329, Application US/09475947A
Factor No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
FAPLICANT: Garner, Jonathan D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REPRENCE: UTSD0667
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 329
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,916 FILING DATE: US/08/687,916 CLASSIFICATION: 800
                                            .;
?;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7.8; DB
Pred. No. 87;
0; Mismatches
Score 7.8; DB Pred. No. 87; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08687916
Patent No. 5908972
GENERAL INFORMATION:
    35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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RESULT 112
US-08-254-81D-5/C
; Sequence 5, Application US/08254811D
; Patent No. 5773213
; GENERAL INFORMATION:
; APPLICANT: GUllans, Steven R.
; APPLICANT: Gullans, Ryoji
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
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; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
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; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
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; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
; TITLE Nucleic Acid
; TITLE Nucleic A
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Patent No.: 5856103
GENERAL INFORMATION:
APPLICANT: Gray, Donald M.
APPLICANT: Clark, Chris L.
TITLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
TITLE OF INVENTION: FOR ANTISENSE TARGETING
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 10;
                                     Score 7.4; DB 1; Length 9;
Pred. No. 6.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 for Windows
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,811D
FILING DATE: 06-UUM-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: MacWright, Robert S.
REGISTRATION UNMBER: 32,425
REFERENCE/DOCKET NUMBER: 32,446101
TELECOMOTNICATION INFORMATION:
TELEFAX: (212) 425-720
TELEFAX: (212) 425-5288
TELEX: 42141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                         33.6%;
88.9%;
                                     Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 10 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                        733 GAGAAACAG 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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US-08-808-474A-3
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Patent No. 6495541

GENERAL INFORMATION.

GENERAL INFORMATION.

TITLE OF INVENTION: SUBUNIT N. METHYLTRANSFERASE AND METHOD OF INACTIVATING

TITLE OF INVENTION: SUBUNIT N. METHYLTRANSFERASE AND METHOD OF INACTIVATING

TITLE OF INVENTION: SUBUNIT N. METHYLTRANSFERASE AND METHOD OF INACTIVATING

TITLE OF INVENTION: SUBUNIT N. METHYLTRANSFERASE ACTIVITY

NUMBER OF SEQUENCES: 30

CORRESPONDENCE: DOANE, SWECKER & MATHIS

STREET: P.O. BOX 1404

CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 6.2e+02;
0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER EADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,614
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,916
FILING DATE:
RIGHT OF ALTONION NUMBER: 08/687,916
FILING DATE:
RESTRATION NUMBER: 40,373
RESTRATION NUMBER: 40,373
RESTRATION NUMBER: 40,373
RESTRATION NUMBER: 40,373
RESTRATION NUMBER: 386-620
TELEPHONE: (703) 836-620
                                                                                                                                                                     028750-138
APPLICATION NUMBER: US 08/391,000
                                                                                      NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 0287F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 11;
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic)
US-08-687-916-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.6%;
88.9%;
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                                  FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 836-665
TELEFAX: (703) 936-2021
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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nucleic acid
DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 111
US-09-138-614-11/c
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Patent No. 601561
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDERSS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
CITY: GARDEN CITY
STATE: HOW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Tlopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOSS/MS-DOS
SOFTWARE: PREACTIN Release #1.0, Version #1.25
CORPUTER: LIBM FC COMPATA:
APPLICATION NUMBER: PM364 (AU)
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: PM302 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM302 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM302 (AU)
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM302 (AU)
FILERPAN: (S16) 742-433
TELECOMMUNICATION INFORMATION:
TELEBRONE: (S16) 742-433
TELEDAX: (S16) 742-433
TELEPAX: (S16) 742-433
TELEPAX: (S16) 742-433
TELEPAX: (S16) 742-433
TELEPAX: (S16) 742-433
                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 477:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.6%;
88.9%;
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 8, Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               738 ACAGAACAC 746
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Best Local Similarity
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Fatent No. 6010895
Fatent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Caper, David
APPLICANT: Cooper, David
CONRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
STREET: New York
COUNTRY: United States
CONPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 14.24
ATTORNEY/AGENT INFORMATION:
NAME: Digialio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 3606
TELECOMMUNICATION: NUMBER: 2606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                          STATE: Dalias
STATE: Dalias
STATE: Texas
COUNTRY: USA
ZIP: 752016776
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,474A
FILING DATE: 03-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: 37,732
REJEPHONE: (214) 740-8800
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: MOCHANICAL acid
TYPE: MICHAEL ACID ACID
        CORRESPONDENCE ADDRESS:
ADDRESSEE: Locke Purnell Rain Harrell
STREET: 2200 Ross Avenue, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                 Dallas
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US-08-388-353-477
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728 GCCAGGAGA 736
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  GENERAL INFORMATION:
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                                                                                                                                                                         Sequence 3, Application US/08522384
| Patent No. 6110667
| CENERAL INFORMATION
| APPLICANT: LOPEZ-NIETO, CARLOS E
| APPLICANT: LOPEZ-NIETO, CARLOS E
| APPLICANT: NIGAM SANJAY KUMAR
| TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR TITLE OF INVENTION: 1984-4029
| CURRENT APPLICATION NUMBER: US/08/522,384
| CURRENT FILING DATE: 1996-11-15
| NUMBER OF SEQ ID NOS: 122
| SOFTWARE PATENTION OF: 2.1
| SEQ ID NO 3
| LENGTH: 10
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APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: MIGAM, SANDAY KUMA
APPLICANT: MIGAM, SANDAY KUMA
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
FILE REFERENCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: Description of Unknown Organism: Primer
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  Mismatches
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; Sequence 36, Application US/08522384
; Patent No. 6110667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-522-384-35/c
; Sequence 35, Application US/08522384
; Patent No. 6110667
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Best Local Similarity 88.5.
Best Aconservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Unknown Organism
Conservative
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                                      738 ACAGAACAC 746
                                                                               2 AGAGAACAC 10
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                         RESULT 116
US-08-522-384-3/c
  8;
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  Matches
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; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: NIGAM, SANGAY KUMAR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; UURBERT FILING DATE: 1996-11-15
; SOFTWARE: PATENTING OF SEQ ID NOS: 122
; SOFTWARE: PATENTING OF SEQ ID NOS: 122
; SOFTWARE: PATENTING OF SEQ ID NOS: 122
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APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: NIGAM, SANJAY KUWAR
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
FILE REFERENCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 36
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 33.6%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 81; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match . 33.6%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 81; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Unknown Organism: Primer US-08-522-384-93
                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown Organism: Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Joyce, Gerald F.
APPLICANT: Breaker, Ronald R.
TILE OF INVENTION: ENYMATIC DNA MOLECULES
FILE REFERENCE: SCR1943S
CURRENT APPLICATION WUMBER: U8/08/849, 567A
CURRENT FILING DATE: 1997-08-25
PRIOR APPLICATION WUMBER: PCT/US95/15580
PRIOR PILING DATE: 1995-12-01
PRIOR PILING DATE: 1995-10-01
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41, Application US/08849567A Patent No. 6326174
                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Unknown Organism
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PRIOR APPLICATION NUMBER: 08/349,023
PRIOR FLING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
```

Query Match
33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 1; Indels 734 AGAAACAGA 742 ð

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Sequence 135, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REPERBACE: UTS0667
CURRENT APPLICATION NHERR: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 135 10 AGAAATAGA 2 RESULT 121 US-09-475-947A-135

33.6%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 81; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 88.5
Matches 8; Conservative

TYPE: DNA ORGANISM: human

US-09-475-947A-135

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US-09-508-7538-36/c

US-09-508-7538-36/c

Sequence 36 Application US/095087538

Patent No. 6544736

GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yako SHIBATA
APPLICANT: Wish Information
APPLICANT: Masanori WATAHIKI
APPLICANT: Wiji OHARA
APPLICANT: WASANORI MATAHIKI
APPLICANTON NUMBER: US/09/508,7538
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: UP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 36
LENGTH: 10
TUDE OF THE PROPERTY OF

TYPE: DNA ORGANISM: Artificial Sequence

; 0 ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-36 PCT-US9-408023-32/C

FCT-US9-408023

GENERAL INFORMATION:

APPLICANT: de Kloet, Siwo R.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Russell, P.A.

STREET: 200 East Broward Boulevard

CITY: Fort Lauderdale

STATE: FL

CONTRY: USA Length 10; 1; Indels COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: THE PC compatible
COMPUTER: THE PC compatible
COMPUTER: THE PC compatible
COMPUTER: THE PC COMPUTER:
COMPUTER: THE COMPUTER:
CO Score 7.4; DB 1; Pred. No. 81; 0; Mismatches 1. Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative 735 GAAACAGAA 743 9 GAAGCAGAA 1 33301

TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) PCT-US94-08023-32

DB 1; Length 10; 33.6%; Score 7.4; DB 88.9%; Pred. No. 81; tive 0; Mismatches Query Match
Best Local Similarity 88.9
Matches 8; Conservative 732 GGAGAAACA 740

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RESULT 124 US-08-237-233-3/c ; Sequence 3, Application US/08237233 ; Patent No. 5414077 GENERAL INFORMATION:
APPLICANT: LIN, KUBI-YING
APPLICANT: MATTEUCCI, MARK 10 GGAGAAAA 2

Mon Oct 18 14:40:09 2004

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APPLICANT: Guilans, Steven R.
APPLICANT: Guilans, Steven R.
APPLICANT: Rolima, Ryoji
APPLICANT: Randall, Jeffrey
TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
TITLE OF INVENTION: Method for Conducting Sequential Nucleic Acid
TITLE OF INVENTION: Hybridization Steps
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: MacWright, Robert S.
STREET: 1 Broadway
CITY: New York
STATE: NY
COUNTRY: NY
                                                                                                                                                                                                                                                                                                                                                                                                       33.6%; Score 7.4; DB 1; Length 11; 77.8%; Pred. No. 91; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.6%; Score 7.4; DB 1; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER EADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NAME:
APPLICATION NAME:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacWright, Robert 5.
RESERENCE/DOCKET NUMBER: 1854/46101
TELECOMMUNICATION:
                  APPLICATION NUMBER: 07/936,531
FILING DATE: August 26, 1992
ATTORNSY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/245
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-254-811D-6/c
; Sequence 6, Application US/08254811D
; Patent No. 5773213
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TELEPHONE: (212) 425-5288
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.00
Best Local 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 11 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                727 TGCCAGGAG 735
                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-435-350-92
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TOPOLOGY: lin
HYPOTHETICAL: N
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TITLE OF INVENTION: PSEUDONUCLEOSIDES AND
TITLE OF INVENTION: PSEUDONUCLEOTIDES AND THEIR POLYMERS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: IRELL & MANELLA
STREET: 545 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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US-08-435-92

Sequence 92, Application US/08435350

Patent No. 5599704

GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: Wennell G. Drapper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: TREATMENT OF BREAST CANCER
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: ADDRESSEE: Lyon & Lyon
STREET: ADDRESSEE: SARCH Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READALE FORM:
MEDULM TYPE: 13 5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: WordPerfect (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,350
FILING DATE: 05-MAY.1995
CLASSIFICATION: 514
                                                                                                                                                                                                ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER I BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/594147
FILING DATE: 09-0CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: WURSAHICE: XATE H.
REGISTRATION NUMBER: 2955
REFERENCE/DOCKET NUMBER: 4610-0006.20
TELEPHONE: 415-327-2550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.6%; Score 7.4; Dl
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
1 TOPOLOGY: linear
US-08-237-233-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        732 GGAGAAACA 740
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USA
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33.6%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 91; tive 0; Mismatches 1; Indels
ADDRESSEB: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
| NAME/KEY: misc_feature | LOCATION: 1..11 |
| OTHER INFORMATION: /product= "MEF-2 MUTANT CONSENSUS" |
| US-08-764-528-8
                                                                                            COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,528
FILING DATE:
CLASSIFICATION: 424
ATTONENY/AGENT INFORMATION:
NAME: VITO, CHRISTINE C.
REGISTRATION NUMBER: 39,061
REGISTRATION SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDENESS: single
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 88.9
Matches 8, Conservative
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                                      Gaps
                                                                                                                                                                                                                                            Sequence 8, Application US/08764522A

Sequence 8, Application US/08764522A

Patent No. 6090544

GENERAL INFORMATION:

APPLICANT: HARADA, SHUN-ICHI

APPLICANT: ROBAN, GIDEON A.

TITLE OF INVENTION: MORPHOGEN AND COMPOSITIONS FOR IDENTIFYING

TITLE OF INVENTION: MORPHOGEN ANALOGS

NUMBER OF SEQUENCES:

ADDRESSE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES

STREET: 45 SOUTH STREET

CITY: HOPKINTON

STATE: NA

COUNTRY: USA

ZIP: 01748

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/764,522A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.6%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 91; tive 0; Mismatches 1; Indels
                                      1; Indels
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LOCATION: 1..11

COTATION: /product= "MEF-2 MUTANT CONSENSUS"

12.02-764-522A-8
            Pred. No. 91;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:

CLASSIFICATION: 435

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: VITO, CHRISTINE C.

REGIETRATION NUMBER: 39,061

REFERENCE/DOCKET NUMBER: CRP-1

REFERENCE/DOCKET NUMBER: CRP-1

REFERENCE/DOCKET NUMBER: CRP-1

TELEPHONE: (617)-248-7000

TELEPHONE: (617)-248-7100

INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:

LENGTH: 11 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
          Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.6
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                   11 AGAACCAGA 3
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US-08-764-522A-8
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US-09-196-523-23

US-09-196-523-23

Sequence 23, Application US/09196523A

Sequence 23, Application US/09196523A

Sequence 23, Application US/09196523A

Patent No. 6248525

GENERAL INPORMATION:
TITLE OF INVENTION: Wethod for Identifying and Inactivating Essential or
TITLE OF INVENTION: Punctional Genes

TITLE OF INVENTION: Punctional Genes

CURRENT APPLICATION NUMBER: US/09/196,523A

CURRENT APPLICATION NUMBER: 06/079,851

EARLIER APPLICATION NUMBER: 60/079,851

SEALIER APPLICATION NUMBER: 60/079,851

EARLIER FILING DATE: 1998-03-30

NUMBER: PatentIn Ver. 2.1

SEQ ID NO 23

LENGTH: 11

TYPE: DAA

ORGANISM: Artificial Sequence ö Gaps . 0 Query Match
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: oligonucleotide US-09-196-523-23

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Gaps
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0
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0
                                              Score 7.4; DB 1; Length 11;
Pred. No. 91;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.6%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Compositions and Methods for Wound TITLE OF INVENTION: Compositions and Methods for Wound TITLE OF INVENTION: Healing; FILE REPERENCE: 00486-78503 CURRENT APPLICATION NUMBER: US/09/249,155A CURRENT FILING DATE: 1999-02-12; PRIOR FILING DATE: 1998-02-13; PRIOR FILING DATE: 1998-08-26; PRIOR FILING DATE: 1998-09-28; PRIOR FILING DATE: 1998-09-28; NUMBER: OF SEQ ID NOS: 346 NUMBER: DESTANCE OF SEQ ID NOS: 346 NUMBER: DESTANCE OF WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound;
TITLE OF INVENTION: Compositions and Methods for Wound;
TITLE OF INVENTION: Healing
FILE REFERENCE: 00486.78503
FILE REFERENCE: 09486.78503
CURRENT APPLICATION NUMBER: US 60/044,737
FRIOR APPLICATION NUMBER: US 60/097,937
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-08-26
FRIOR FILING DATE: 1998-08-26
FRIOR FILING DATE: 1998-09-38
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Pred. No. 91;
0; Mismatches 1
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FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-249-155A-124
; Sequence 124, Application US/09249155A
; Patent No. 6538173
                                                                                                                                                                                                                                                                                                                                Sequence 86, Application US/09249155A Patent No. 6538173 GENERAL INFORMATION:
                                                 33.6%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.6%;
Best Local Similarity 88.9%;
Matches 8; Conservative
                                           Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                   734 AGAAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       738 ACAGAACAC 746
                                                                                                                                                                                                     3 AGAAAAAGA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACAGAACTC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Mus :
US-09-249-155A-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-249-155A-86
US-08-722-015A-4
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SEQ ID NO 124
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Sequence 4. Application US/08722015A
Sequence 4. Application US/08722015A
Setting Normation
Setting Normation
APPLICANT: Schultemaker, Johanna
TITLE 0F INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCYTIU
TITLE 0F INVENTION: NUCLEIC ACIDS AND NON SYNCYTIUM INDUCING VARIANTS OF THE HUMAN INMUNC
FILE REPERENCE: 9250.25
CURRENT APPLICATION NUMBER: US/08/722,015A
CURRENT PILING DATE: 1996-11-19
NUMBER OF SEQ ID NOS: 258
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                  Sequence 25, Application US/08930828A
Patent No. 6261768
GENERAL INFORMATION:
APPLICANT: TODD, Alison
TITLE OF INVENTION: METHOD FOR AMPLIFYING SPECIFIC NUCLEIC
TITLE OF INVENTION: ACID SEQUENCES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: RECOMPY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                             STATE: U.C.
COMPUTRY: USA
ZIP: 20004

ZIP: 20004

COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30

CURENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/930,828A
FILING DATE: 16-JAN-1998
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: KORNBAU Anne M.
REFERENCY/DOCKET 10/MBER: 25,884
FREFERENCY/DOCKET 10/MBER: 202-202-2197
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-3528
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
TUNTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORALIFICIAL Sequence ORGANISM: Artificial Sequence ORHER INFORMATION: Synthetic Oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.6%; Score 7.4; DE Best Local Similarity 88.9%; Pred. No. 91; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            729 CCAGGAGAA 737
2 CCTGGAGAA 10
                                                                                                                                                                                                                                                                                                                                        ADDA-
STREET: 419 SC.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCAGGAGGA 9
                                                                       RESULT 130
US-08-930-828A-25
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US-08-722-015A-4
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Gaps
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US-08-859-954-30/C

Sequence 30, Application US/08859954

Fatera No. 6038595

Fatera No. 6038595

FATERAL INFORMATION:

APPLICANT: Hardin, Busan H.

APPLICANT: Hardin, Paul E.

TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Design and Optimized Primer Library for STREES: 1301 Workings Second Convention of Method Thereof Convention of Method Thereof STREE: Texas

STREE: Texas

CONVENT: 108.A.

ZIP: 7701-3039

CONFETT: Texas

CONFUTER: Texas

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Query Match 31.8%; Score 7; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 137
US-08-859-954-541/c
'S-08-859-954, Application US/08859954
'; Patent No. 6083695
'; GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 7; Conservative
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ANTI-SENSE: YES

US-08-859-954-30
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US-08-376-376-275-376
Sequence 3, Application US/08376362A
Sequence 3, Application US/0837636
Sequence 3, Application US/08376362A
Sequence 3, Application US/0837664
Sequence 3, Application US/0837636A
TITLE OF INVENTION MEHOD OF IDENTIFYING SUBSTANCES WHICH STIMULATE OR BLOCK
TITLE OF INVENTION MEHOD OF IDENTIFYING SUBSTANCES WHICH STIMULATE OR UNWARTON
TITLE OF INVENTION SALTY TASTE PROCEST OF SEQUENCES SALTY TASTE SALTY TASTE SALTY TASTE SALTY TO SECUENCE SALTY SALT
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33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                              5214136-10/c
;Patent No. 5214136
APPLICANT: LIN, KUEL-YING;MATTEUCCI, MARK
TITLE OF INVENTION: ANTHRAQUINONE-DERIVATIVES;
OLIGONUCLECTIDES
NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/482,941
FILING DATE: 20-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           732 GGAGAAACA 740
                                                             738 ACAGAACAC 746
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US-08-376-362A-3
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SEQ ID NO:10:
:
LENGTH: 11
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CITY: Franklin Lakes
STATE: New Jersey
CONTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPRY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,642
FILING DATE: 19910801
    APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-No. RE38392-2001
CLASSIFICATION: CURNOWID
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: REMEDICA, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 36,902
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOMMUNICATION INFORMATION:
TELEFRANCE, 202-639-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 31.8%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
CORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-985-799-19
                                                                                                                                                                                                                                                                                                                                                                TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION
TELEPHONE: 201-848-5317
TELEFAX: 201-848-9228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt,, Brian K.
REGISTRATION NUMBER: 33,21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 199108
CLASSIFICATION: 435
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TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pemsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Le...
No. 7e+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 31.8%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 70+
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
negrathTION: /desc = "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTE: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ Vorsion 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE: THORMATION:
ATTORNEY/ABENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELECHONE: 713/651-5325
                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09985799
Patent No. RE38392
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 713/61-5246
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         730 CAGGAGA 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ANTI-SENSE:
US-08-859-954-541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 138
US-09-985-799-19
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Gaps
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0
                                              0; Indels
Length 10;
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US-07-739-642-13
Sequence 13, Application US/07739642
Fatent No. 5173427
GENERAL INFORMATION:
APPLICANT: Mallonee, Richard L.
TITLE OF INVENTION: Vectors And Hosts With Increased
TITLE OF INVENTION: Expression Of HBCAg
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
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Length 10;
                                                                                                                                                                                                                                                                                                                                                                                          US-07-739-643-13

Sequence 13, Application US/07739643

Patent No. 5175094

GENERAL INFORMATION:

TITLE OF INVENTION: Increased Expression of HBCAG NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE Richard R. Rodrick STREET: 1 Becton Drive CITY: Franklin Lakes STRATE: 10 W Jersey

COUNTRY: U.S.A.

ZIPP: 07417-1880

COMPUTER: IBM PC compatible COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

MEDIUM TYPE: Plopy disk COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/07/739,643

FILING DATE: 19910801

CLASSIFICATION NUMBER: 9-2090

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-848-5317

TELEPHONE: 201-848-5317

TELEPHONE: 201-848-5317

TELEPHONE: 201-848-5317

TELEPHONE: 201-848-5317

TELEPHONE: SCOLD NUMBER: PLONE SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: NUCLEIC ACID

STREADENDENTES: SINGIE
                                                                                                                                          Query Match 31.8%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches
LENGTH: 10 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                        737 AACAGAA 743
                                                                                                                                                                                                                                                                                  1 AACAGAA 7
                                                                         , TOPOLOGY:
US-07-739-642-13
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US-07-739-643-13
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31.8%; Score 7; DB 1; Length 10; 100.0%; Pred. No. 95; ative 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity Matches 7; Conserva linear US-07-739-643-13

737 AACAGAA 743 1 AACAGAA 7 d

RESULT 141

18-07-139-142-13

18-07-139-142-13

18-07-13-13-142-13

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18-07-142-142

18-07-142-142

Length 10; COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/739,142

FILING DATE: 19310801

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAMME: Stierwalt, Brian K.

REGISTRATION NUMBER: P-2271

TELEFAMINICATION INFORMATION:

TELEFAMINICATION INFORMATION:

TELEFAMINICATION INFORMATION:

TELEFAM: 201-848-5218

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

STRANDEDNESS: single

10S-07-739-142-13 ADDRESSEE: Richard R. Rodrick STREET: 1 Becton Drive STREET: 1 Becton Director CITY: Franklin Lakes STATE: New Jersey COUNTRY: U.S.A. ZIP: 07417-1880

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; 0 Query Match 31.8%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 95; Matches 7; Conservative 0; Mismatches

RESULT 142
US-08-548-199-14/C
| Sequence 14, Application US/08548199
| Patent No. 5652106
| Fatent No. 5652106
| GENERAL INFORMATION:
| APPLICANT: Plikaytis, Bonnie B. APPLICANT: Plikaytis, Bonnie B. APPLICANT: Plikaytis, Bonnie B. APPLICANT: Crawford, Jack T. ITLE OF INVENTION: RAPID AMPLIFICATION-BASED SUBTYPING OF TITLE OF INVENTION: WACOBACTERIUM TUBERCULOSIS
| NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSE: SALE SUITE 1200, The Candler Building STREET: 127 Peachtree Street, N.E. CITY: Atlanta STATE: Georgia COUNTY: USA STATE: Georgia COUNTY: USA STATE: Georgia COUNTY: USA STATE: PLODRY disk COMPUTER: IBM PC COMPATION: PLODS/MS-DOS SOFTWARE: PLODRY MISK COMPUTER: IBM PC COMPATION OF STEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/548,199 FILING DATE: 2-CCT-1995 CLASSIFICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION NUMBER: US/08/548,199 FILING DATE: 04 UNDER: US/08/548,199 FILING DATE: DESTYMANT, DAVIG G. REGISTRATION NUMBER: 33,438 REFERENCE/DOCKET NUMBER: 33,438 REFERENCE/DOCKET NUMBER: 11414.062

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schultz1-727.rni

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31.8%; Score 7; DB 1; Length 10;
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Query Match

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RESULT 144
US-08-440-787A-70/c
US-08-440-787A-70/c
Sequence 70, Application US/08440787A
Patent No. 5770434
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
TITLE OF INVENTION: Same.
TITLE OF INVENTION: Same.
NUMBER OF SEQUENCES: 174
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
STATE: California
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                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/08594031
Sequence 19. Application US/08594031
Sequence 10. 5783182
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSED: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OOPBATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,787A
FILING DATE: 15-MAY-1995
CLASSIFICATION NUMBER: US/09/440,787A
FILING DATE: 10-NOV-1992
ATONEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/978,893
FILING DATE: 10-NOV-1992
ATONEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 25-901
TELEPHONE: (619) 535-901
TELEPHONE: (619) 535-901
TELEPAX: (619) 535-949
INPORMATION FOR SEQ ID NO: 70:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1;
Pred. No. 95;
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100.0%; Pred. No. 20.
0; Mismatches
Pred. No. 95;
0; Mismatches
100.0%;
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Best Local Similarity 100.
Best Local Similarity 100.
Matches 7; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                               737 AACAGAA 743
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US-08-594-031-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Huse, William D.
TITLE OF INVENTION: Soluble Peptides Having Constrained,
TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
TITLE OF INVENTION: Same.
CORRESPONDENCES: 174
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      /number= 10
/note= "Consensus sequence of 10 bp tandem repeat
of MPTR (Hermans et al. 1992)"
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,787A
FILING DATE: 15-MAY-1995
PROOR APPLICATION: 435
PRIOR APPLICATION: WAS PRIOR APPLICATION NUMBER: US 07/978,893
FILING DATE: 10-NOV-1992
ATTONBEY/AGENT INPORMATION:
ATTOMBEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....KESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 31.8%; Score 7; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P.IX 1586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 143
US-08-440-787A-66/C
; Sequence 66, Application US/08440787A
; Patent No. 5770434
; GENERAL INFORMATION:
APPLICANT: Huse, William D.
                      TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                        DNA (genomic)
YES
                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1..10
OTHER INFORMATION: /numb
OTHER INFORMATION: /note
OTHER INFORMATION: of MP
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.8
Best Local Similarity 100.
Matches 7; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      742 AACACCG 748
                                                                                                                                                                               linear
                                                                                                                                                                             TOPOLOGY: lir
MOLECULE TYPE:
HYPOTHETICAL: )
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Sequence 481, Application US/08488551B

Sequence 481, Application US/08488551B

Patent No. 6015661

GENERAL INFORMATION:

APPLICANT: Nicholas J. Deacon

APPLICANT: David Cooper

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 841

CORRESPONDENCE ADDRESS:

ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: AGADEM CITY

STREET: AGADEM CITY

STREET: NEW YORK

COUNTRY: U.S.A.

ZIP: 11530-029

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

TILING DATE: 07-JUN-1995

APPLICATION NUMBER: PM4002 (AU)

FILING DATE: 11-FEB-1994

APPLICATION NUMBER: PM401

FILING DATE: 12-FEB-1994

APPLICATION NUMBER: PM3021/95

FILING DATE: 17-MAY-1995

APPLICATION NUMBER: PM3021/95

FILING DATE: 17-MAY-1995

APPLICATION NUMBER: PM3021/95

FILING DATE: 17-MAY-1995

ATTORNEY/AGBYT INFORMATION:

NAME: FRANK S: DIGIGLIO

REFERENCE/DOCKET NUMBER: 9606Z

TELECOMMUNICATION INFORMATION:

FILING DATE: 17-MAY-1943

APPLICATION NUMBER: PM3021/95

FILING DATE: 17-MAY-1995

APPLICATION NUMBER: PM3021/95

FILING DATE: 17-MAY-1995

APPLICATION NUMBER: PM3021/95

FILING DATE: 17-MAY-1995

ATTORNEY/AGBYT INFORMATION:

FELECOMMUNICATION INFORMATION:

FELECOMMUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.8%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches
                              ALIONANE: Didigito, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4346
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 481:
SEQUENCE GIRARGERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-481
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INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            741 GAACACC 747
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US-08-388-353-481
i Sequence 481, Application US/08388353
patent No. 6010895
i GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Cooper, Dale A.
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSES: Scully, Scott, Murphy & Presser
CITY: Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City Plaza
COUNTRY: United States
STRET: New York
COUNTRY: United States
COMPUTER: IB30
COMPUTER: IB30
COMPUTER: IB40
COMPATION: APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.8%; Score 7; DB 1;
100.0%; Pred. No. 95;
tive 0; Mismatches
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM:
DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY, AGENT INFORMATION:
NAVE: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
FINGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
CRIGINAL SOURCE:
US-08-594-031-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Sequence 3, Application US/09640953
Patent No. 64923410
GENERAL INFORMATION:
APPLICANT: Meyer, Rich
TITLE OF INVENTION: IMPROVED HYBRIDIZATION AND
TITLE OF INVENTION: CONJUGATED TO MINOR GROOVE BINDERS
CONJUGATED TO MINOR GROOVE BINDERS
                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
SOFTWARE: FastSEQ for Windows
TLUNG DATE: 16-Aug-2000
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US/09/640,953
FILING DATE: 03-APR-1998
APPLICATION NUMBER: 08/415,370
FILING DATE: 03-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34469-20004.20
                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                  Query Match 31.8%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 95; Matches 7; Conservative 0; Mismatches
                                                                34469-20004.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brennan, Sean M
REGISTRATION NUMBER: 39,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                    NAME: Brennan, Sean M
REGISTRATION WUMBER: 39,917
REFRENCE/DOCKET NUMBER: 34465
TELEPHONE: 650-813-560
TELEPHONE: 650-813-560
TELERX: 650-494-0792
TELEX: 706141
INPORMATION POR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
ATTORNEY/AGENT INFORMATION: NAME: Brennan, Sean M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                        736 AAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AAACAGA 10
                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                   TOPOLOGY:
US-09-054-832-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-640-953-3
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                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Meyer, Rich TITLE OF INVENTION: IMPROVED HYBRIDIZATION AND TITLE OF INVENTION: IMPROVED HYBRIDIZATION AND TITLE OF INVENTION: MIGMATCH DISCRIMINATION USING OLIGONUCLEOTIDES TITLE OF INVENTION: CONJUGATED TO MINOR GROOVE BINDERS CORRESPONDENCE ADDRESS:
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APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: MIGAM, SANDAY KUMAR
APPLICANT: MIGAM, SANDAY KUMAR
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
FILE REFERENCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARR: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Description of Unknown Organism: Primer US-08-522-384-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                      0; Indels
                                                                                        Length 10;
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FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.8%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches
                                                                                        Query Match 31.8%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches
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APPLICATION NUMBER: US/09/054,832
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/415,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08522384
Patent No. 6110667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09054832
Patent No. 6312894
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Wind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Unknown Organism
                                                                                                                                                                                  741 GAACACC 747
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         TOPOLOGY: linear
                                                                                                                                                                                                                         1 GAACACC 7
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                           , MOLECULE TYPE:
US-08-488-551B-481
                                                                                                                                                                                                                                                                                                               US-08-522-384-13/c
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| FALCHLE NO. DODOLSO. |
| GENERAL INFORMATION: SHIV |
| APPLICANT: STAVASTANA, SHIV |
| APPLICANT: MOUL, JUDD W. |
| APPLICANT: MOUL, JUDD W. |
| APPLICANT: MOUL, JUDD W. |
| APPLICANT: SEGAWA, TAKEHIKO |
| TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED |
| TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED |
| TITLE OF INVENTION: POYNUCLEOTIDE ARRAY |
| FILE REPRENENCE: 04995-0057-00000 |
| CURRENT APPLICATION NUMBER: US/09/769,482 |
| CURRENT APPLICATION NUMBER: 60/178,772 |
| PRIOR APPLICATION NUMBER: 60/178,772 |
| PRIOR APPLICATION NUMBER: 60/178,772 |
| PRIOR APPLICATION NUMBER: 60/179,045 |
| PRIOR APPLICATION NUMBER: 60/179,045 |
| RATOR FILING DATE: 2000-01-31 |
| NUMBER OF SEQ ID NOS: 67 |
| LENGTH: 10 |
| LENGTH
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GENERAL INFORMATION:

APPLICANT: Akira SHIMAMOTO

APPLICANT: Yasuhiro FURUICHI

APPLICANT: Yuko SHIBATA

APPLICANT: Hiroko FUNAKI

APPLICANT: Hiroko FUNAKI

APPLICANT: Hiroko FUNAKI

APPLICANT: Masanori WATAHIKI

TITLE OF INVENTION: Method for Synthesizing CDNA from mRNA sample

FILE REFERENCE: 00162/HG

CURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT FILING DATE: 2000-06-16

PRIOR FILING DATE: 1997-09-18

NUMBER OF SEQ ID NOS: 472

SEQ ID NO 319
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CRGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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31.8%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.8%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 95; Matches 7; Conservative 0; Mismatches
                                                                                                                          US-09-508-753B-319/c
; Sequence 319, Application US/09508753B
; Patent No. 6544736
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; Sequence 22, Application US/09769482
; Patent No. 6566130
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ORGANISM: Artificial Sequence
FEATURE:
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9 GGAGAAA 3
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                                        Gabs
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Patent No. 6544736

Patent No. 6544736

APPLICANT: Akira SHIMAMOTO

APPLICANT: Yaku SHIMAMOTO

APPLICANT: Yaku SHIMAMOTO

APPLICANT: Hicko FUNAXI

APPLICANT: Hicko FUNAXI

APPLICANT: Hicko FUNAXI

APPLICANT: Hicko FUNAXI

APPLICANT: Masanori MaTHAHIKI

TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

FILE REFERENCE: 00162/HG

CURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: UP 9/270324

PRIOR FILING DATE: 1997-09-18

NUMBER OF SEQ ID NOS: 472

SEQ ID NO 135

LENGTH: 10
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; CIHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-7538-135
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31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                     0; Indels
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                                                                                                                                                                                                               RESULT 151
US-09-867-915-21
Sequence 21. Application US/09867915
Patent No. 6521747
GRNERAL INFORMATION:
APPLICANT: Anastasio, Alison E. APPLICANT: Anastasio, Alison E. APPLICANT: Roshy, Beena
APPLICANT: Finkel, Kevin
APPLICANT: Lee, Helen H.
TITLE OF INVENTION: HAPLOYPES OF THE AGTRI GENE
FILE REFERENCE: AGTR1-11364est
CURRENT PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 21
LENGTH: 10
Best Local Similarity 100.0%; Pred. No. 95; Matches 7; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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CORGANISM: Homo sapiens
US-09-867-915-21
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US-09-508-753B-135/c
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; OTHER INFORMATION: Description of Artificial Sequence: No. 6632919el Sequence
US-09-083-235A-52
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                                                                                                                      GENERAL INFORMATION:

APPLICANT: SRIVASTAVA, SHIV

APPLICANT: MOUL, JUDD W.

APPLICANT: W. LINDA L.

APPLICANT: W. LINDA L.

TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

TITLE OF INVENTION: POYNCLEOTIDE ARRAY

TITLE OF INVENTION: BOYNER: US/09/769,482

CURRENT FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/179,045

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PATENTING NOS: 67

SOFTWARE: PATENTING NOS: 67

SOFTWARE: PATENTING NOS: 67
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Sequence 52, Application US/09083235A

Patent No. 6632919

GENERAL INFORMATION:
APPLICANT: Nielsen, Peter E
APPLICANT: Bldrup, Anne B
TITLE OF INVENTION: Peptide Nucleic Acid Monomers and Oligomers
FILE REFERENCE: 1583044

CURRENT APPLICATION NUMBER: US/09/083,235A

CURRENT PILING DATE: 1997-05-23

PRIOR PILING DATE: 1997-05-33

NUMBER: OF SEQ ID NOS: 87

SOFTWARE: PatentIn Ver: 2.1

SEQ ID NO 52

LENGTH: 10

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CTHER INFORMATION: Description of Artificial Sequence: Synthetic
CTHER INFORMATION: oligonucleotide
US-09-769-482-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.8%; Score 7; DB 1; Length 10; 100.0%; Pred. No. 95; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.8%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches
US-09-769-482-29; Sequence 29, Application US/09769482; Patent No. 6566130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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AGAACAC 2

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; OTHER INFORMATION: Description of Artificial Sequence: No. 6632919el Sequence US-09-083-235A-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                 GENERAL INFORMATION:

APPLICANT: Nielsen, Peter E
APPLICANT: Nielsen, Gerald
APPLICANT: Bldrup, Anne B
ITILE OF INVENTION: Peptide Nucleic Acid Monomers and Oligomers
FILE REFERENCE: IS183044
CURRENT APPLICATION NUMBER: US/09/083,235A
CURRENT FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 08/862,629
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 87
SOFTHARE: Patentin Ver. 2.1
SEQ ID NO 56
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10;
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US-07-681-703B-55
Sequence 55, Application US/07681703B
Patent No. 5443965
GENERAL INCRNATION:
APPLICANT: Reyes, Gregory
APPLICANT: MocKAI, Randolph
TITLE OF INVENTION: Hepatitis C Virus Epitopes
TITLE OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Defilinger & Associates
STREET: -10 Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILICATION NUMBER: US/07/681.7020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
31.8%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/681,703B FILING DATE: 05-APR-1991 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 505,611 PILING DATE: 06-APR-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 594,854 FILING DATE: 09-OCT-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERNCE/DOCKET NUMBER: 4600-076.21
TELECOMMUNICATION:
TELECOMMUNICATION:
(415) 324-0880
JS-09-083-235A-56/c
; Sequence 56, Application US/09083235A
; Patent No. 6632919
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 324-0880 INFORMATION FOR SEQ ID NO: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     740 AGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AGAACAC 2
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ZIP: 943
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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SEQUENCE CHARACTERISTICS

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Indels
 5
 0; Mismatches
 8; Conservative
                    732 GGAGAAACAG 741
 Matches
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Gaps

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10 GGAGAAGTAG 1
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                                                                                                                                                                                           Score 6.8; DB 1; Length 10;
Pred. No. 1e+02;
0; Mismatches 2; Indels
                                                                                                   ; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDVIDUAL ISOLATE: Codon Change, Example 20
US-07-681-703B-55
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                             Query Match 30.9%;
Best Local Similarity 80.0%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                    734 AGAAACAGAA 743
                                                                                                                                                                                                                                                                                                      1 AGAAGAAGAA 10
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US-08-049-283A-32/C

Sequence 32, Application US/08049283A

Sequence 32, Application US/08049283A

PEREMAL INFORMATION

APPLICANT: Panen, Daniel G.

APPLICANT: Burn, Timothy C.

TILLE OF INVENTION: Cell Specific Promoter and Uses Thereof

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRES: 3

STREET: Two Militia Drive

START: Tay Militia Drive

START: Massachusetts

COUNTRY: USA

COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,283A
FILING DATE: 14-APR-1993
CLASSIFICATION OPTER: 08/020,465
FILING DATE: 19-FEB-1993
CLASSIFICATION WHERE: 07/837,776
FILING DATE: 19-FEB-1992
CLASSIFICATION A 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/837,776
FILING DATE: 11-FEB-1992
CLASSIFICATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 21,592
TELECOMUNICATION NUMBER: BIH91-03'A
TELEFROND: (617) 861-6240
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CLASSIFICS:

TYPE: nucleic acid STRANDEDNESS: single

30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02; Query Match Best Local Similarity

US-07-949-541A-13 ; Sequence 13, Application US/07949541A ; Patent No. 5552270

GENERAL INFORMATION:
APPLICANT: Khrapko, Konstantin R.
APPLICANT: Knorlin, Alexandr A.
APPLICANT: Taron'in, Alexandr A.
APPLICANT: Iranov, Igor B.
APPLICANT: Lysov, Jury P.
APPLICANT: Lysov, Jury P.
APPLICANT: Plorentiev, Vludimir L.
APPLICANT: Mirzabekov, Andrei D.
TITLE OF INVENTION: Method for Determining a DNA Nucleotide
TITLE OF INVENTION: Sequence and a Device for Carrying Out Same
TITLE OF INVENTION: Sequence and a Device for Carrying Out Same
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Laddas & Parry
STREET: 26 West 61st Street

CITY: New York STATE: New York COUNTRY: USA

ZIP: JUSAA
ZIP: JUSAA
ZIP: JUSAA
ZIP: JUSAA
ZIP: JUSAA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IEM PC/XT/AT or compatibles
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US. 552270-1992
PRIOR APPLICATION NUMBER: PCT/RU92/00052
FILING DATE: 18-Mar-1992
APPLICATION NUMBER: PCT/RU92/00052
FILING DATE: 18-Mar-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet I. Cord
REGISTRATION UNHBER: 33,778
REGISTRATION UNHBER: 33,778

REFERENCE/DOCKET NUMBER: U-

TELEPHONE: (212) 708-1800 TELEFAX: (212) 246-8959 TELEX: 233288 INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: 1: 10 bases nucleic acid

The sequence is listed from 3' to 5' left to right and this is a part of SEQ ID NO:4. Score 6.8; DB 1; Length 10; Pred. No. 1e+02; 0; Mismatches 2; Indels 30.9%; Ouery Match
Best Local Similarity 80.v
Best Local 8; Conservative OTHER INFORMATION: COTHER INFORMATION: US-07-949-541A-13

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Gaps

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| Sequence 4, Application US/0808658
| Patent No. 5641625
| GENERAL INFORMATION:
| APPLICANT: Ecker, David J. |
| APPLICANT: Benchardt, Ole |
| APPLICANT: Bench, Michael |
| APPLICANT: Berg, Rolf H. |
| APPLICANT: Miles |
| AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
STREBT: One Liberty Place - 46th Floor
CIIX: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                         Patent No. 5612455
; Patent No. 5612455
; GENERAL INFORMATION:
APPLICANT: HOEY, Timothy
TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,479B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION ...
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59450-1/RAO
TELEPHONE: (415) 494-870
TELEPHONE: (415) 494-871
TELEPKX: 210 27729
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                    Application US/08396479B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.9
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               732 GGAGAAACAG 741
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RESULT 161
US-08-396-479B-16
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US-08-658-4
                                                                                    Sequence 16,
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; Sequence 15, Application US/08818823
; GENERAL INFORMATION:
; APPLICANT: HOEY, Timothy
; TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY
; CORRESPONDENCE ADDRESSE: 18
; CORRESPONDENCE ADDRESSE: ADDRESSES: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURITY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,823
FLING DATE: 14-MAR.1997
CLASSIFICATION 1536
PRIOR APPLICATION NUMBER: 08/396,479
FILING DATE: 02-MAR.1995
ATONEY/AGENT INPORMATION:
NAME: COMMAN ALCHARCH
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REBERENCE/DOCKET NUMBER: 36,627
TELECOMMUNICATION INPORMATION:
                                                                   CURRATION SYSTEM: E-LOSYMS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATY APPLICATION DATA:
APPLICATION NUMBER: US/08/088,658
FILING DATE: 19930702
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: 08/054,363
APPLICATION NUMBER: 08/054,363
APPLICATION NUMBER: 18.0 19.3
APPLICATION NUMBER: 18.0 19.3
ATTORNEY/AGNIT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 1SIS-1052
TELECOMMUNICATION NUMBER: 1SIS-1052
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 15.5 68-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 10.0 580 1D NO: 4:
SEQUIENCE CHARACTERISTICS:
                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 210 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80...
Best Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         736 AAACAGAACA 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-088-658-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415)
MEDIUM TYPE:
COMPUTER: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-818-823-16
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US-08-847-108-49
Sequence 49, Application US/08847108
Sequence 49, Application US/08847108
Patent No. 5736336
TITLE OF INVENTION: Binding Affinity, Sequence Specificity
TITLE OF INVENTION: Binding Affinity, Sequence Specificity
Patent No. 5736336
TITLE OF INVENTION: And Solubility
NUMBER OF SEQUENCES: 53
CORRESPONDENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5736336ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                              APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5719262ris LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                   STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: WORDFREECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,484
FILING DATE: 24-UUL-1996
CLASSIFTCATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY AGBUT INFORMATION:
NAME: MIChael P. Straher
REGISTRATION NUMBER: 38,325
REFREENCE/DOCKET NUMBER: 181S-2270
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3439
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/847,108
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   736 AAACAGAACA 745
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                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 164

US-08-686-116A-49

Sequence A application US/08686116A

Patent No. 5/14331

GENERAL INFORMATION:

PAPLICANT: Buchardt et al.

TITLE OF INVENTION: Binding Affinity, Sequence Specificity

TITLE OF INVENTION: ans Solubility

NUMBER OF SEQUENCES: 53

CORRESONDENCE ADDRESS:

ADDRESSER: WoodCock Washburn Kurtz Mackiewicz & No. 5714331ris illy

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STREET: One Liberty Place - 46th Floor

CITY: Bhiladelphia

STREET: One Liberty Place - 46th Floor

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

STREET: WoodCock Washburn Kurtz Mackiewicz & No. 5714331ris illy

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STREET: One Liberty Place - 46th Floor

COUNTRY: U.S.A.

COUNTRY: U.S.A.

STREET: One Liberty Place - 46th Floor

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STREET: One Liberty Place - 46th Floor

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STREET: ONE WOODCETTURE WINDER: US-051

FILING DATE: 22-NOV-193

ATTORNEY/AGENT INFORMATION:

RESISTRATION NUMBER: 181-2271

PRICE RESISTRATION NUMBER: 181-2271

PRICE RESISTRATION NUMBER: 181-2271

PRICE RESISTRATION NUMBER: 181-2271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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Pred. No. 1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                         Score 6.8; DB 1; Length 10;
Pred. No. 1e+02;
0; Mismatches 2; Indels
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US-08-685-484-49
Sequence 49, Application US/08685484
, Patent No. 5719262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAK: 215-568-3439
INPORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.9%;
                                                                                                                                                                               Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPDLOGY: linear
MOLECULE TYPE: CDNA
US-08-818-823-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
US-08-686-116A-49
                                                                                                                                                                                                                                                                                                    732 GGAGAAACAG 741
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Best Local Similarity
Matches 8; Conserva
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| Sequence 49, Application US/08847095A
| Patent No. 5786461
| GENERAL INFORMATION:
| APPLICANT: Buchardt et al.
| TITLE OF INVENTION: Side Chains
| TITLE OF INVENTION: Side Chains
| NUMBER OF SEQUENCES: 53
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5786461ris LLP
| STREET: One Liberty Place - 46th Floor
| CITY: Philadelphia
                                                                                    Gaps
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US-08-465-590-148
; Sequence 149, Application US/08465590
; Patent No. 5824770
; Patent No. 5824770;
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
                                           30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.9%; Score 6.8; DB 1; Length 10;
80.0%; Pred. No. 1e+02;
tive 0; Mismatches 2; Indels
                                                                                    Mismatches
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ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORZHERECT 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,095A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFRENCE/DOCKET NUMBER: ISIS-2270
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,484
FILING DATE: 24-JUL-1996
APPLICATION NUMBER: 08/108,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INPERMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 30.9
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                             736 AAACAGAACA 745
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-847-095A-49
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                                         Query Match
Best Local Similarity
Matches 8; Conserv
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CLASSIFICATION:
  US-08-686-113A-56
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Patent No. 5766855
GENERAL INFORMATION:
TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
TITLE OF INVENTION: Affinity And Sequence Specificity
TITLE OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5766855ris
STREET: One Liberty Place - 46th Floor
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Pred. No. 1e+02;
0; Mismatches 2; Indels
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER. IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,113A
FILING DATE: July 24, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
RESISTRATION NUMBER: 181S-2273
TELECOMMUNICATION NUMBER: 181S-2273
TELECOMMUNICATION NUMBER: 181S-2273
TELEFAX: 215-568-3100
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   ISIS-2271
               CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straha:
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: 1SIS-227
TELEPHONE: 215-568-3439
INFORMATION FOR SEQ ID NO: 49:
ELEPAX: 10 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-847-108-49
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US-08-686-113A-56
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Gaps
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Pred. No. 1e+02;
0; Mismatches 2; Indels
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US-08-173-489C-67
| Sequence 67, Application US/08173489C
| Patent No. 5861244
| GENERAL INFORMATION:
| APPLICANT: WANG, C. -G.
| APPLICANT: WANG, C. -G.
| TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
| NUMBER OF SEQUENCES: 365
| CORRESPONDENCE ADDRESS: ADDRESSE: PROFILE DIAGNOSTIC SCIENCES, INC.,
| STREET: 510 EAST 73RD STREET,
| CITY: NEW YORK |
| STREET: NEW YORK |
| STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDION TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1 BM PCXTYAT
COPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Worldperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 DCT 1992
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 DCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 246-8959
INFORMATION POR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: esterage D gene (Accession # M13450)
DESCRIPTION: esterage D gene (Accession # W13750)
                                                                           NAME: MAYIELD, Defise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTDAL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (214) 740-8800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative (
FILING DATE: 03-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     729 CCAGGAGAAA 738
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US-08-808-474A-4

Sequence 4, Application US/08808474A

Sequence 4, Application US/08808474A

Patent No. 5856103

GENERAL INFORMATION:
APPLICANT: Gray, Donald M.
APPLICANT: Gray, Donald M.
TILLE OF INVENTION: METHOD FOR SELECTIVELY RANKING SEQUENCES
TITLE OF INVENTION: FOR ANTISENSE TRRGETING
TITLE OF INVENTION: FOR ANTISENSE TRRGETING
CORRESPONDENCE ADDRESS:
ADDRESSEE: Locke Purnell Rain Harrell
STREET: 2200 Ross Avenue, Suite 2200
CITY: Dallas
STATE: Texas
COUNTRY: USA
COUNTRY: USA
COMPUTER READBRIE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: EMADRIES: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/808,474A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                 COMPUTER REALBLE FORM:

MEDIUM TYPE: Floppy disk
COMPOTER: IBM FC compatible
COMPOTER: IBM FC compatible
COMPOTER: IBM FC compatible
CORPOTER: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/465,590
FILING DATE: 05-UN-1995
PRIOR APPLICATION DATA:
PRING APPLICATION NAMER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NAMER: US 08/238,212
FILING DATE: 14-SEP-1993
PRIOR APPLICATION NAMER: US 07/946,233
FILING DATE: 14-SEP-1993
PRIOR APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATPORMATION: UNMBER: 35,695
RESTERNEY POOKET NUMBER: 35,695
RESTERNEY COKET NUMBER: 35,695
RESTERNEY (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SED ID NO: 148:
SEQUENCE CHARACTERISTICS:
LO DASS PAIRS
                                       ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUCETTS
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      731 AGGAGAACA 740
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US-08-465-590-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Query Match 30.9%; Score 6.8; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 1e+02; Matches 8; Conservative 0; Mismatches 2; Indels
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in E coli
. Nature
                                                                                                                                                                                                                                                                                                                                            Sequence 151, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C.-G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                      72 : FROM 1 TO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET; 510 EAST 73RD STREET, CITY: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: hepatitis B virus ayw isolate,
DESCRIPTION: nucleotides 807 to 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 12.
PRIOR APPLICATION BUTA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTONEY/AGENT INPORMATION:
NAME: Handelman, Joseph H.
RECISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U5518-6
TELECOMMUNICATION INFORMATION:
TELEPAX: (attorney) (212) 246-8959
INPORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 18M PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFFORTION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS: Galibert, F, Mandart, E, AUTHORS: Tiollais, P, Charnay, P. TITLE: Nucleotide sequence of the
               RELEVANT RESIDUES IN SEQ ID NO:
US-08-173-489C-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Hepatitis B virus INDIVIDUAL ISOLATE: avw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                          734 AGAAACAGAA 743
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                     US-08-173-489C-151/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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DESCRIPTION: third strand derived from esterase D
DESCRIPTION: sequence region in Seq ID No. 586124471
HYPOTHETICAL: Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 72, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
     ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 13
MAP POSITION: 13q14.1-q14.2
PUBLICATION INFORMATION:
AUTHORS: Lee, E Y H P, Lee, W H.
TITLE: Molecular cloning of the
TITLE: human esterase D gene, a genetic marker of
TITLE: retinoblastoma
                                                                                                                                                                                                                                                                                                                 DATE: 1986
RELEVANT RESIDUES IN SEQ ID NO: 67 :FROM 1 TO 10
US-08-173-489C-67
                                                                                                                                                                                                         Proceedings of the National Academy of Sciences, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET; S10 EAST 73RD STREET, CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 18M PC/XI/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOSTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION APA:
APPLICATION APA:
APPLICATION APA:
APPLICATION APA:
APPLICATION OF 436
FILING DATE: 2 DGC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY AGENT INFORMATION:
NAME: Handelman, Joseph H.
REFERENCE/DOCKET NUMBER: U56.179
REPERENCE/DOCKET NUMBER: U56.179
REPERENCE/COMPUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (attorney) (212) 246-8959
INPORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
LENGTH: 10 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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MEDIUM TYPE: 3.5 incl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 172
US-08-173-489C-72/c
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                                                                                                                                                                                                                        JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Gaps

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Query Match 30.9%; Score 6.8; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 1e+02; Matches 8; Conservative 0; Mismatches 2; Indels
       ; RELEVANT RESIDUES IN SEQ ID NO: 175 :FROM 1 TO 10 US-08-173-489C-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT

OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordpoerfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/ABGIT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REPRENCE/DOCKET NUMBER: U9518-6
TELECHONE: (attorney) (212) 708-1880
TELECHONE: (attorney) (212) 708-1880
TELECHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 205: SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: hepatitis B virus adr isolate,
DESCRIPTION: hepatitis B virus adr isolate,
HYPOTHETICAL: no
                                                                                                                                                                                            734 AGAAACAGAA 743
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                                                                                                                                                                                                                                                                                                        RESULT 174
US-08-173-489C-175
i Sequence 175, Application US/08173489C
j Patent NO. 5861244
j GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
INVERTOR SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET, STO BAST 73RD STREET,
CITY: NEW YORK
STREET: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Heparitis B virus
INDIVIDUAL ISOLATE: adw2
INDIVIDUAL ISOLATE: adw2
AUTHORS: Valenzuela, P, Quiroga, M, Zaldivar, J, AUTHORS: Valenzuela, P, Ruter, W J.
TITLE: The nucleotide sequence of
TITLE: the Heparitis B viral genome and the
TITLE: identification of the major viral genes
JOURNAL: Jaenisch, R, Fox C F eds
VOLUME:
PAGES: 57-70
DATE: 1980
; RELEVANT RESIDUES IN SEQ ID NO: 151 :FRCM 1 TO 10 US-08-173-489C-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: hepatitis B virus adw2 isolate,
DESCRIPTION: nuclectides 563 to 572
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPER: 3.5 inch, 1.44Mb storage COMPUTER: IBM PC/XY/AT OPERATING SYSTEM: Mordperfect Version 6.2 SOFTWARE: Wordperfect Version 5.1 CSOFTWARE: Wordperfect Version 5.1 CSOFTWARE: Wordperfect Version 5.1 CSOFTWARE: Wordperfect Version 5.1 CHING DATE: 2 DEC 1993

FILING DATE: 2 DEC 1993

FILING DATE: 2.9 OCT 1992

ATTORNEY/AGENT INFORMATION: NAME: Handelman, Joseph H. REGISTRATION NUMBER: U9518-6

TELEPHONE: (attorney) (212) 708-1880

TELEPHONE: (attorney) (212) 708-1880

TELEPHONE: (attorney) (212) 246-8959

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYRE: nucleic acid

STRANDEDNESS: double stranded
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10 AGAAGAAGAA 1
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AWIT-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Hepatitis B virus
ORGANISM: Hepatitis B virus
INDIVIDUAL ISOLATE: adr
PUBLICATION INFORMATION:
AUTHORS: Pujiyama, A, Miyanohara, A, No. 5861244aki, C,
AUTHORS: Toneyama, T., Ohromo, N, Matsubara, K.
TITLE: analysis of Hepatitis B virus DNAs subtype adr
JOURNAL: Nucleic Acids Research
VOLUME: 11
PAGES: 4601-4610 Sequence 205, Application US/08173489C

Fatent No. 5861244

GENERAL INFORMATION:

APPLICANT: WANG, C. -G.

APPLICANT: HEPBURN, A. G.

TITLE OF INVENTION: TRIPLE-STRAND FORMATION.

NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS:

ADDRESSEE: STO EAST 73RD STREET,

CITY: NEW YORK

STATE: NEW YORK DATE: 1983 ; RELEVANT RESIDUES IN SEQ ID NO: 205 :FROM 1 TO 10 US-08-173-489C-205

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                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: O'Malley, David M.
APPLICANT: Scderoff, Ronald R.
APPLICANT: Grattapaglia, Dario
APPLICANT: Grattapaglia, Dario
APPLICANT: Brillip Wilcox
APPLICANT: Hillip Wilcox
TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Siblev
STREET: Post Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                              Score 6.8; DB 1; Length 10;
Pred. No. 1e+02;
                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDTUM TYPE: FILIPOPY disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PATENTIN PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545,253A

FILING DATE:

CLASSIFICATION: APPLICATION: APPLICATION: APPLICATION NUMBER: US/08/545,253A
                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-281
TELECOMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEPHONE: (919) 881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/08471907A; Patent No. 5986053
                                                                                                                                                                                                                                                                                                                                                                                   US-08-545-253A-5
; Sequence 5, Application US/08545253A
; Patent No. 5908978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Charlotte
STATE: No. 5908978th Carolina
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 575102
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                    30.9%;
80.0%;
                                                           Query Match
Best Local Similarity 80.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.9
Best Local Similarity 80.0
Matches 8; Conservative
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lin
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US-08-286-819A-48
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US-08-471-907A-4
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Sequence 48 Application US/0826819A

Sequence 48 Application US/0826819A

Sequence 48 Application US/0826819A

Setting 1900

APPLICANT: APTHUR

APPLICANT: DUKTA-MALEN, STLVIE

APPLICANT: MOLINAS, CATHERINE

TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE

TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

NUMBER OF SEQUENCE SIS 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STRATE: Virginia

STRATE: Virginia
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                                                                                             Gaps
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                               Score 6.8; DB 1; Length 10;
Pred. No. 1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819A
FILING DATE: 08-AUG 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 29-OCT-1991
FILING DATE: 29-OCT-1991
FILING DATE: 29-OCT-1991
FILING APPLICATION NUMBER: RESOLDS PRIOR APPLICATION NUMBER: PTILING DATE: 29-OCT-1991
FILING DATE: 29-OCT-1991
FILING DATE: 31-OCT-1990
CLASSIFICATION NUMBER: RESOLDS PRIOR APPLICATION NUMBER: RESOLDS PRIOR APPLICATION NUMBER: RESOLDS PRIOR APPLICATION NUMBER: GO-060-0 PCT
FILING DATE: 31-OCT-1990
CLASSIFICATION NUMBER: 660-060-0 PCT
TELESSIFICATION NUMBER: 660-060-0 PCT
TELESSIFICATION NUMBER: 660-060-0 PCT
TELESSIFICATION NUMBER: CASSIFICATION NUMBER: CASSIFICATI
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                               Query Match 30.9%;
Best Local Similarity 80.0%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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Score 6.8; DB 1; Length 10;
Pred. No. 1e+02;
0; Mismatches 2; Indels
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/NS-DOS
SOFTHANS: IEM PC-DOS/NS-DOS
SOFTHANS: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,353
FILING DATE: 14-FEB-1995
CLASSIFCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELEFAX: 0510 NO. 73.
TELEFAX: (516) 742-436
TELEFAX: (516) 742-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  728 GCCAGGAGAA 737
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                                      APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Ole
APPLICANT: Benolm, Michael
APPLICANT: Nelsen, Peter E.
APPLICANT: Nelsen, Peter E.
APPLICANT: Milegaard, Niels E.
TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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US-08-388-353-73
i Sequence 73, Application US/08388353
j Patent No. 6010895
i GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Nicholas J.
APPLICANT: Crowe, Suzanne
APPLICANT: Croper, David
ITILE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
CORRESPONDENCES: 800
CORRESPONDENCES: Scully, Scott, Murphy & Presser
STREE: ADDRESSE: ADDRESS:
CITY: Garden City Plaza
CITY: Garden City
STATE: New York
COUNTY: United States
ZIP: 11530
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Philadelphia
CITY: Philadelphia
COUTRY: U.S.A.
ZUDIR: PA
COUTRY: U.S.A.
ZUP: 19103
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION:
APPLICATION:
APPLICATION NUMBER: 08/088,658
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Pred. No. 1e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Luccl, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPKX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Best Local Similarity 80.0%;
Matches 8; Conservative
                   Ecker, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          736 AAACAGAACA 745
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Gaps .; 0

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US-UB-188-19-1/b

Sequence 175, Application US/08388353
Fatent No. 6010855
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: McPhee, Dale A.
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STREET: New York
COUNTRY: United States
COMPUTER: New York
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: 1230
COMPUTER: 18M PC COMPANIAN:
MEDIUM TYPE: 14-FEB-1995
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: STATES
FILLEADONE: (516) 743-4443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR ESQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
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APPLICANT: ARTHUR. MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: OCURVALIN
APPLICANT: OCURVALIN
APPLICANT: OCURVALIN
APPLICANT: OCURVALIN
APPLICANT: OCURVALIN
APPRICE
TITLE OF INVENTION: IN GRAM-FOSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS: 54
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02; tive 0; Mismatches 2; Indels
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                         APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
AUGHER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States

ZIP: 11330

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353

FILING DATE: 14-FEB-1995

CLASSIFICATION: 424
                                                                                                                                                                                                                                                          ADDRESSEE: Scuily, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 48, Application US/08980357
Patent No. 6013508
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: DNA (genomic)
US-08-388-353-187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (516) 742-4343
TELERX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 18'
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      732 GGAGAAACAG 741
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGAGGAAGAG 10
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1755 S.
CITY: Arlington
STATE: Virginia
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-980-357-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
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                                                                                                                                                                      Score 6.8; DB 1; Length 10; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: ULLICAL

ZUP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMB PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/388,353
FLING DATE: 14 FPB-195
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAMME: DIGIGALON: PRANK S.
REGISTRATION NUMBER: 9606
TELERENCE/DOCKET NUMBER: 9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States
                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 186, Application US/08388353; Patent No. 6010895
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US-08-388-353-187
; Sequence 187, Application US/08388353
; Patent No. 6010895
                                                            TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) MOLECULE TYPE: DNA (genomic)
US-08-388-353-186
                                                                                                                                                                                Query Match 30.9%;
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731 AGGAGAAACA 740
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30.9%; Score 6.8; DB 1; Length 10;
80.0%; Pred. No. 1e+02;
tive 0; Mismatches 2; Indels
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,551B
FILING DATE: US-0.00.1955

PRIOR APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994

APPLICATION NUMBER: PM002 (AU)
FILING DATE: 23-DEC-1994

APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994

APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995

APPLICATION NUMBER: US 08/388,353
FILING DATE: 17-MAY-1995

ATTORNEY, AGENT INFORMATION:
NAME: FRANK S. DIGIGILO

REFERENCE/DOCKET NUMBER: 9606Z

TELECOMOVICATION INFORMATION:
TELEPHONE: (516) 742-4343

TELEPHONE: (516) 742-4346

INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           728 GCCAGGAGAA 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-488-5518-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-488-551B-175
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   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
                                                                                                                                                                                                                                     FILLING DATE:

CLASSIFICATION:

RELIGATION DATA:

APPLICATION NUMBER: US 08/286,819

FILLING DATE: 28-DEC-1993

PRICA APPLICATION NUMBER: US 08/174,682

FILLING DATE: 28-DEC-1993

FRICA APPLICATION DATA:

APPLICATION NUMBER: US 07/917,146

FILLING DATE: 10-AGC-1992

PRICA APPLICATION DATA:

APPLICATION NUMBER: PCT/FR/91/00855

FILLING DATE: 28-OCT-1991

PRICA APPLICATION DATA:

APPLICATION NUMBER: FR 9013579

FILLING DATE: 31-OCT-1991

PRICA PRICATION NUMBER: FR 9013579

FILLING DATE: 31-OCT-1991

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 2200

TELEFAX: (703) 413-220

TELEFAX: (703) 413-2220

TELEFAX: (703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: RBS
LOCATION: 1..10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-980-357-48
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Gaps

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US-084-88-51B-175

Sequence 175, Application US/08488551B

Patent No. 6015661

APPLICANT: Nicholas J. Deacon
APPLICANT: Daid A. McPhee
APPLICANT: Daid A. McPhee
APPLICANT: Daid A. McPhee
APPLICANT: Daid Cooper
ITILE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GABDEN CITY PLAZA
CITY: GARDEN CITY
STREET: 400 GABDEN CITY PLAZA
CITY: GARDEN CITY
STREET: US-029
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PARABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BRADABLE FORM:
APPLICATION NUMBER: W4002 (AU)
FILING DATE: 21-FBB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FBB-1994
APPLICATION NUMBER: PM3024 (AU)
FILING DATE: 21-FBB-1994
APPLICATION NUMBER: US-08938333
FILING DATE: 14-FBB-1995
APPLICATION NUMBER: US-089383353
FILING DATE: US-0895
APPLICATION NUMBER: US-089383333
FILING DATE: US-089364
APPLICATION NUMBER: US-089364
APPLICATION UMBER: US-089364
APPLICATION UMBER: US-089364
APPLICATION UMBER: US-089364
APPLICATION U
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RESULT 184

US-08-488-551B-73

Sequence 73. Application US/08488551B

Patent No. 6015661

GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: CORRESONDENCES: 841
CORRESONDENCES: 841
CORRESONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
CONTRY: GARDEN CITY
CITY: GARDEN CITY
COMPITER: NEW YORK
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25

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Mon Oct 18 14:40:09 2004

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                                                                                          Query Match 30.9%; Score 6.8; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 1e+02; Matches 8; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 187, Application US/08488551B
Patent No. 601561
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR PEPLICATION NUMBER: PM3864 (AU)
PILING DATE: 14-FBB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FBB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 33-BC-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 14-FBB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: 9606Z
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGILO
REFERENCE/DOCKET NUMBER: 9606Z
TELESHONE: (516) 742-4343
TELESHONE: (516) 742-4343
TELESHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 base pairs
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         ; MOLECULE TYPE:
US-08-488-5518-186
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US-08-488-551B-187
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STATE: WEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,531B
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PW4002 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/388,353
FILING DATE: 17-MAY-1995
ATTACKNEY/AGENT NUMBER: 9606Z
TELECOMMUNICATION INPORMATION:
MATE: PERANK S. DIGIGLION
MATE: PERANK S. DIGIGLION
MATE: PERANK S. DIGIGLION:
MATE: PERANK S. DIGIGLION
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PATENT NO. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
30.9%; Score 6.8; DB 1;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGICLIO
REFERENCE/DOCKET NUMBER: 96065
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS; single
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INFORMATION FOR SEQ ID NO: 186
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: lines-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 AGAAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGAAGCACAA 10
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US-08-488-551B-175
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WESULT 190

US-08-724-466B-26

i Sequence 26, Application US/08724466B

i Sequence 26, Application US/08724466B

i Patent No. 6063606

GENERAL INFORMATION:

APPLICANT: Petkovich, P. Martin, White, Jay A.,

APPLICANT: Beckett, Barbara R., Jones, Glenville

TITE OF INVENTION: Retinoid Metabolizing Protein

NUMBER OF SEQUENCES:

ADDRESSEE: Blake, Cassels & Graydon

STREET: Box 25, Commerce Court West

CITY: Toronto

ZIP: M5L 1A9

COMPUTES: Canada

COMPUTES: COMPATE: Compatible

OPERATION NUMBER: US/08/724,466B

FILING DATE: October 1, 1996

PRICATION NUMBER: 316,244

REGISTRATION NUMBER: 36,424

REGISTRATION NUMBER: 36,424

REFERENCE/DOCKET NUMBER: 50727/00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 10;
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                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMP PC compatible
COMPUTER: EMP PC compatible
COMPUTER: EMP PC compatible
COMPUTER: BMP PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,337
FILING DATE: 25-SEP-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/184,567
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REBERBINGE/DOCKET NUMBER: 5051-247
TELEFPHONE: (919) 881-3175
TELEFPHONE: (919) 881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.9%; Score 6.8; DB 1;
80.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 50767/00004 TELECOMMUNICATION:
STATE: No. 6054634th Carolina COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 575102
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDENBES: single
TOFOLLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Patent No. 6054634

GENEAL INFORMATION:
APPLICANT: O'MAILEY, David M.
APPLICANT: Sederoff, Ronald R.
TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
NUMBER OF SEQUENCE: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenneth D. Sibley
STREET: Post Office Drawer 34009
CITY: Charlotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1 _ NOTE= "AT THE TERMINUS IS AN AMINOHEXYL OTHER INFORMATION: ALKYLATED GROUP"
US-08-993-303-2
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80.0%; Pred. No. 1e+02;
iive 0; Mismatches 2; Indels
      COUNTRY: USA

ZIP: 2000-5701
COUNTRY: USA

ZIP: 2000-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,303
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERMAN, Richard B.
REGISTRATION NUMBER: 99.107
REFERENCE/DOCKET NUMBER: 99.107
REFERENCE/DOCKET NUMBER: 91614-7082
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LEMGTH: 10 base pairs
TYPE: nuclaic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "OLIGODEOXYRIBONUCLEOTIDE"
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Best Local Similarity 80.0
Matches 8; Conservative
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US-08-719-337-5
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APPLICANT: No. 6228982den, Benget
APPLICANT: No. 6228982den, Benget
APPLICANT: Wittung, Pernilla
APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Egholm, Michael
APPLICANT: Egholm, Michael
APPLICANT: Berg, Rolf
ITILE OF INVENTION: Double-Stranded Peptide Nucleic Acids
FILE REPRENCE: ISISIL108
CURRENT APPLICATION NUMBER: US/08/086,661F
CURRENT FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR FILING DATE: 1993-04-26
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.9%; Score 6.8; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 1e+02; Matches 8; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                  NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUTCATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPRAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 148:
                          FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
            APPLICATION NUMBER: 08/238,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/08088661F Patent No. 6228982
                                                                                                                                                                                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.vv,
and 8; Conservative
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US-08-088-661F-30
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TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
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APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: NIGAM, SANJAY KUMAR
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
FILE REFERENCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 121
LENGTH: 10
                                                                                                                                                                                                            30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Unknown Organism: Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/711,417C
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-711-417C-148
; Sequence 148, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-522-384-121/c
; Sequence 121, Application US/08522384
; Patent No. 6110667
TELEFAX: (416) 863-2653

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-724-466B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
                                                                                                                                                                                                            Query Match 30.9
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                      727 TGCCAGGAGA 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           728 GCCAGGAGAA 737
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US-08-522-384-121
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; OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence
US-08-088-661F-20
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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0
      gequence 30, Application us/Obsessif
patent No. 6289832
GENERAL INFORMATION:
APPLICANT: No. 628982den, Benget
APPLICANT: No. 628982den, Benget
APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Ole
APPLICANT: Berg Rolf
APPLICANT: Berg Rolf
TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
FILE REFERENCE: ISISINOB
CURRENT APPLICATION NUMBER: US/O8/O88,661F
CURRENT APPLICATION NUMBER: US/08/088,61F
FILE REFERENCE: ISISINOB
FILENCE APPLICATION NUMBER: DO/O2
PRIOR FILING DATE: 1993-04-26
PRIOR FILING DATE: 1993-04-26
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 30
LENGTH: 10
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Pred. No. 1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        30.9%; Score 6.8; DB 1; Length 10;
80.0%; Pred. No. 1e+02;
tive 0; Mismatches 2; Indels
Sequence 30, Application US/08088661F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.9%;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80...
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Primer US-09-245-041-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       734 AGAAACAGAA 743
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US-08-882-164D-26
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Sequence 26, Application US/08692164D

PREERIN NO. 6350241

APPLICANT: Bethoria, P. Martin, White, Jay A.;
APPLICANT: Bethoria, P. Martin, White, Jay A.;
APPLICANT: Bethoria, B., Jones, Johnshing Protein,
COMESSANDENCE, Barbara E., Jones, Johnshing Protein,
COMESSANDENCE ADDRESS:
ADDRESSES Blake, Casels & Graydon
STREET: Box 25, Commerce Court West
COMPUTER: CORPOY, IBM PC Compatible
COMPATIBLE
COMPUTER: CORPOY, IBM PC COMPATIBLE
COMPUTER: REALCALION DATA:
COMPUTER: REALCALION DATA:
COMPUTER: CORPOY, IBM COMPATIBLE
COMPUTER: COMPATIBLE
COMPUTER: COMPATIBLE
COMPUTER: COMPATIBLE
COMPUTER: COMPUTER: COMPATIBLE
COMPUTER: CO
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Sequence 14, Application US/08150156A

Sequence 14, Application US/08150156A

Sequence 14, Application US/08150156A

Parent No. 6357163

Farent No. 6357163

TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES NUMBER OF SEQUENCES: 40

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: THY PC Compatible

COMPUTER: THY PC Compatible

COMPUTER: THY PC Compatible

COMPUTER: THY PC Compatible

COMPUTER: FIRM PC Compatible

COMPUTER: FIRM PC COMPATIBLE

COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE USE OF NUCLEIC ACID ANALOGUES IN DIAGNOSTICS AND ANALYTICAL PROCEDURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.9%; Score 6.8; DB 1; Length 10;
80.0%; Pred. No. 1e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
PUBLICATION INFORMATION:
DOCUMENT: NUMBER: WO PCT/EP92/01220
US-08-150-156A-14
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,156A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/150,156A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: THE USE OF NUCLE
TITLE OF INVENTION: DIAGNOSTICS AND
NUMBER OF SEQUENCES: 40
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
PILING DATE: 24-MAY-1991
PRIOR APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
FILING DATE: 24-MAY-1991
FILING DATE: 24-MAY-1991
PRIOR APPLICATION NUMBER: DK 0510/92
FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 200
US-08-150-156A-17/c
; Sequence 17, Application US/08150156A
; Patent No. 6357163
; APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.9
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            736 AAACAGAACA 745
1 AAAAACAAAA 10
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TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
NUMBER OF SEQUENCES: 40
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: OCOMPAS:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: US/08/150,156A
SOFWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DX 0987/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DX 0510/92
FILING DATE: 12-ARY-1991
APPLICATION NUMBER: DX 0510/92
FILING DATE: 12-ARY-1991
APPLICATION NUMBER: DX 0510/92
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH 10 base pairs
TYPE: NUCLEIC acid
STREE CHARADENESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 30.9%; Score 6.8; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 1e+02; Matches 8; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/EP92/01220
FILING DATE: 22-MAY-1992
US-08-1564-5
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/EP92/01220
US-08-150-156A-6
                       PRIOR APPLICATION DATA:
APPLICATION WOMER: DK 0510/92
FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 198
US-08-150-156A-6
; Sequence 6, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE; DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
  FILING DATE: 24-MAY-1991
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Pred. No. 1e+02;
0; Mismatches 2; Indels
            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MIDIUM TYPE: Floppy disk
MIDIUM TYPE: Floppy disk
COMPUTER: IEM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,834C
FILING DATE: 19-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 US-08-618-834C-45

Sequence 45, Application US/08618834C

Sequence 45, Application US/08618834C

Patent No. 6361937

GENERAL INFORMATION:

APPLICANT: Stryer, Lubert

TITLE OF INVENTION: Computer-Aided Nucleic Acid

TITLE OF INVENTION: Sequencing

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ritter, Van Pelt & Yi LLP

STREET: 4906 El Camino Real, Suite 205

CITY: Los Altos

STATE: CA
            ..
            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08108591B
Patent No. 6395474
GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Baholm, Michael
APPLICANT: Nelsen, Peter Eigil
APPLICANT: Nelsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TILLE OF INVENTION: Peptide Nucleic Acids
FILE REPERENCE: ISISOS40
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CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
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ATTORNEY/AGENT INFORMATION:
NAME: Ritter, Michael J.
REGISTRATION NUMBER: 36,653
REFERENCE/DOCKET NUMBER: AFF)
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-903-3501
TELEFAX: 650-903-3501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.9%;
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            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                         738 ACAGAACACC 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: LOS
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 203
US-08-108-591B-8
            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 6.8; DB 1; Length 10;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTEXT: USA
CONTEXT: USA
CONTEXT: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,834C
FLING DATE: 19-MR-1996
CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: SISSION OF FRIENDED FROM THE STATE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-618-834C-33
; Sequence 33, Application US/08618834C
; Sequence 33, Application US/08618834C
; Patent No. 6361937
; GENERAL INFORMATION:
; APPLICANT: Stryer. Lubert
; TITLE OF INVENTION: Computer-Aided Nucleic Acid
; TITLE OF INVENTION: Sequencing
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; CITY: CANTER C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/EP92/01220
FILING DATE: 22-MAY-1992
APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0510/92
FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.9%;
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Best Local Similarity
Matches 8, Conserva
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Best Local Similarity
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US-08-618-834C-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-150-156A-17
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Score 6.8; DB 1; Length 10;
Pred. No. 1e+02;
0; Mismatches 2; Indels
                                                                                                                                                          RESULT 206
US-08-108-591B-15/C
| Sequence 15, Application US/08108591B
| Patent No. 6395474
| GENERAL INFORMATION:
| APPLICANT: Buchard: Michael
| APPLICANT: Beloam, Michael
| APPLICANT: Berg, Rolf Henrik
| TILE OF INVENTION: Peptide Nucleic Acids
| FILE REFERENCE: ISISO540
| CURRENT APPLICATION NUMBER: US/08/108,591B
| CURRENT PILING DATE: 2001-08-13
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 15.
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GAPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Ole
APPLICANT: Bacholm, Michael
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Barg, Rolf Henrik
TITLE REFERENCE: IS150540
CURRENT FILING PATE: 2001-08-13
CURRENT FILIOR DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patchtin version 3:1
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y OTHER INFORMATION: No. 6395474el Sequence

US-08-108-591B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
    30.9%;
    Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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LENGTH: 10
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30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels
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; Sequence 9, Application US/08108591B
; Sequence 9, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Bacolm, Michael
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; TILE REFERENCE: ISISO540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 9
; LENGTH: 10
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GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Befolm, Michael
APPLICANT: Nelsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
ITILE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISOSA
CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENTH: 10
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US-08-108-591B-12
                                                                                                              FEATURE:
OTHER INFORMATION: No. 6395474el Sequence
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        SOFTWARE: PatentIn version 3.1 SEQ ID NO 8 LENGTH: 10 TYPE: DA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
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; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Hypothetical sequence to demonstrate application.

US-09-394-457C-7
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                                                                     30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02; tive 0; Mismatches 2; Indels
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APPLICANT: Variagenics, Inc.
TITLE OF INVENTION: A Method for Analyzing Polynucleotides
FILE REFERENCE: 246/020
CURRENT APPLICATION NUMBER: US/09/394,457C
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                           RESULT 210
US-09-154-750A-54

Sequence 54, Application US/09154750A
FREET NO. 6432640
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
APPLICANT: Kinzler, Kenneth
APPLICANT: Rolyak, Kornelia
FILE REFRENCE: 1107-7537
CURRENT APPLICATION NUMBER: US/09/154,750A
CURRENT APPLICATION NUMBER: 60/059,153
FRIOR PILING DATE: 1998-09-17
PRIOR PILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 54
LENGTH: 10
TYPE: DNA
CUSCANISM: Homo sapiens
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US-09-1394-457C-7/c
; Sequence 7, Application US/09394457C
; Patent No. 6440705
                                                                                                      Best Local Similarity 80.0
Matches 8; Conservative
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             US-09-154-750A-14
                                                                         Query Match
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Pred. No. 1e+02;
0; Mismatches 2; Indels
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US-09-154-750A-14/C
; Sequence 14, Application US/09154750A
; Patent No. 6432640
GENERAL INFORMATION:
APPLICANT: VOGEStein, Bert
APPLICANT: Kinzler, Kenneth
APPLICANT: RILISER, Kornelia
TITLE OF INVENTION: p53-Induced Apoptosis
FILE REFERENCE: 1107.7537
CURRENT APPLICATION NUMBER: 105/09/154,750A
CURRENT APPLICATION NUMBER: 60/059,153
PRIOR APPLICATION NUMBER: 60/059,153
PRIOR PILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-03-30
NUMBER: OF SEQ ID NOS: 93
SEQ ID NO 14
LENGTH: 10
SEQ ID NO 14
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LENGTH: 10
SEQ ID NO 14
CENGTH: 10
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INFORMATION FOR SEQ ID NO: 56;
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
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Best Local Similarity 80.0°
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-686-1148-56
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RESULT 208
US-08-686-114B-56
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US-09-486-853-8/c
US-09-486-853-8/c
US-09-486-853-8/c
Sequence 8, Application US/09486853
Patent No. 6461871
GENERAL INFORMATION:
APPLICANT: KUBISTA, MICKEL
APPLICANT: WESTMAN, GUNNAR
TITLE OF INVENTION: WESTMAN, GUNNAR
TITLE OF INVENTION WHERE: US/09/486,853
CURRENT APPLICATION NUMBER: US/09/486,853
CURRENT APPLICATION NUMBER: E2/05-04-05
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
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| Sequence 106, Application US/09475947A
| Patent No. 6471154
| GENERAL INFORMATION:
| APPLICANT: Marne, John D.
| APPLICANT: Minna, John D.
| TITLE OF INVENTION: FOLYMORPHIC Repeats in Human Genes
| FILE REFERENCE: US/00677
| CURRENT APPLICATION NUMBER: US/09/475,947A
| CURRENT APPLICATION NUMBER: 1999-12-31
| NUMBER OF SEQ ID NOS: 346
| SOFTWARE: Patentin Ver. 2.1
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US-09-475-947A-122/c
Sequence 122, Application US/09475947A
Ferent No. 6472154
GENERAL INFORMATION:
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Matches 8; Conservative
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731 AGGAGAAACA 740
                                                      10 AGGAGGAATA 1
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ORGANISM: human
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US-08-275-951-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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US-09-709-596A-7
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30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels
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APPLICANT: Variagenics, Inc.
APPLICANT: Variagenics, Inc.
TITLE OF INVENTION: A Method for Analyzing Polynucleotides
FILE REFERENCE: 258/239
CURRENT APPLICATION NUMBER: US/09/709,596A
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO: 17
LENGTH: 10
                                                                                                                                                           APPLICANT: Griffin, Michael
APPLICANT: Coull, James M.
APPLICANT: Coull, James M.
APPLICANT: Coull, James M.
APPLICANT: Coull, Deter
APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Ole
APPLICANT: Ducholm, Kim L.
APPLICANT: Christensen, Lein
TITLE OF INVENTON: Linked Peptide Nucleic Acids
FILE REFERENCE: ISISIS77
CURRENT APPLICATION NUMBER: US/08/275,951
CURRENT APPLICATION NUMBER: 08/108,591
PRIOR APPLICATION NUMBER: 08/088,658
PRIOR FILING DATE: 1993-07-02
PRIOR FILING DATE: 1993-07-02
PRIOR FILING DATE: 1993-07-02
PRIOR PLING DATE: 1991-05-22
PRIOR PLING DATE: 1991-05-22
PRIOR PLING DATE: 1991-05-24
PRIOR FILING DATE: 1991-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09709596A Patent No. 6458945
                              Sequence 61, Application US/08275951
Patent No. 6451968
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ORGANISM: Artificial Sequençe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                  GENERAL INFORMATION:
APPLICANT: Egholm, Michael
APPLICANT: Kiely, John
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Best Local Similarity
Matches 8; Conserva
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APPLICANT: Le Mouellic, Herve
APPLICANT: Le Mouellic, Philippe
TITLE OF INVENTION: Procedure for Specific Replacement of a Copy of a
Gene Present in the Recipient Genome by the Integration of
That Where the Integration is Made
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US-09-655-104A-7
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                                                                                                                                                                                                                                                   Score 6.8; DB 1; Length 10;
Pred. No. 1e+02;
0; Mismatches 2; Indels
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80.0%; Pred. No. 1e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Variagenics, Inc.
TITLE OF INVENTION:
FILE REPERENCE: 257/078
CURRENT APPLICATION NUMBER: US/09/655,104A
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
    PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 30
SCFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                   ) OTHER INFORMATION: tag or tag concatamer US-09-916-228-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1300 I Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-655-104A-7/c
; Sequence 7, Application US/09655104A
; Patent No. 6500650
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08301037; Patent No. 6528313; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                     30.9%;
80.0%;
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STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
Matches 8, Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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US-08-301-037-7/c
                                                                                                                                                                FEATURE:
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Sequence 7, Application US/09916228
Setent No. 6498013
GENERAL INFORMATION:
APPLICANT: Sparks, Andrew
APPLICANT: Wintler, Kenneth
APPLICANT: Wodelstein, Bert
TITLE OF INVENTION: Serial analysis of transcript expression
TITLE OF INVENTION: Serial analysis of transcript expression
FILE REFERENCE: 001107.00172
CURRENT APPLICATION NUMBER: US/09/916,228
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/221,556
PRIOR PLING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/233,431
                                                                                                                                                                                                                                                                                                                                        30.9%; Score 6.8; DB 1; Length 10;
80.0%; Pred. No. 1e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels
APPLICANT: Garner, Harold R.

APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE CANT: Minna, John D.
TITLE CEREBRICE: UTSD067
FILE REPREBRICE: UTSD067
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SSCTWARE: PatentIn Ver. 2.1
SSCTWARE: DA
LENGTH: 10
TYPE: DNA
CORGANISM: human
US-09-475-947A-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-914-259-101/c

Sequence 101, Application US/09914259

Patter No. 6495336

GENERAL NIPORMATION:
APPLICANT: MAKOWSKi, Lee

APPLICANT: HYMMAN, Paul
APPLICANT: MAILiams, Mark
ITILE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999

CURRENT APPLICATION NUMBER: US/09/914,259

CURRENT FILING DATE: 2000-11-21

NUMBER OF SEQ ID NOS: 180

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 101

LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
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US-09-916-228-7
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Sequence 53, Application US/09394455
Patent No. 6531305
GENERAL INFORMATION
Sequence 53, Application US/09394455
Patent No. 6531305
GENERAL INFORMATION
APPLICANT: Witman, George F.
APPLICANT: San Agustin, Jovenal
APPLICANT: Bas YK, John D.
TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE
FILE REPERENCE: 07917/078001
CURRENT APPLICATION NUMBER: US 60/09/394,455
CURRENT APPLICATION NUMBER: US 60/099,771
PRIOR PLILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        02356-0053-05000
                                                                FILING DATE: 13-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,679
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/596,679
FILING DATE: 19-MAR-1990
PRIOR APPLICATION NUMBER: WO PCT/FR90/00185
FILING DATE: 19-MAR-1990
PRIOR APPLICATION NUMBER: FR 8903630
PRIOR APPLICATION NUMBER: R 8903630
ATTONERY/ABROT INFORMATION:
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 02356-0053-05001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                UMBER: US 07/867,744
13-APR-1992
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US-09-508-753B-37
; Sequence 37, Application US/09508753B
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Best Local Similarity 80.0%;
Matches 8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION: 435
PRIOR APPLICATION DATA
APPLICATION NUMBER:
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CRGANISM: Homo sapiens
US-09-394-455-53
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LENGTH: 10
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Sequence 7, Application:
APPLICANT: Ballet, Philipps
APPLICANT: Ballet, Philipps
TITLE OF INVENTION: Procedure for Specific Replacement
TITLE OF INVENTION: of a Copy of a Gene Present in the Recipient Genome by the
TITLE OF INVENTION: is Made
TITLE OF INVENTION: is Made
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
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                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/301,037

FILING DATE: 06-SEP-1994

APPLICATION NUMBER: US 07/867,744

FILING DATE: 13-APR-1992

APPLICATION NUMBER: US 07/598,679

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: WO PCT/FR90/00185

FILING DATE: 19-MAR-1990

APPLICATION NUMBER: R 8903630

APPLICATION NUMBER: R 8903630

APPLICATION NUMBER: R 8903630

APPLICATION NUMBER: B 8903630

ATTORNEY/AGENT INFORMATION:

NAME: POTCE: Jane E.

REGISTRATION NUMBER: 33,332

REGISTRATION NUMBER: 33,332

REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
COUNTRY: USA
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,539
FILING DATE: 06-UUN-1995
CLASSIFICATION: 435
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301,037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/301,037
FILING DATE: 06-SEP-1994
                                                  FILING DATE: 06-Sep-1994 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELBPAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.9
Best Local Similarity 80.0
Matches 8; Conservative
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TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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                Yasuhiro FURUICHI
                                                         Yuko SHIBATA
Hiroko FUNAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               732 GGAGAAACAG 741
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US-09-508-753B-51

y Sequence 51, Application US/09508753B

y Eatent No. 6544736

general INFORMATION:
y APPLICANT: Akira SHIMAMOTO
y APPLICANT: Yashino FURUICHI
y APPLICANT: Yashino FURNICHI
y APPLICANT: Washino FURNICHI
y APPLICANT: Masanori WATAHIKI
y APPLICANT: Masanori WATAHIKI
y TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
y FILE REFERENCE: 0165/HG
current APPLICATION NUMBER: US/09/508,753B
current PILING DATE: 2000-6-16
y PRIOR APPLICATION NUMBER: US/09/508,753B
y NUMBER OF SEQ ID NOS: 472

SEQ ID NO 51

LENGHH: 10
y TURNE NUMBER: NUMBER:
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| Patent NO. 6544736
| GENERAL INFORMATION:
| APPLICANT: Akira FURMANTO|
| APPLICANT: Yasuhiro FURUICHI
| APPLICANT: Yuko SHIBATA|
| APPLICANT: Hiroko FUNAKI|
| APPLICANT: Hiroko FUNAKI|
| APPLICANT: Masanori WATAHIKI|
| TITLE OF INVENTION: Wathod for Synthesizing cDNA from mRNA sample|
| FILE REFERENCE: 00162/HG|
| CURRENT APPLICATION NUMBER: US/09/508,753B|
| PRIOR APPLICATION NUMBER: US/09/508,753B|
| PRIOR PILING DATE: 1997-09-18|
| PRIOR PILING DATE: 1997-09-18|
| NUMBER: OF SEQ ID NOS: 472|
| LENGTH: 10
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-7538-37
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30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels
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US-09-508-753B-76/c
; Sequence 76, Application US/09508753B
; Detent No. 6544736
; GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 8; Conserv
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| Sequence 133, Application US/09508753B |
| Patent No. 6544736 |
| GENERAL INFORMATION: |
| APPLICANT: Avira SHIMAMOTO |
| APPLICANT: Avira SHIBATA |
| APPLICANT: Hiroko FURNICHI |
| APPLICANT: Masanori WATAHIKI |
| FILE REPERBNCE: 00162/HG |
| CURRENT FILING DATE: 2000-06-16 |
| FRIOR PFLING DATE: 1997-09-18 |
| NUMBER OF SEQ ID NOS: 472 |
| LENGTH OF SEQ ID NOS: 473 |
| LENGTH
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APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NMERR: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
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; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-133
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                                                                   CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 131
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; Sequence 157, Application US/09508753B
; Patent No. 6544736
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
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ORGANISM: Artificial Sequence
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APPLICANT: Yasuhiro FURUICHI
YUSO SHIBATA
APPLICANT: Hiroko FURAKI
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Matches 8; Conservative
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                                    FILE REFERENCE: 00162/HG
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APPLICANT: AALTA SHIMAMOTO
APPLICANT: Yasuhiro FTRUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Eiji OHARA
APPLICANT: Eiji OHARAIKI
APPLICANT: Eiji OHARAIKI
APPLICANT: OLOGO O
APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REPERENCE: 00.0162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR PILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 82
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APPLICANT: Hiroko FUNAKI
APPLICANT: Biji OHARA
APPLICANT: Biji OHARA
APPLICANT: Masanori WATAHIKI
IIILE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
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Sequence 131, Application US/09508753B
Patent No. 6544736
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ORGANISM: Artificial Sequence
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APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
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Best Local Similarity 80.0.
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Best Local Similarity 80.0
Matches 8; Conservative
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RESULT 234

US-10-42-111-43/C

1 Sequence 43, Application US/10042111

1 Patent No. 6551476

2 GBNERAL INFORMATION:

APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES

APPLICANT: CHEN, JINGING

1 TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS

1 TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS

1 FILE REFERENCE: ref.

1 CURRENT APPLICATION NUMBER: US/10/042,111

2 CURRENT APPLICATION NUMBER: CM 99124511.3

PRIOR FILING DATE: 1999-11-09

3 NUMBER OF SEQ ID NOS: 46

3 SOFTWARE: Patentin version 3.1

3 SEQ ID NO 43

1 LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence PEATURE: PATURE: OPTHER INFORMATION: Used to demonstrate how indicated aspect of invention works. US-09-394-467-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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US-09-34467-7/c
; Sequence 7, Application US/09394467
; Patent No. 6566059
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TILLE OF INVENTION: A Method for Analyzing Polynucleotides
FILE REFERENCE: 245/287
; CURRENT APPLICATION NUMBER: US/09/394,467
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 10
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30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                               Score 6.8; DB 1; Length 10;
Pred. No. 1e+02;
0; Mismatches 2; Indels
) ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KRY: misc_feature
; CTHER INFORMATION: primer
US-10-042-111-42
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.0%;
Matches 8; Conservative (
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OTHER INFORMATION: primer
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US-10-042-111-42

Sequence 425 Application US/10042111

Patent No. 6551476

GENERAL INFORMATION:

APPLICANT: ZHEJING ACADEMY OF AGRICULTURAL SCIENCES

APPLICANT: ZHEJING ACADEMY OF AGRICULTURAL SCIENCES

APPLICANT: CHEN, Jinging

TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS

TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS

TITLE OF INVENTION NUMBER: US/10/042,111

CURRENT FILING DATE: 2002-05-08

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1

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Fatent No. 6544736

GENERAL INFORMATION:
APPLICANT: Akira SHINAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Hiroko FURATA
APPLICANT: Hiroko FURAKA
APPLICANT: Biji OHARA
APPLICANT
APPLICA
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PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 157
LENGTH: 10
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ORGANISM: Artificial Sequence
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Matches 8; Conservative
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US-09-508-753B-160
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
OTHER INFORMATION: DNA
US-09-989-789-1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-789-1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1334, Application US/09989789
Patent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.20 / 811-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085.
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APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / $11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1335
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.9%; Score 6.8; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 1e+02; Matches 8; Conservative 0; Mismatches 2; Indels
     TRIPLETS BY ZINC FINGERS
TITLE OF INVENTION: TRIPLETS BY ZINC FING FILE REPREBNCE: 8325-0011.20 / $11-US2 CURRENT APPLICATION NUMBER: US/09/989,789 CURRENT FILING DATE: 2002-03-25 NUMBER OF SEQ ID NOS: 4085 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1333 LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1335, Application US/09989789
Patent No. 6588746
                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 80.0.
".hea 8;. Conservative
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LENGTH: 10
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; OTHER INFORMATION: Hypothetical sequence to demonstrate application.
US-10-104-818-7
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US-09-989-789-1332/c
US-09-989-789-1332/c
Partent No. 6588746
GENERAL INFORMATION:
FEBTIONAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRATBLETS BY ZINC FINGERS
TITLE REPERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION: TRATBLETS BY ZINC FINGERS
TOTHER PELICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFUTANEE: ParentIn Ver. 2.0
SEQ ID NO 1332
LENGTH: 10
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; Sequence 1333, Application US/09989789
; Parent No. 5888746
; GENERAL INFORMATION;
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
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                                                                                                                                                                                                                         APPLICANT: Varigenics, Inc.

TITLE OF INVENTION: A Method for Analyzing Polynucleotides
FILE REFERENCE: 265/034
CURRENT APPLICATION NUMBER: US/10/104,818
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 09/394,774
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                sequence 7, Application US/10104818; Patent No. 6582923; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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                               10 AGGAGGAATA 1
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                                                                                                         RESULT 236
US-10-104-818-7/c
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WESULY 23-909-148

Sequence 148, Application US/09723909

Patent No. 6530441

THIRD SOURTH Georgopoulos, Katia A,

TITLE OF INVENTION:

APPLICANT: Georgopoulos, Katia A,

TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 202

CORRESPONDENCE ADDRESS:

ATTREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

STATE: MA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COURDITER: THE COUNTRY: USA

MEDIUM TYPE: Diskette

COMPUTER: THE COUNTRY: USA

SOFTWARE: TSAESQ for Windows Version 2.0b

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/711,417

FILING DATE: 02-MAY-1994

APPLICATION NUMBER: US/08/711,417

FILING DATE: 02-MAY-1994

APPLICATION NUMBER: 03/121,438

FILING DATE: 14-SEP-1993

ATTORNEY AGENT INFORMATION:

NAME: MANER INFORMATION:

NAME: MANER INFORMATION:
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                                                                                                                                                Score 6.8; DB 1; Length 10;
Pred. No. 1e+02;
0; Mismatches 2; Indels
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30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION:
TELEPHONE: 617/542-5070
TELEPRAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO: 148:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                   Query Match 30.9%;
Best Local Similarity 80.0%;
Matches 8; Conservative
  ; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Adenovirus type 2
US-09-855-159A-7
                                                                                                                                                                                                                                                  734 AGAAACAGAA 743
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APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Michael
APPLICANT: Buchardt, Michael
APPLICANT: Buchardt, Michael
APPLICANT: Beig, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids Having 2, 6-Diaminopurine Nucleobases
TITLE OF INVENTION: Peptide Nucleic Acids Having 2, 6-Diaminopurine Nucleobases
FILE REFERENCE: ISIS-3809
CURRENT FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 08/686,114
PRIOR APPLICATION NUMBER: 08/686,114
PRIOR FILING DATE: 1991-05-24
PRIOR PELING DATE: 1991-05-24
PRIOR APPLICATION NUMBER: 987/91
PRIOR PELING DATE: 1991-05-24
PRIOR APPLICATION NUMBER: 510/92
PRIOR PELING DATE: 1991-05-24
PRIOR PELING DATE: 1992-04-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 56
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09855159A
Patent No. 6620595
GENERAL INFORMATION:
APPLICANT: Cannon, Paula
APPLICANT: Barcova, Maria
TITLE OF INVENTION: Structure
FILE REFERENCE: 4-31439A/USC
CURRENT APPLICATION NUMBER: US/09/855,159A
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/203,884
PRIOR APPLICATION NUMBER: US 60/203,884
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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; OTHER INFORMATION: Description of Artificial Sequence: example target ; OTHER INFORMATION: DNA US-09-989-789-1335
                                                                                                                                                     Gaps
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                                                                                               Query Match
30.9%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels
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Pred. No. 1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-337-304-56
                                                                                                                                                                                                                                                                                                                      RESULT 241
US-09-337-304-56
; Sequence 56, Application US/09337304
; Patent No. 6613873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                 737 AACAGAACAC 746
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US-09-855-159A-7/c
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GENERAL INFORMATION:

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APPLICANT: Matteucci, Mark D.
APPLICANT: Krawczyk, Steven
TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
TITLE OF INVENTION: DUPLEX DNA
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
/note= "T-T, linking group o-xyloso (nucleotides
that have xylose sugar linked via the o-xylene
iing)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IFN PC compatible
COMPUTER: IFN PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: PCT/US91/03680
FILING DATE: 19910524
CLASSIFICATION: 435
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/note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "5-methylcytosine"
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/note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4610-0011.40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 461
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75:
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LOCATION: 10
OTHER INFORMATION: /mod_b
OTHER INFORMATION: /note=
OTHER INFORMATION: that h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFHONE: 415-327-7250
TELEFAX: 415-327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified_base
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TELEX: 706141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 8; Conserv
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Matches
                                                                                  Sequence 7, Application US/08466699
| Patent No. 6638768
| GENERAL INFORMATION:
| APPLICANT: Le Mouellic, Herve | APPLICANT: Brulet, Philippe | TITLE OF INVENTION: Procedure for Specific Replacement of a Copy | TITLE OF INVENTION: of a Gene Present in the Recipient Genome by the Integration of TITLE OF INVENTION: Different From That Where the Integration is Made | CORRESPONDENCE | CORRESPONDENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UGA
ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,699
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/301,037
FILING DATE: 06-SEP-1994
FILING DATE: 13-APR-1992
PRIOR APPLICATION NUMBER: US 07/867,744
FILING DATE: 13-APR-1992
PRIOR APPLICATION NUMBER: US 07/598,679
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/598,679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 02.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33,332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Potter, Jane E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202-408-4400
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Matches 8; Conserv
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STRANDEDNESS:
                              RESULT 244
US-08-466-699-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-466-699-7
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RESULT 246 PCT-US93-08743-148 ; Sequence 148, Application PC/TUS9308743

RESULT 245 PCT-US91-03680-75/c ; Sequence 75, Application PC/TUS9103680

10 CATGCGAAAC 1

10 GAGAAGAAGA 1

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Sequence 14, Application US/07739142

Sequence 14, Application US/07739142

Patent No. 5175272

Patent No. 5175272

Patent No. 5175272

TITLE OF INVENTION: DNA Sequences With Increased Expression TITLE OF INVENTION: DA Sequences With Increased Expression TITLE OF INVENTION: DA HBCAG

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSE: Richard R. Rodrick

STREET: 1 Becton Drive

CITY: Franklin Lakes
                                                                         Score 6.4; DB 1; Length 8;
Pred. No. 7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.1%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 7e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/07739643

Patent No. 5175094

GENERAL INPORMATION:
TITLE OF INVENTION:
INTERE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Rodrick
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07417-1880
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC c
                                                                                      29.1%;
87.5%;
                                                                                 Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 87.5 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 8 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                         737 AACAGAAC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     737 AACAGAAC 744
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        US-07-739-642-14
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US-07-739-643-14
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 248
US-07-739-643-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                             TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.9%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 1e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/07739642

Patent No. 5173427

GENERAL INPORMATION:

APPLICAMY:
APLICAMY:
APPLICAMY:
APPLICAMY:
APPLICAMY:
APPLICAMY:
APPLICAMY:
AND SERION:
ADDRESSE:
Richard R. Rodrick
STREET:
Becton Drive
CITY:
Franklin Lakes
STREET:
Becton Drive
CITY:
STREET:
Becton Drive
CITY:
Franklin Lakes
STATE:
COMPUTER:
Becton Drive
COMPUTER:
Becton Drive
COMPUTER:
COMPUTER:
COMPUTER:
FRADALE PORM:
MEDIUM TYPE:
FLORDY disk
COMPUTER:
DEP PO. 502/MS-DOS
SOFTWARE:
PATORNER:
PATORNER:
PATORNER:
PATORNER:
PATORNER:
PATORNER:
PATORNER:
PATORNER:
PATORNER:
REGISTRATION:
REGISTRATION NUMBER:
REG
                                                                                                                                                                                                                                                     OPERATING SIGNAL
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
APPLICATION NUMBER: US 946, 233
FILING DATE: 14.5EP-1992
FILECAMINICATION INFORMATION:
FILEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
ENWOTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 80.v
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   731 AGGAGAAACA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 8 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGAGGAAAA 10
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US93-08743-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-739-642-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 247
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/desc = "oligonucleotide"
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TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMUNICATION:
TELEPHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
                                                  LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  (617)227 - 5941
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 base pairs
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                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGGGGAAA B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                            ;
US-08-465-590-117
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US-08-859-954-38
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Patent No. 5824770
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.1%; Score 6.4; DB 1; Length 8; Best Local Similarity 87.5%; Pred. No. 7e+02; Matches 7; Conservative 0; Mismatches 1; Indels
                                                  COMPUTER RELABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Elab PC compatible
COMPUTER: Elab PC compatible
COMPUTER: Elab PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,142
FILING DATE: 19910801
CLESSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: Stierwalt, Brian K.
REGISTRATION NUMBER: P-2271
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 201-848-517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT AFFLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/121,438
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-193
FILING DATE: 14-SEP-193
FILING DATE: 14-SEP-193
FILING DATE: 14-SEP-193
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-193
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REPRENCE/DOCKET UMBER: MRY
TELECOMMUNICATION (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 60 SIG.-CITY: BOSTON
CITY: BOSTON
SIGATE: MASSACHUCETIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   737 AACAGAAC 744
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           COUNTRY:
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Gaps
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1 Sequence 38 Application US/08859954
5 Sequence 38 Application US/08859954
5 Patent NO. 6083695
6 Patent INO. 6083695
7 Patent INFORMATION:
7 PAPPLICANT: Hardin, Banin
7 PTLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof NUMBER OF SEQUENCES: 56
7 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Fulbright & Jaworski L.L.P.
8 STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
Query Match 29.1%; Score 6.4; DB 1; Length 8; Best Local Similarity 87.5%; Pred. No. 7e+02; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
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US-08-711-417C-117

US-08-711-417C-117

Sequence 117, Application US/08711417C

Sequence 117, Application US/08711417C

GENERAL INFORMATION:

TITLE OF INFORMATION:

TITLE OF INFORMATION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 202

CORRESPONDENCE ADDRESS:

STREET: 225 Franklin Street

CITY: BOSTON

STREET: 225 Franklin Street

CITY: BOSTON

STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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29.1%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: OZIJO-ZBA
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
COMPATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-SEP-1996
PRIOR APPLICATION NUMBER: 08/28,212
FILING DATE: 02-MAY-1994
                                                                                                        COUNTRY: HOUSEON
STATE: HOUSEON
COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/632,782
RILING DATE:
ATTORNEY/AGENT:
RILING DATE:
ATTORNEY/AGENT:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELEPHONE: 713/651-5325
INFORMATION FOR SEQ ID NO: 375:
SEQUIRNE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
                          E: Fulbright & Jaworski L.L.P.
1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         729 CCAGGAGA 736
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                                                                                          Houston
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                                                                                                                                                             JULY 1997-1994-200

JULY 1997-1994-200

JULY 1997-1994-200

JULY 1997-1904

JULY 1997-100

JULY 1997-100

JULY 1997-100

JULY 1907-100

JULY 
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Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Ramin
APPLICANT: Hardin, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof NUMBER OF SEQUENCES: 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.1%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 7e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 8 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 735 GAAACAGA 742
                                                                                                                                                   US-08-859-954-205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE:
US-08-859-954-205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 253
US-08-859-954-375
                                                                                                              RESULT 252
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5. Application US/08088658

Sequence 5. Application US/08088658

Batent No. 5641625

GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Application, Michael
APPLICANT: Applicant, Peter E.
APPLICANT: Milegard, Niels E.
TILLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
TILLE OF INVENTION: MUCLEIC ACIDS
OUNDER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117, Application PC/TUS9308743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.1%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 7e+02;
                                                                                                                                                                                     29.1%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 7e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 7e+0
0; Mismatches
                                                                                          MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 946, 233
FILING DATE: 14-SEP-1992
TELECHONNICATION INFORMATION:
TELECHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
     LENGIH: 8 base pairs
                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                         ropology: linear
                                                                                                                                                                                       Query Match
Best Local Similarity 87.5;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.1
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS.
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  731 AGGAGAAA 738
                                                                                                                                                                                                                                                                                       731 AGGAGAAA 738
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                                                                                                                                             US-09-723-909-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 257
US-08-088-658-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117, Application US/09723909
Patent No. 6630141
GENERATION: GEORGOPOULOS, Katia A.
APPLICANT: GEORGOPOULOS, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.1%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,909
FILING DATE: 28-No. 6630141-2000
PRIOR APPLICATION DATA:
                                                                                                                        NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOWAUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALLON ANTELLALION DAILS

PAPLICATION NUMBER: US/08/711,417

PILING DATE: 05-8ep-1996

APPLICATION NUMBER: 08/238,212

FILING DATE: 02-MAY-1994

APPLICATION NUMBER: 08/121,438

FILING DATE: 14-8EP-1993

APPLICATION NUMBER: 07/946,233

FILING DATE: 14-8EP-1993

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-08-711-417C-117
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                          TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ 1D NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 117
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.1
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 731 AGGAGAAA 738
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Query Match
29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               Length 9;
                                                                                                                                                                                                                                                                                                                          29.1%; Score 6.4; DB 1; 87.5%; Pred. No. 6.2e+02; trive 0; Mismatches 1
                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "OTHER NUCLEIC ACID,

DESCRIPTION: SYNTHETIC DNA"

US-08-410-779B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OCMENTINE: IBM PC compatible
OCHIVATE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-WAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
(619) 550-7675
                     INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            727 TGCCAGGA 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                                    linear
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i Sequence 28, Application US/08410779B

i Patent No. 5814517

j GENERAL INFORMATION:

APPLICANT: SEIDEL, H. MARTI

APPLICANT: LAMB, I. PETER

ITTLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 166

CORRESPONDENCE ADDRESS:

ADDRESSE: LIGAND PHARMACEUTICALS INCORPORATED

STREET: 9393 TOWNE CENTRE DRIVE

CITY: AND DIEGO

STATE: CALIFORNIA

COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.1%; Score 6.4; DB 1; Length 9; 87.5%; Pred. No. 6.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                             OUREMAING SISIEM: EV-LOCS/NB-LOCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/088,658
FILING DATE: 19930702
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
NAME: LUCC., JOSEPH
REGISTRATION NUMBER: 181S-1052
TELECOMMUNICATION NIFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3139
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TELEPHONE: CAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READALLE FORM:
MEDLUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEM PC COMPASSOR
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
FILING DATE: 27-WAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/228,935
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: UTRGENSEN, THOMAS E
REGISTRATION NUMBER: 34,195
REFERENCE/DOCKET NUMBER: 016-0013A.US
TELECOMMUNICATION INFORMATION:
                     COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 29.1
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           731 AGGAGAAA 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGAGAAA 8
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; 0 ö Gaps Sequence 126, Application US/08465590

Fatent No. 5824770

GENERAL INFORMATION:

APPLICANT: Georgopoulos, Katia A.

TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

MUMBER OF SEQUENCES: 164

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 STATE STREET, Suite 510

CITY: BOSTON

STATE: MASSACHUCETTS

COUNTRY: USA .. ö

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Mismatches, and Application to the Detection of Base Substitutions or Deletions in Nucleotide Sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ecker, David J.
APPLICANT: Buchardt, Ole
APPLICANT: Beholm, Michael
APPLICANT: Nielsen, Peter E.
APPLICANT: Berg, Rolf H.
APPLICANT: Milegaard, Niels E.
APPLICANT: Milegaard, Niels E.
APPLICANT: Milegaard, Niels E.
APPLICANT: NUTURION: HICH ORDER STRUCTURE AND BINDING OF PEPTIDE
TITLE OF INVENTION: NUCLEIC ACIDS
NUMBER OF SEQUENCES: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.1%; Score 6.4; DB 1; Length 9; Best Local Similarity 87.5%; Pred. No. 6.2e+02; Matches 7; Conservative 0; Mismatches 1; Indels
TITLE OF INVENTION: Mismatches, and Application to th
TITLE OF INVENTION: Substitutions or Deletions in Nuc
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                              COUNTRY: USA

ZIF: 20002-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,163
FILING DATE: 08-MAR-1996
CLASSIFICATION NUMBER: 1996
ATTORNEY/AGENT INFORMATION:
NAME: MAYORY: Kenneth J.
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05986.0005-00000
TELEPHANICATION INFORMATION:
TELEPHANICATION 10000000
TELEFAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,907A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08471907A Patent No. 5986053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            739 CAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CAGAGCAC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linea
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                                                                                                                                                                                            STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-605-163-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-471-907A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                              APPLICANT: Meo, Tommaso
APPLICANT: Tosi, Mario
APPLICANT: Tosi, Mario
APPLICANT: Using Michel
APPLICANT: Biasotto, Michel
TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
TITLE OF INVENTION: Containing Nucleotide Mismatches and the Base
TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-605-163-18/c

Sequence 18, Application US/08605163

Patent No. 5879886

GENERAL INFORMATION:

APPLICANT: Meo, Tommaso

APPLICANT: Verpy, Elisabeth

APPLICANT: Verpy, Elisabeth

APPLICANT: Biscotto, Michel

TILE OF INVENTION: Method for Detecting Molecules

TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner Bunner 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,163 FILING DATE: 08-MAR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05986.0005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0. v
                                                                                                                                                                            US-08-605-163-7/c
; Sequence 7, Application US/08605163
; Patent No. 5879886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 408-44-00
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.1
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                               732 GGAGAAG 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            739 CAGAACAC 746
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                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Meo, T
                                                                            1 GGAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                     ) NAME/KEY: misc_feature
) LOCATION: 1..9
CTHER INFORMATION: /note= "This sequence represents
) CTHER INFORMATION: mutation of base 2486 of Seq Id No. 60546333"
US-08-461-607-21
                                                                                                                                                                                                                                                                                                                                                              US-08-711-417C-126

Sequence 126, Application US/08711417C

Sequence 126, Application US/08711417C

Sequence 126, Application US/08711417C

Patent No. 18228611

APPLICANT: Georgopoulos, Katia A.

TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

STREET: 225 Franklin Street

CITY: Boston

STATE: MA.
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                                                                                                                                                                       Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTE: USA

ZIP: 02110-2804

ZONPUTER REDABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows Version 2.0b

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/711,417C

FILING DATE: 05-89-1996

FILING DATE: 02-89-1994

APPLICATION NUMBER: 08/121,438

FILING DATE: 14-SEP-1993

ATTORNEY/AGRIT INFORMATION:

MANAYER WANNEY WINDER: 170192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

29.1%; Score 6.4; DB 1;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1;
                                                                                                                                                                     Query Match

29.1%; Score 6.4; DB 1;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10287/007001
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MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-08-711-417C-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 9 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    732 GGAGAAAC 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 33301
ZIP: 33301
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,607
            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/088,658
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LAUCCI, JOSEPH)
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 1SIS-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPACK: 215-568-3139
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: US 07/874,974
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-1
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/379,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 2'SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.5-
                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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US-08-471-907A-5
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Gaps

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USA

COUNTRY:

FILING DATE

SOFTWARE:

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Sequence 23, Application US/09163485
Sequence 10. 627-1634 No. 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                           ; LOCATION: 1..9—
; OTHER INFORMATION: /note= "This sequence represents
; OTHER INFORMATION: mutation of base 2486 of Seq Id No. 62325243"
US-09-363-600-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.1%; Score 6.4; DB 1; Length 9; 87.5%; Pred. No. 6.2e+02; tive 0; Mismatches 1; Indels
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    728 GCCAGGAG 735
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APPLICANT: AUERNHAMMER, CHRISTOPH J.
APPLICANT: AUERNHAMMER, CHRISTOPH J.
APPLICANT: AUERNHAMMER, SHLONG
TITLE OF INVENTION: SUPPRESSOR OF CYTOKINE SIGNALING
TITLE OF INVENTION: IN HUMANS
TITLE OF INVENTION: IN HUMANS
FILE REFERENCE: P07 42591 (18810-803
FURRANT APPLICATION NUMBER: US/09/327,138C
CURRANT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide, consensus sequence from human OTHER INFORMATION: matrix metalloproteinases
TITLE OF INVENTION: KNOWN AND NOVEL MEMBERS OF GENE FAMILIES FILE REFERENCE: VCUIP4B
CURRENT APPLICATION UNDER: US/09/163,485
CURRENT FILING DATE: 1998-08-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 6.4; DB 1; Length 9;
Pred. No. 6.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.1%; Score 6.4; DB 1; Length 9; 87.5%; Pred. No. 6.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: promoter LOCATION: (-74)...(-66)
LOCATION: (-74)...(-66)
PEATURE: INFORMATION: STAT-BINDING SITE AT -74 TO -66
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mutation
LOCATION: (0)...(0)
OTHER INFORMATION: STAT-BINDING SITE AT -74 TO -66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: mutation
; LOCATION: (0)...(0)
; OTHER INFORMATION: STAT-BINDING SITE AT -74 TO 66
US-09-327-138C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 267
US-09-377-138C-13
Sequence 13, Application US/09327138C
Patent No. 6541244
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 268
US-09-989-789-530/c
; Sequence 530, Application US/09989789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.1%;
Best Local Similarity 87.5%;
Matches 7; Conservative (
                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  731 AGGAGAAA 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: promoter LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TTCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 13
LENGTH: 9
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                                                                                                                JOHN COURT STREET SOURCE STREET SCHOOL STREET SCHOOL STREET STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION WNBER: US 07/874,974
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MAINE: 32,264
REGISTRATION WNMER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-1
TELECHONE: 305-527-2498
TELEPAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 33301
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SBQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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STRANDEDNESS

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TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                      730 CAGGAGAA 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 AGGAGAAA 738
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US-09-989-789-2021
; Sequence 2021, Application US/09989789
; Parent No. 6588746
; GRNERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; TITLE OF INVENTION: 120 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SEQ ID NO 2021
; LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-789-789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: example target; CTHER INFORMATION: DNA
US-09-989-789-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 270
US-09-989-789-2022
| Sequence 2022, Application US/09989789
| Patent No. 6588746
| GENERAL INFORMATION:
| APPLICANT: LIU, Qiang
| TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
| TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
| TITLE OF INVENTION: POSITION OF SIZE
| TITLE OF INVENTION: POSITION OF SIZE
| CURRENT APPLICATION NUMBER: US/09/989,789
| CURRENT APPLICATION NUMBER: US/09/989,789
| CURRENT FILING DATE: 2002-03-25
| NUMBER OF SEQ ID NOS: 4085
| SOFTWARE: PATENTIN VET. 2.0
| SEQ ID NO 2022
PARENT NO. 6588746
GENERAL INFORMATION:
GENERAL INFORMATION:
THILL OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
SUFTWARE: PARENTIN Ver. 2.0
SEQ ID NO 530
LENGTH: 9
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.1%; Score 6.4; DB 1; Length 9; 87.5%; Pred. No. 6.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 87.5
Matches 7; Conservative
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US-09-989-789-2401
j Squence 2401, Application US/09989789
j Patent No. 6888746
j GENERAL INFORMATION:
j APPLICATION
j TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
j TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
j TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
j TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
j CURRENT APPLICATION NUMBER: US/09/989,789
j CURRENT FILING DATE: 2002-03-25
j NUMBER OF SEQ ID NOS: 4085
j SOFTWARE: PatentIN Ver. 2.0
j SEQ ID NO 2401
j LENGTH: 9
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) TYPE: DNA
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2022
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Patent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, Qiana
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: PRIPLETS BY ZINC FINGERS
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOUTHARE: Patentin Ver. 2.0
SEQ ID NO 2402
LENGTH: 9
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29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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29.1%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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29.1%; Score 6.4; DB 1;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1;
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Gaps

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PCT-US95-04477-28/C

FCT-US95-04477-28/C

Sequence 28, Application PC/TUS9504477

GENERAL INFORMATION:

APPLICANT:

ITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE

TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 165

COMPUTER READABLE FORM:

MEDIUM TYPE: FLORDY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 126, Application PC/TUS9308743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         29.1%; Score 6.4; DB 1; Length 9; 87.5%; Pred. No. 6.2e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-09-723-909-126
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CURRENT APPLICATION DATA:
APPLICATION NUBER: PCT/US93/08743
FRIOR APPLICATION DATA:
APPLICATION NUBER: US 946,233
FILING BATE: 14-SEP-1992
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: CATALON NUBER: SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                              TELEFAX: 617/542-8906
                                                                      TELEX: 200154
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                      GENERAL INCORNATION:
GENERAL INCORNATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT PILLING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2403
LENGTH: 9
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Patent No. 6630141
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,909
FILING DATE: 28-No. 6630141-2000
FRION APPLICATION NUMBER: US/08/711,417
FILING DATE: 05-SEP-1996
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
                                                                                                                                                                                        Sequence 2403, Application US/09989789
Patent No. 6588746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                         731 AGGAGAAA 738
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/228,935
FILING DATE: 14-APR-1994
INFORMATION POR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLIGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
CORRECTION: /desc = "OTHER NUCLEIC ACID,
CORRECTION: /desc = "OTHER NUCLEIC ACID,
CORRECTION: SYNTHETIC DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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Sequence 9242, Ap Sequence 169, App Sequence 170, App Sequence 878, App Sequence 42, Appl	269,	1258 2390	444 404 900, 1000,	454	NN	99	i a a	312	7.00	o H M	10	25		7 -	d d (7 7 7		9.5	1 10 10	9 9	ω r	5.0	'' (A	<u> </u>	- m -	3 01 0	3 42 5	7 2	7 8	0.4.1
US-10-287-949A-9242 US-10-669-841-169 US-10-669-841-170 US-10-669-841-878 US-08-911-824-42	US-10-453-792-269 US-10-453-792-271 US-08-841-636A-40	US-10-060-756A US-10-138-674-	US-10-28/-349A-239 US-10-782-002-40 US-10-825-378-40 US-09-776-474-983	US-10-238-700-133 US-10-230-006-788 US-10-297-068-119	US-10-138-674- US-10-287-9492	US-09-504-231A-65 US-09-274-553D-65	US-10-056-414- US-10-116-993- US-10-743-163-	US-10-339-674- US-10-339-674- US-10-717-897-	US-10-146-058-125 US-09-877-478-603	US-10-339-674- US-10-339-674- US-10-339-674-	US-10-056-414-11 US-10-669-841-243	US-09-997-326-2 US-09-504-231A-71	US-09-2	US-09-274-553D-71 US-09-835-694-19	US-10-339-674-420 US-10-339-674-421	US-09-504-231A-71 US-09-274-553D-71 US-09-504-231A-13	US-09-2	US-10-1	US-09-5	US-10-347-510A-95 US-09-544-934B-95	US-10-3	US-10-1	US-10-07	US-10-0	US-10-131-337-1 US-10-146-058-35	US-10-01	US-09-26	US-10-7	US-709-90	,US-10-6 US-10-6 US-10-6
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GenCore v Copyright (c) 1993 -	nucleic 1 on:	(Wilnow alguments) 165.484 Million cell updates/sec	Title: US-09-695-451-1 Perfect score: 22 Sequence: 1 tgccaggagaaacaccg 22	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 0.5	3761 residue	Total number of hits satisfying chosen parameters: 572	Minimum DB seq length: 8 Maximum DB seq length: 30	Post-processing: Minimum Match 0% Maximum Match 100%	first 27.sed:	ed. No. is the number of results predi	l to the score of the result being prof the total score distribution.	SUMMARIES	Query Match Langth Do In	Score Match Length UB ID Description	2 16.4 74.5 22 1 US-10-403-10/A-1 Sequence L. 2 16.4 74.5 22 1 UG-10-31-039-633 Sequence 6.	14.6 66.4 22 1 US-10-270-258-7 Sequence 2:	6 14.6 66.4 22 1 US-10-270-258-11 Sequence 1.7 14.6 66.4 22 1 US-10-270-258-17 Sequence 1.	8 14.2 64.5 21 1 US-09-904-968A-29 Sequence 20 14 63.6 18 1 US-10-453-792-276 Sequence 2	0 13.4 60.9 18 1 US-10-453-792-270 Sequence 2 ^o 1 13.4 60.9 18 1 US-10-453-792-272 Sequence 2 ^o	12 13.4 60.9 18 1 US-10-453-792-273 Sequence 2' 13 12.8 58.2 17 1 US-10-060-756A-1254 Sequence 1.	14 12.8 58.2 17 1 US-10-060-756A-1255 Sequence 13 12.4 56.4 17 1 US-10-060-756A-1256 Sequence 13	16 12.4 56.4 17 1 US-10-060-756A-1257 Sequence 17 12.4 56.4 18 1 US-10-453-792-275 Sequence 27	18 12.4 56.4 18 1 US-10-453-792-278 Sequence 27 19 12.4 56.4 19 1 US-09-898-533-28 Sequence 28	20 12.2 55.5 18 1 US-10-349-143-4649 Sequence 46 21 12 54.5 17 1 US-10-676-154-188 Sequence 18	22 11.8 53.6 17 1 US-09-877-478-169 Sequence 16 23 11.8 53.6 17 1 US-08-877-478-170 Sequence 16	24 11.8 53.6 17 1 US-09-877-478-878 Sequence 1.25 11.8 53.6 17 1 US-10-342-007-150 Sequence 18.	25 11.8 53.6 17 1 US-10-342-902-170 Sequence 17 1 1 US-10-342-902-170 Sequence 17 1 US-10-342-902-170 Sequence 17 1 US-10-343-902-170 Sequence 17 1 US-10-343-903-170 Sequence 17 1 US-10-343-903-903-903-903-903-903-903-903-903-90	24 11.0 53.6 17 1 US-10-342-902-8/8 Sequence 8 11.8 53.6 17 1 US-10-060-7564-1253 Sequence 12 12 12 12 12 12 12 12 12 12 12 12 12	29 11.8 53.6 17 1 US-10-156-306-4512 Sequence 45 30 11.8 53.6 17 1 US-10-156-306-5193 Sequence 51	31 11.8 53.6 17 1 US-10-156-306-519 32 11.8 53.6 17 1 US-10-339-793-241 33 11.8 53.6 17 1 US-10-138-674-924

Sequence 1363, App Sequence 47, Appl Sequence 57, Appl Sequence 537, App Sequence 537, App Sequence 537, App Sequence 613, App Sequence 741, Appl Sequence 17, Appl Sequence 18, Appl Sequence 13, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 52, Appl Sequence 51, Appl Sequence 5	eduence eduenc
1 US-10-330-627-1363 1 US-10-434-479-47 1 US-10-450-797-47 1 US-10-450-797-532 1 US-10-450-797-532 1 US-10-450-797-613 1 US-09-179-536B-86 1 US-09-179-536B-86 1 US-09-263-959-795 1 US-09-263-959-755 1 US-09-263-959-755 1 US-09-263-959-755 1 US-09-263-959-756 1 US-10-391-32 1 US-10-391-32 1 US-10-330-627-77 1 US-10-310-655-898-6 1 US-10-266-138B-6 1 US-10-310-677-27	- Sn
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Sequence 3, Appli Sequence 4, Appli Sequence 5, Appli Sequence 6, Appli Sequence 8, Appli Sequence 28, Appli Sequence 29, Appli Sequence 29, Appli Sequence 31, Appli Sequence 32, Appli Sequence 44, Appli Sequence 45, Appli Sequence 77, Appli Sequence 77, Appli Sequence 177279, Sequence 37, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 177279, Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 17, Appli Sequence 29, Appli Sequence 4, Appli Sequence 31, Appli Sequence 31, Appli Sequence 44, Appli Sequence 46, Appli Sequence 46, Appli Sequence 46, Appli Sequence 46, Appli Sequence 46, Appli	
US-09-152-059-3 US-09-152-059-4 US-09-152-059-4 US-09-152-059-6 US-09-152-059-6 US-09-152-059-6 US-09-152-059-6 US-09-152-059-7 US-09-152-059-9 US-09-152-059-9 US-09-152-059-9 US-09-152-059-9 US-09-152-059-9 US-09-152-059-32 US-09-152-059-44 US-09-152-059-44 US-09-152-059-44 US-09-152-059-44 US-09-152-059-44 US-09-152-059-44 US-09-152-059-44 US-09-152-059-47 US-09-059-47 US-09-059-48 US-09-059-48 US-09-059-49 US-09-059-069-059-09 US-09-059-069-059-09 US-09-059-069-059-09 US-09-059-069-059-09 US-09-059-069-059-09 US-09-059-069-059-09 US-09-059-069-059-09 US-09-059-069-069-069 US-09-059-069-069-069 US-09-059-069-069-069 US-09-059-069-069-069 US-09-059-069-069-069-069 US-09-059-069-069-069-069-069-069-069-069-069-06	US-10-008-029-48 Sequence US-10-008-029-71 Sequence US-10-008-029-71 Sequence US-10-008-029-77 Sequence US-10-008-029-77 Sequence US-10-208-650-3 Sequence US-10-208-650-4 Sequence US-10-208-650-4 Sequence US-10-208-650-8 Sequence US-10-208-650-9 Sequence US-10-208-650-9 Sequence US-10-208-650-39 Sequence US-10-208-650-39 Sequence US-10-208-650-44 Sequence US-10-208-650-44 Sequence US-10-208-650-44 Sequence US-10-208-650-44 Sequence US-10-208-650-44 Sequence US-10-208-650-44 Sequence US-10-208-650-47 Sequence US-10-208-650-47 Sequence US-10-208-650-71 Sequence US-10-208-650-72 Sequence US-10-208-650-74 Sequenc
Sequence 1152-059-3 Sequence 5-152-059-4 Sequence 6-152-059-6 Sequence 6-152-059-6 Sequence 6-152-059-6 Sequence 6-152-059-9 Sequence 6-152-059-9 Sequence 6-152-059-9 Sequence 6-152-059-9 Sequence 6-152-059-4 Sequence 6-152-059-8 Sequence 6-152-059-4 Sequence 6	1 US-10-008-029-48 Sequence 1 US-10-008-029-71 Sequence 2 US-10-208-650-3 Sequence 2 US-10-208-650-4 Sequence 2 US-10-208-650-6 Sequence 2 US-10-208-650-6 Sequence 2 US-10-208-650-9 Sequence 2 US-10-208-650-9 Sequence 2 US-10-208-650-9 Sequence 2 US-10-208-650-3 Sequence 2 US-10-208-650-3 Sequence 2 US-10-208-650-4 Sequence 2 US-10-208-650-7 Sequence 2 US-10-203-145-1215 Sequence 2 US-10-33-145-1215 Sequence 2 US-10-3
US-09-152-059-3 Sequence US-09-152-059-4 Sequence US-09-152-059-5 Sequence US-09-152-059-5 Sequence US-09-152-059-5 Sequence US-09-152-059-6 Sequence US-09-152-059-6 Sequence US-09-152-059-8 Sequence US-09-152-059-3 Sequence US-09-152-059-3 Sequence US-09-152-059-3 Sequence US-09-152-059-3 Sequence US-09-152-059-3 Sequence US-09-152-059-3 Sequence US-09-152-059-4 Sequence US-09-152-059-4 Sequence US-09-152-059-4 Sequence US-09-152-059-4 Sequence US-09-152-059-7 US-09-09-05-2 US-09-09-09-09-2 US-09-09-09-2 US-09-09-09-2 US-09-09-09-2 US-09-09-09-2 US-09-09-2 US-09-09-2 US-09-09-2 US-09-09-09-2 US-09-09-2	0.0 13 1 US-10-008-029-48 Sequence 13 1 US-10-008-029-71 Sequence 13 1 US-10-008-029-71 Sequence 13 1 US-10-008-029-74 Sequence 13 1 US-10-208-650-3 Sequence 13 1 US-10-208-650-4 Sequence 13 1 US-10-208-650-4 Sequence 13 1 US-10-208-650-6 Sequence 13 1 US-10-208-650-6 Sequence 13 1 US-10-208-650-6 Sequence 13 1 US-10-208-650-9 Sequence 13 1 US-10-208-650-44 Sequence 13 1 US-10-208-650-74 Sequence 14 US-10-208-650-74 Sequence 15 US-10-208-650-74
Sequence (1) 1 (US-09-152-059-3) (Sequence (2) (1) 1 (US-09-152-059-4) (Sequence (2) (1) 1 (US-09-152-059-4) (Sequence (2) (1) 1 (US-09-152-059-6) (Sequence (2) (1) 1 (US-09-152-059-8) (Sequence (2) (2) (2) (2) (2) (2) (2) (2) (2) (2)	8 40.0 13 1 US-10-008-029-48 Sequence 8 40.0 13 1 US-10-008-029-71 Sequence 8 40.0 13 1 US-10-008-029-71 Sequence 8 40.0 13 1 US-10-008-029-77 Sequence 18 40.0 13 1 US-10-208-650-5 Sequence 18 40.0 13 1 US-10-208-650-6 Sequence 18 40.0 13 1 US-10-208-650-6 Sequence 18 40.0 13 1 US-10-208-650-7 Sequence 18 40.0 13 1 US-10-208-650-9 Sequence 18 40.0 13 1 US-10-208-650-30 Sequence 18 40.0 13 1 US-10-208-650-30 Sequence 18 40.0 13 1 US-10-208-650-43 Sequence 18 40.0 13 1 US-10-208-650-40 Sequence 19 10 US-10-308-650-40 Sequence 19

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RESULT 3

US-09-736-084-45/C

Sequence 45, Application US/09736084

Sequence 45, Application US/09736084

Parent No. US20020107211A1

GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY

APPLICANT: THE ROCKEFELLER UNIVERSITY

ITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

ITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSE: Klauber & Jackson

STREET: 411 Hackensack

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER: READABLE FORM:

INTERIOR READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                 DB 1; Length 22;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NDRER: US/09/736,084
FILING DATE: 13-Dec-2000
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
APPLICATION NUMBER: 08/347,563
FILING DATE: NO. US20020107211Alember 30, 1994
APPLICATION NUMBER: 08/292,345
FILING DATE: ANGUST 17, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
74.5%; Score 16.4; DE
Best Local Similarity 94.4%; Pred. No. 8.8;
Matches 17; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         727 TGCCAGGAGAACAGAAC 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic US-10-321-039-633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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Publication No. US20040053288A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, Shigeto
APPLICANT: YAMAMOTO, Kozo
TITLE OF INVENTION: Action
TITLE OF INVENTION: Actor
TITLE OF INVENTION: Actor
TITLE OF INVENTION: Actor
CURRENT APPLICATION NUMBER: US/10/409,107A
CURRENT FILING DATE: 2003-04-19
PRIOR APPLICATION NUMBER: UP 107126/2002
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.2
IENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide used as primer for PCR detection of TNF-R55 mRNA US-10-409-107A-1
Sequence 1342, Ap
Sequence 1396, Ap
Sequence 1419, Ap
Sequence 1773, Ap
Sequence 261, App
Sequence 261, App
Sequence 287, App
Sequence 59, Appl
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Sequence 626, App
Sequence 631, App
Sequence 1118, App
Sequence 1280, Ap
Sequence 1286, Ap
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399, App
399, App
82, App
86, App
86, App
66, App
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81, App
81,
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                                                               ALIGNMENTS
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Best Local Similarity 100.0
Matches 20; Conservative
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US-10-409-107A-1
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ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 274:
US-10-453-792-274
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TYPE: nucleic acid
STRANBDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                 728 GCCAGGAGAAACAGA 742
                                                                                                                                                                                                                                                                                                                         18 GCCAGGAGAAACAGA 4
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Best Local Similarity 100.0
Matches 15; Conservative
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US-10-270-258-7
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Best Local S
Matches 17
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ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTYR: U.S.A.
ZIP: 22201-4714
COMPUTER: READBELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOREID FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOREID FORM:
MEDIUM TYPE: PLOSS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
SOFTWARE: PATENTIN Release
FILING DATE: 04-Unn-2003
CLASSIFICATION NUMBER: US/10/453,792
FILING DATE: 04-Unn-2003
CLASSIFICATION NUMBER: US/09/155,885A
                                                                                                                                                                                                                                                                               DESCRIPTION: sequence tagged-site specific PCR primer HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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  REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,663
REGISTRATION NUMBER: 36,663
REPERRORS/POCKET NUMBER: 2551-5
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 274:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 274, Application US/10453792
Publication No. USZU0040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
                                                                     TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (primer)
                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-10-453-792-274/c
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US-1U-2/U-220-//C
Sequence 7. Application US/10270258
Fublication No. US2030148951A1
GENERAL INFORMATION:
GARDRAL INFORMATION:
APPLICANT: Gordon, Siamon
SAPPLICANT: Gordon, Andrew J.
APPLICANT: Isis Innovation Limited
ITLE OF INVENTION: Human EMR2, A G-Protein Coupled Receptor from the EGF-TM7 Family
FILE REFERENCE: 1365.061US1
CURRENT APPLICATION NUMBER: US/10/270,258
CURRENT APPLICATION NUMBER: US/10/210
FILE REPERENCE: 2002-10-11
FRIOR APPLICATION NUMBER: PGT/GB01/01729
FRIOR APPLICATION NUMBER: GB 0009181.9
FRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 22
SEG ID NO 7
LENGTH: 22
LENGTH: 22
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Publication No. US20030148951A1
GENERAL INFORMATION:
APPLICANT: Mornight, Andrew J.
APPLICANT: Mornight, Andrew J.
APPLICANT: Mornight, Andrew J.
APPLICANT: Stacey, Martin
APPLICANT: Isis Innovation Limited
TILLE OF INVENTION: Human EMR2, A G-Protein Coupled Receptor from the EGF-TM7 Family
FILE REPERENCE: 1365.061US1
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: PGT/GB01/01729
PRIOR APPLICATION NUMBER: GB 0009181.9
PRIOR FILING DATE: 2000-04-17
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 22
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68.2%; Score 15; DB 1; Length 18; 100.0%; Pred. No. 13; tive 0; Mismatches 0; Indels
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                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: VICEINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE PORDY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-JUM-2003
CLASSIFICATION NUMBER: US/9/155,885A
FILING DATE: 108-Oct-1998
APPLICATION NUMBER: PS/T/EP97/02002
FILING DATE: 21-APR-1996
APPLICATION NUMBER: PP 96870053.4
APPLICATION NUMBER: PP 96870053.4
APPLICATION NUMBER: PP 96870053.4
APPLICATION NUMBER: SP 96870053.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 276. Application US/10453792

Publication No. US20040029110A1

GENERAL INFORMATION:

ROSSAU, RUDI

MARTENS, GERT

TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

NUMBER OF SEQUENCES: 313

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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Pred. No. 18;
0; Mismatches
                                                                                                                                                                              0; Mismatches
                                                                                                                    Score 14.2;
Pred. No. 19;
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SAUTI SENSE: NO
SAUTI SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-453-792-276
                             CTHER INFORMATION: PCR primer 5F1 US-09-904-968A-29
                                                                                                                                                                                                                                           728 GCCAGGAGAACAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 276:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                  3 GCCAGGAGGAGCAGAACCC 21
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                    Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          728 GCCAGGAGAAACAG 741
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-10-453-792-276/c
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; Sequence 17, Application WG20030148951A1
CENERAL INFORMATION:
APPLICANT: Hsi-Hsi-Hsi-Msi and an applicant on a particolar; Stacey, Martin
APPLICANT: Stacey, Martin
APPLICANTON NUMBER: US/10/270,258
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: GB 0009181.9
PRIOR PELING DATE: 2000-04-13
PRIOR PELING DATE: 2000-04-13
PRIOR PELING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 17
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/0990496BA
; Bublication No. US2003000828BA1
; GENERAL INFORMATION.
; APPLICANT: HE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, GREGORY
; APPLICANT: HARDERITCHAROEN, Bunyong
; APPLICANT: WATNICK, Terry
; TITLE OF INVENTION DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US 60/283,691
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PATENT OF SEQ ID NOS: 113
; SOFTWARE: PATENT OF SEQ ID NOS: 120
; SEQ ID NO 29
; LENGTH: 21
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                                                                                                                                                                              66.4%; Score 14.6; DB 1; Length 22; 81.0%; Pred. No. 17; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.4%; Score 14.6;
81.0%; Pred. No. 17
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                                                                                                                                                                                                                                                  17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Conservative
                                                             TYPE: DNA
ORGANISM: Homo sapiens
US-10-270-258-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                              Best_Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-904-968A-29
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SEQ ID NO 11
LENGTH: 22
                                                                                                                                                                                    Query Match
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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Matches 14; Conservative
                                            ARLINGTON
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COMPUTER READABLE FORM:

MEDIUM TYEE: Floppy disk

COMPUTER: ENDRELE FORM:

MEDIUM TYEE: Floppy disk

COMPUTER: ENDRE FORM:

COMPUTER: ENDRE FLOPSY GISK

COMPUTER: ENDRE FORM:

COMPUTER: ENDRE FORM:

COMPUTER: ENDRE FORM:

COMPUTER: ENDRE FORM:

APPLICATION NUMBER: US/10/453,792

FILING DATE: 04-JUN-2003

CLASSIFICATION: CURLOWN:

APPLICATION NUMBER: US/09/155,885A

FILING DATE: 11-ARR-1997

APPLICATION NUMBER: EP 96870053.4

FILING DATE: 11-ARR-1996

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REGISTRATION NUMBER: 36,663

REGISTRATION NUMBER: 2551-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROSSAU, RUDI
MAENTENS, GERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                                                                                                       MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSES: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.9%; Score 13.4; DB 1; Length 18, 93.3%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 270: US-10-453-792-270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 270:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                            Sequence 270, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 272, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYNER, LIEVEN
ROSSAU, RUDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                               APPLICANT: STUYVER, LIEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                728 GCCAGGAGAAACAGA 742
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-453-792-272/c
                                            -10-453-792-270/c
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STATE: VIRGINIA

STATE: VIRGINIA

CONDUTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC Compatible

COMPUTER: IBM FC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/453,792

FILLING DATE: 04-Jun-2003

CLASSIFICATION: <Unknown>
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 222014714
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.9%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 23;
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                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-0ct-1998
APPLICATION NUMBER: PCT/RE97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 272:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 273, Application US/10453792
Publication No. US20040029110A1
GENERAL INPORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 272: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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STRANDEDNESS: single
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Gaps

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Sequence 1255, Application US/10060756A

Publication No. US20030046717A1

GENERAL INFORMATION:

APPLICANT: Zhang, Jian

TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REPERENCE: PBD177

CURRENT APPLICATION NUMBER: US/10/060,756A

CURRENT FILING DATE: 2002-01-30

PRIOR PELION NUMBER: PCT/US01/00664

PRIOR PLILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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                                                      Indels
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                                                      ..
         87.5%; Pred. No. 27;
tive 0; Mismatches
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                                                                                                                                       727 TGCCAGGAGAACAGA 742
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         Best Local Similarity 87.5
Matches 14; Conservative
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CORGANISM: Homo sapiens
US-10-060-756A-1255
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US-10-060-756A-1255/c
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WS-10-060-756A-1254/C

Sequence 1254, Application US/10060756A

PULICANT: Zhang, Jian

TITLE OF INVORMATION:
TITLE OF INVORMATION:
CURRENT FILING DATE: 2002-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.9%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 23;
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: -(Juhranowa)
PRIOR APPLICATION NUMBER: US/09/155,885A
APPLICATION NUMBER: US/09/155,885A
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 13-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
RAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REGISTRATION NUMBER: 36,663
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 273:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 273: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 728 GCCAGGAGAACAGA 742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 14; Conserva
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RESULT 15

US-10-060-756A-1256/C

US-10-060-756A-1256/C

Sequence 1256, Application US/10060756A

Publication No. US20030046717A1

GENERAL INFORMATION:

APPLICANT: Zhang, Jian

ITLLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

CURRENT APPLICATION NUMBER: US/10/060, 756A

CURRENT PILING DATE: 2002-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
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Length 17;

DB 1;

Score 12.8;

58.2%;

Query Match

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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-453-792-278/c
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TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
FILE REFERENCE: PB0177
CURRENT APPLICATION NUMBER: US/10/060,756A
CURRENT FILING DATE: 2002-01-30
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Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUTVER, LIEVEN
ROSSAU, RUDI
MARKTERS, GERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
                                                                                                                                                                                                                                                                                                           56.4%; Score 12.4; DB 1; Length 17; 92.9%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 17;
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Pred. No. 32;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELICATION NUMBER: PCT/US01/00664
PRIOR PELICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/327,898
PRIOR RELING DATE: 2001-10-09
PRIOR PELING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/327,898
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4804
SOFTWARE: Aeemica Sequence Listing Engine
SEQ ID NO 1256
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1257, Application US/10060756A Publication No. US20030046717A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                 727 TGCCAGGAGAACA 740
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 92.9
Matches 13, Conservative
                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -10-060-756A-1257/c
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MAERTENS, GERRT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.4%; Score 12.4; DB 1; Length 18; 92.9%; Pred. No. 33; tive 0; Mismatches 1; Indels
ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 275:
                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 2551-5
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 275:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                             NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
                                CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 278, Application US/10453792
Publication No. US200040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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COMPUTER READABLE FORM:
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Sequence 4649, Application US/10349143
Publication No. US20040005584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
TITLE OP INVENTION: Biallaic markers for use in constructing a high density...
FILE REFRENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR PELING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1998-04-21
PRIOR PELING DATE: EARLIER FILING DATE: 1998-04-21
PRIOR PELING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 4649
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-16740 for SEQ 715,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 55.5%; Score 12.2; DB 1; Length 18; Best Local Similarity 82.4%; Pred. No. 36; Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  731 AGGAGAAACAGAACACC 747
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Matches 12; Conservative
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CRGANISM: Homo Sapiens
US-10-676-154-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-676-154-188/c
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Sequence 28, Application US/09898533

Fatent No. US202020106656A1

GENERAL INFORMATION:
APPLICANT: Genmill, Robert M.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION:
FILE OF INVENTION:
CURRENT APLICATION NUMBER: US/09/898,533

CURRENT FILING DATE: 2001-07-02

PRIOR FILING DATE: 2001-07-02

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 28

LENGIH: 19
  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION **CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/15,885A
FILING DATE: 04-OCT-1998
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, 8.J.
REGISTRATION NUMBER: 36,663
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 2551-5
TELECOMMUNICATION NUMBER: 256-63
TELECOMMUNICATION NUMBER: 256-63
TELECOMMUNICATION NUMBER: 256-6400
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Pred. No. 34;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 278:
US-10-453-792-278
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 278:
SEQUENCE CHRACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative
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Best Local Similarity 92.9%;
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-09-898-533-28
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US-10-349-143-4649/c
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                                                                                                                                                                                                                                 Sequence 188, Application US/10676154

Publication No. US20040081996A1

GENERAL INFORMATION:

APPLICANT: John Landers

APPLICANT: John Landers

APPLICANT: Barbara Jordan

CURRENT APPLICATION NUMBER: US/10/676,154

CURRENT FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-09-25

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 691

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 17
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TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication FILE REFERENCE: MBHB00-845-H (400/029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.6%; Score 11.8; DE Best Local Similarity 86.7%; Pred. No. 39; Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE REFERENCE: MEHBOO-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 09/831,025
PRIOR FILING DATE: 1992-05-14
PRIOR FILING DATE: 1992-05-30
PRIOR FILING DATE: 2000-320
PRIOR FILING DATE: 1995-05-7
PRIOR FILING DATE: 1995-05-7
PRIOR FILING DATE: 1995-05-04
PRIOR PRIOR PRIOR DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR PRIOR PRIOR DATE: 1995-05-04
PRIOR PRIOR PRIOR DATE: 1995-05-04
PRIOR PRIOR DATE: 1995-05-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Dave
          US 08/434,504
                                                                           09/436,430
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; Sequence 169, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 878, Application US/09877478
Publication No. US20030068301A1
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PRIOR APPLICATION NUMBER: US 08/, PRIOR FILING DATE: 1995-05-06/, PRIOR APPLICATION NUMBER: US 09/, PRIOR FILING DATE: 1999-11-08 , NUMBER OF SEQ ID NOS: 6586 , SOFTWARE: Patentin version 3.0 , SEQ ID NO 170
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                                                                                                                                                                                                                                                                                                            ORGANISM: Hepatitis B virus US-09-877-478-170
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                TYPE: RNA
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                                                                                                                                                                                             APPLICANT: NIDOZYME FDARMAGEULICALS, INC.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Mcaniggen, Jüm
APPLICANT: Mcariggen, Jüm
APPLICANT: Mcrisey, Dave
TILLE REPREBRICE: MBH800-845-H (400/029)
TILLE REPREBRICE: MBH800-845-H (400/029)
CURRENT APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR FILING DATE: 1992-05-14
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-01-0-24
PRIOR FILING DATE: 2000-01-0-24
PRIOR FILING DATE: 2000-01-0-24
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1999-11-08
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APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
FILE REFERENCE: MBHB00-845-H (400/029)
CURRENT APPLICATION NUMBER: US 09/827, 478
FRIOR FILING DATE: 1992-05-14
FRIOR FILING DATE: 1992-05-14
FRIOR FILING DATE: 2000-00-20
FRIOR FILING DATE: 2000-00-20
FRIOR FILING DATE: 2000-08-09
FRIOR FILING DATE: 2000-08-09
FRIOR FILING DATE: 2000-10-24
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53.6%; Score 11.8; Di
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches
                                                                                  Sequence 169, Application US/09877478
Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
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Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
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APPLICATION NUMBER: US 08/433,993
FILING DATE: 1995-05-04
                                                                       Application US/09877478
5. US20030068301A1
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SEQ ID NO 169
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US-09-877-478-170/c
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US=10-342-902-879/C

1 Sequence 879, Application US/10342902

1 Sequence 879, Application US/10342902

2 Publication No. US20040054156A1

3 Publication No. US20040054156A1

3 APPLICANT: Sirna Therapeutics, Inc.

4 APPLICANT: Blatt, Larry

4 APPLICANT: Blatt, Larry

5 APPLICANT: Marked and Reagent for Inhibiting Hepatitis B Virus Replication

7 TILE OF INVENTION WHERE: US/10/342, 902

7 TILE OF INVENTION WHERE: US 09/877, 478

PRIOR APPLICATION WHERE: US 09/877, 478

PRIOR APPLICATION WHERE: US 09/877, 478

PRIOR APPLICATION WHERE: US 09/836,385

PRIOR PRILNG DATE: 2000-00-09

PRIOR PRILNG DATE: 2000-00-09

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR PLING DATE: 1994-02-07

PRIOR PLING DATE: 1999-02-07

PRIOR PLING DATE: 1999-02-07

PRIOR PLING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 6592

SEQ ID NO 978

LENGTH: 17
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Sequence 1253, Application US/10060756A

Sequence 1253, Application US/10060756A

Publication No. US20030046717A1

GENERAL INFORMATION:
APPLICANT: Zhang, Jian
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/060, 756A

CURRENT APPLICATION NUMBER: US/10/0667

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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Pred. No. 39;
0; Mismatches
                                                                                                                   Query Match 53.6%; Score 11.8; I Best Local Similarity 86.7%; Pred. No. 39; Matches 13; Conservative 0; Mismatches
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86.7%; Pred
0;
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    ; ORGANISM: Hepatitis B virus US-10-342-902-170
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Best Local Similarity 86.7
Matches 13; Conservative
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Publication No. US20040054156A1

GENERAL INFORMATION:

APPLICANT: Sinna Therapeutics, Inc.

APPLICANT: Blact, Larry

APPLICANT: Blact, Larry

APPLICANT: Morrises, Dave

ITLE OF INVENTION WHOMER: US/10/342,902

CURRENT APPLICANTON WHOMER: US/10/36.08

PRIOR APPLICANTON WHOMER: US/10/36.08

PRIOR APPLICANTON WHOMER: US/10/36.385

PRIOR PRING DATE: 2000-08-09

PRIOR PRILING DATE: 2000-08-09

PRIOR PRILING DATE: 2000-08-09

PRIOR PRILING DATE: US/10/36.385

PRIOR PLILING DATE: US/10/36.385

PRIOR PLILING DATE: US/10/36.347

PRIOR PLILING DATE: 193-4-02-07

PRIOR APPLICATION WUMBER: US/183,627

PRIOR PLILING DATE: 193-4-02-07

PRIOR APPLICATION WUMBER: US/89436,430

PRIOR APPLICATION WUMBER: US/89436,430

PRIOR APPLICATION WUMBER: US/8952

PRIOR PLILING DATE: 193-11-08

PRIOR APPLICATION WUMBER: US/8952

PRIOR PLILING DATE: 193-11-08

PRIOR APPLICATION WUMBER: US/8952

PRIOR PLILING DATE: 193-11-08

PRIOR APPLICATION WUMBER: US/8952

PRIOR APPLICATION WUMBER: US/8952

PRIOR PLILING DATE: 193-10-08

PRIOR APPLICATION WUMBER: US/8952

PRIOR PLILING DATE: 193-11-08

PRIOR APPLICATION WUMBER: US/8952

PRIOR PLILING DATE: 193-11-08

PRIOR APPLICATION WUMBER: US/8952

PRIOR PLING DATE: 193-11-08

PRIOR APPLICATION WUMBER: US/8953

PRIOR PLING DATE: 193-11-08

PRIOR PLING DATE: 193-11-08

PRIOR PLING DATE: PRIOR PRI
                                                                                          APPLICANT: BLACK, DAILY
APPLICANT: MCSWiggen, Jim
APPLICANT: MCSWiggen, Jim
APPLICANT: MCSWiggen, Jim
APPLICANT: MCSWiggen, Jim
APPLICANT: MCSWiggen, June
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MBHB00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2000-03-01-15
FRIOR FILING DATE: 2000-03-20
FRIOR APPLICATION NUMBER: US 09/636,385
FRIOR APPLICATION NUMBER: US 09/636,385
FRIOR PILING DATE: 2000-10-24
FRIOR FILING DATE: 1994-02-07
FRIOR FILING DATE: 1994-02-07
FRIOR APPLICATION NUMBER: US 08/193,627
FRIOR FILING DATE: 1994-02-07
FRIOR APPLICATION NUMBER: US 09/436,430
FRIOR FILING DATE: 1999-11-08
FRIOR FILING DATE: 1990-11-08
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Pred. No. 39;
0; Mismatches
APPLICANT: Sirna Therapeutics, Inc
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Best Local Similarity 86.7%;
Matches 13; Conservative
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CRGANISM: Hepatitis B virus
US-10-342-902-169
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relater
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILE REPERBNCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: ParentIn version 3.0
SEQ ID NO 5:94
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Sequence 241. Application US/2030180764A1

Sequence 241. Application No. US20030180764A1

Sequence 241. Application No. US2003018076A1

Publication No. US2003018076A1

APPLICANT: Shang, Jin

APPLICANT: Shang, Jin

TITLE OF INVENTION: GRNES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS

TILLE REFERENCE: 37-000310US

CURRENT APPLICATION NUMBER: US/10/339,793

CURRENT PLIAGO DATE: 2003-01-08

NUMBER OF SEQ ID NOS: 443

SOFTWARE: Patentin version 3.1
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                                                                   53.6%; Score 11.8; Di
86.7%; Pred. No. 39;
tive 0; Mismatches
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86.7%; Pred. No. 39;
Live 0; Mismatches
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86.7%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                  Sequence 5194, Application US/10156306
Publication No. US20030119017A1
GENERAL INFORMATION:
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US-10-138-674-9242/c
; Sequence 9242, Application US/10138674
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                                                                                                                                                                                                      16 receasesascas 2
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                                                         Query Match
Best Local Similarity 86.75
Warches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-10-156-306-5194
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US-10-339-793-241
; ORGANISM: Homo sapiens
US-10-156-306-5193
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Best Local Similarity
Matches 13; Conserv
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APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of IXK-Gamma and PKR
TITLE OF INVENTION: Levels of IXK-Gamma and PKR
TITLE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: Patentin version 3.0
SEQ ID NO 5193
LENGTH: 17
TYPE: RNA
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Publication No. US20030119017A1

FORDERAL INPORMATION:
APPLICANT: MCSWiggen, James
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
FILLE REFERENCE: MBHB01-664-A (400/050)

CURRENT FAPLICATION WUBBER: US/10/156,306

CURRENT FILING DATE: 2002-05-28

NUMBER OF SEQ ID NOS: 8013

SEQ ID NO 4512

LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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86.7%; Pred. No. 39;
tive 0; Mismatches
                     PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-05-23
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4804
SEQ ID NO 1253
    APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5193, Application US/10156306 Publication No. US20030119017A1 GENERAL INFORMATION:
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Best Local Similarity 86.7
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-10-156-306-4512
                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 30
US-10-156-306-5193/c
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APPLICANT: Renact, proberts
APPLICANT: Relisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLECTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIE OF INVENTION: OLIGONUCLECTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS REPLICATION
FILE REPERENCE: 400/0420S (MERBRO 2-24)
FILE REPERENCE: 400/0420S (MERBRO 2-24)
CURRENT APPLICATION NUMBER: US 100/069,841
CURRENT APPLICATION NUMBER: US 60/296,876
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR PLING DATE: 2001-10-26
PRIOR PLING DATE: 2001-12-05
PRIOR PLING DATE: 2001-12-05
PRIOR PLING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/336,124
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2000-12-18
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
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Sequence 170, Application US/10669841

PUDIcation No. U520040127446A1

SEQUENCE INCOMPATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: David, Morrissey

APPLICANT: David, Morrissey

APPLICANT: David, Morrissey

APPLICANT: David, Morrissey

APPLICANT: Parrice, Lee

APPLICANT: Parrice, Lee

APPLICANT: Remeth, Draper

APPLICANT: Remeth, Draper

APPLICANT: Remeth, Draper

APPLICANT: Remeth, Draper

APPLICANT: Remeth, Outgoutcheoribe Mediated No. 18 (1998)

TITLE OF INVENTION: OLIGOUTCHEORIBE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA:

TITLE OF INVENTION: OLIGOUTCHEORIBE WEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA:

TITLE OF INVENTION: OLIGOUTCHEORIBE WEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA:

TITLE OF INVENTION: OLIGOUTCHEORIBE WEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA:

TITLE OF INVENTION: OLIGOUTCHEORIBE WEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA:

TITLE OF INVENTION NUMBER: US 103-09-23

FRIOR APPLICATION NUMBER: US 60/235, 059

PRIOR APPLICATION NUMBER: US 60/337, 055

PRIOR APPLICATION NUMBER: US 60/337, 055
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53.6%; Score 11.8; D
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches
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; ORGANISM: Hepatitis B Virus
US-10-669-841-169
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US-10-287-949A-9242/c

Sequence 9242, Application US/10287949A

Sequence 9242, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:

APPLICANT: Ribozywe Pharmaceuticals, Inc.

APPLICANT: Ribozywe Pharmaceuticals, Inc.

APPLICANT: Ribozywe Pharmaceuticals, Inc.

APPLICANT: Stanchcomb, Dam

APPLICANT: Stanchcomb, Dam

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

CURRENT FILLING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0

SEQ ID NO 9242

LENGTH: 17
Publication No. US20040077565A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Fam
APPLICANT: Pavco, Pau
APPLICANT: Stinchcomb, Dan
APPLICANT: McSwiggen, Uim
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9242
LENGTH: 17
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86.7%; Pred. No. 39;
tive 0; Mismatches
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US-10-669-841-169/C
Sequence 169, Application US/10669841
Sequence 169, Application US/10669841
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Damis, Macejak
APPLICANT: James, Macejak
APPLICANT: Pamela, Pacigen
APPLICANT: Pamela, Pavco
APPLICANT: Pamela, Pavco
APPLICANT: Patrice, Lee
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Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-10-287-949A-9242
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CORGANISM: Homo sapiens
US-10-138-674-9242
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APPLICANT: Abboto Laboratories
APPLICANT: Abboto Laboratories
APPLICANT: Yamaguchi, Julie
APPLICANT: Yamaguchi, Julie
APPLICANT: Golden, Alan M.
APPLICANT: Golden, Alan M.
APPLICANT: Golden, Alan M.
APPLICANT: Hickman, Robert K.
APPLICANT: Hickman, Robert K.
APPLICANT: Hickman, Novel ANTIGEN CONSTRUCTS USEFUL IN THE
ITILE OF INVENTION: DETECTION AND DIFFERENTIATION OF ANTIBODIES TO HIV
FILE REPERENCE: 6165.US.01
CURRENT APPLICATION NUMBER: US/08/911,824
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 42
LENGTH: 18
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TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: URGINIA
COUNTY: U.S.A.
ZIP: 22201-4114
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 (BPO)
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                                                                                                                                                                                                                             0; Mismatches
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Mismatches
                                                                                                                                                   Query Match 53.6%; Score 11.8; I
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches
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APPLICATION NUMBER: US/10/453,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.6%; Score 11.8; Best Local Similarity 86.7%; Pred. No. 41 Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human Immunodeficiency Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: PCR Primer 41sy-3
US-08-911-824-42
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US-10-453-792-269/c
; Sequence 266, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 42, Application US/08911824
Publication No. US20030004323A1
                                                                                                                                                                                                                                                                                                           728 GCCAGGAGAACAGA 742
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           ; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-878
                                                                                                                                                                                                                                                                                                                                                                                 15 GCCAAGAGAAACGGA 1
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APPLICANT: Parala, Paraco
APPLICANT: Parala, Paraco
APPLICANT: Parala, Paraco
APPLICANT: Renneth, Dager
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION O'LIGOM/CLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TITLE OF INVENTION O'LIGOM/CLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TITLE OF INVENTION O'LIGOM/CLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
TITLE OF INVENTION O'MERR: US/0.069,441
CURRENT FILING DATE: 2003-09-23
CURRENT FILING DATE: 2003-09-26
PRICH APPLICATION NUMBER: US 60/296,876
PRICH PILING DATE: 2001-10-24
PRICH PILING DATE: 2001-10-24
PRICH PILING DATE: 2001-10-24
PRICH PILING DATE: 2001-10-34
PRICH PILING DATE: 2001-0-3-1
PRICH PILING DATE: 2001-0-3-1
PRICH PILING DATE: 2001-0-3-26
PRICH PILING DATE: 2001-0-3-1
PRICH PILING DATE: 2000-0-3-1
PRICH PILING DATE: 2000-0-3-1
PRICH PILING DATE: 2000-0-1-3
PRICH PILING DATE: 2000-0-1-3
PRICH PILING DATE: 2000-0-1-3
PRICH PILING DATE: 2000-0-1-5
PRICH PILING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.6%; Score 11.8; 1
86.7%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 878, Application US/10669841 Publication No. US20040127446A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sirna Therapeutics, Inc. APPLICANT: Lawrence, Blatt APPLICANT: Dennis, Macejak APPLICANT: James, McSwiggen APPLICANT: David, Morrissey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728 GCCAGGAGAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Hepatitis B Virus
US-10-669-841-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GCCAAGAGAACGGA 2
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Best Local Similarity 86.73
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 37
US-10-669-841-878/c
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APPLICANT: Miettinen-Oinonen, Arja
APPLICANT: Miettinen-Oinonen, Arja
APPLICANT: Undesborough, John
APPLICANT: Vehmaanper, Jari
APPLICANT: Haakana, Heli
APPLICANT: Hautto, Raija
APPLICANT: Hautto, Raija
APPLICANT: Elovainio, Minna
APPLICANT: Elovainio, Minna
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: Washington
STATE: D.C.
COUNTRY: USA
ZIUD: ACADAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.6%; Score 11.8; DB 1; Length 18; Best Local Similarity 86.7%; Pred. No. 41; Matches 13; Conservative 0; Mismatches 2; Indels
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ZIP: X. USA
ZIP: X. USA
ZIP: Z0005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: IBM PC compatible
COMPUTER: But PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/841,636A
FILING DATE: 30-ARR-1997
CLASSIFICATION: 435
PRICATION NUMBER: US 60/005,335
FILING DATE: 17-OCT-1995
PRICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 04-DEC-1995
                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPHONE: TELEPHONE: 271:
TELEPHONE: CHARACTERISTICS:
TENGRATION: 271:
TYPE: uncleic acid
TYPE: Uncleic a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-841-636A-40; Sequence 40, Application US/08841636A; Publication No. US20020168751A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728 GCCAGGAGAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 GCCATGAGAAACGGA 4
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: AND SERVED CORRESPONDENCE ADDRESSES: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VARGINIA
CONDUTE: VARGINIA
CONDUTER: ED200-4714
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATORIE: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION NUMBER: US/09/155,885A
FILING DATE: 08-OCT-1998
APPLICATION NUMBER: PCT/RE97/02002
FILING DATE: 19-ARP-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-ARR-1996
ATTORNEY/AGENT INFORMATION:
NAME: CANOUR E. ALAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 271, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUTYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 53.6%; Score 11.8; DB 1; Length 18; Best Local Similarity 86.7%; Pred. No. 41; Matches 13; Conservative 0; Mismatches 2; Indels
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGANT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR EQUINO: 269:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANBEDNESS: single
STRANBEDNESS: single
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 269:
US-10-453-792-269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 728 GCCAGGAGAACAGA 742
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US-10-453-792-271/c
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; Sequence 2390, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
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US-10-702-002-40
; Sequence 40, Application US/10782002
; Publication No. US2004014244A1
; GENERAL INFORMATION:
; APPLICANT: Miettinen-Oinonen, Arja
; APPLICANT: Vehmaanpera, John
; APPLICANT: Vehmaanpera, Jari
; APPLICANT: Haakana, Heli
; APPLICANT: Mantyla, Arja
; APPLICANT: Mantyla, Arja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    733 GAGAACAGAACA 745
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Best Local Similarity 92.33
Matches 12, Conservative
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Best Local Similarity 92.3
Matches 12, Conservative
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CORGANISM: Mus musculus
US-10-287-949A-2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
US-10-138-674-2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-287-949A-2390
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LENGTH: 17
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APPLICANT: Zhang, Jian

TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

FILE REFERENCE: PED177

CURRENT APPLICATION NUMBER: US/10/0667

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1258, Application US/10060756A Publication No. US20030046717A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-138-674-2390; Application US/10138674; Publication No. US20040077565A1
FILING DATE: 17-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Timochy J. Shea, Jr.
REGISTRATION NUMBER: 41,306
REFERENCE/DOCKET NUMBER: 1716.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
INFORMATION EQ SEQ ID NO: 40: SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs
TYPE: mucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      735 GAAACAGAACACCG 748
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CORGANISM: Homo sapiens
US-10-060-756A-1258
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserva
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US-10-060-756A-1258/c
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Bscobedo, Jame
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: PavCo, Pam
APPLICANT: BavCo, Pam
APPLICANT: Stinchcomb, Dam
APPLICANT: Stinchcomb, Dam
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re)
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Walnumber: us/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARES PATENT VERSION 3.0
SEQ ID NO 2: 2092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.8%; Score 11.4; DB 1; Length 17; 92.3%; Pred. No. 46; tive 0; Mismatches 1; Indels
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Elovainio, Minna
Joutsjoki, Vesa
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APPLICANT:
APPLICANT:
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APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
APPLICANT: Booher, Robert
APPLICANT: Holman, Patridia
APPLICANT: Holman, Patridia
APPLICANT: McSwiggen, Jim
APPLICANT: McSwi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication V0. U020030153521A1

Publication No. U020030153521A1

Publication No. U020030153521A1

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels

FILE REFERENCE: 400/057 (MBHB01-1158-A)

CURRENT PELLING DATE: 2002-09-18

PRIOR APPLICATION NUMBER: PCT/US 02/16840

PRIOR APPLICATION NUMBER: US 60/218,471

PRIOR PILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 46;
4; Mismatches
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Best Local Similarity 81.2%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
              SEQ ID NO 40
LENGTH: 17
TYPE: DNA
TYPE: DNA
PRATURE:
FRATURE:
OTHER INFORMATION: PCR Primer
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                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

; LOCATION: (9)...(9)

; OTHER INFORMATION: n is a,

US-10-825-378-40
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Best Local Similarity 64.5-
9, Conservative
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                                                                                                                                                                                                                        FEATURE:
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US-10-825-378-40

Sequence 40, Application US/10825378

Sequence 40, Application US/10825378

Publication No. US20040185498A1

GENERAL INFORMATION:
APPLICANT: Metrinen-Orinonen, Arja
APPLICANT: Vehmampera, Jarii
APPLICANT: Wentampera, Jarii
APPLICANT: Mantyla, Arja
APPLICANT: Mantyla, Arja
APPLICANT: Blovaino, Mina
APPLICANTON NUMBER: US 08/41,636
PRICH APPLICATION NUMBER: US 08/732,181
PRICH APPLICATION NUMBER: US 60/020,840
PRICH FLING DATE: 1996-10-17
PRICH APPLICATION NUMBER: US 60/020,840
PRICH FLING DATE: 1996-10-16
PRICH FLING DATE: 1995-12-04
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVEXMION: Novel Cellulases, The Genes Encoding Them and Uses Thereof
FILE REPRENCE: 1116.051.000A
CURRENT APPLICATION NUMBER: US/10/782,002
CURRENT APPLICATION NUMBER: US 08/81,636
PRIOR FILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-04-30
PRIOR APPLICATION NUMBER: US 08/732,181
PRIOR APPLICATION NUMBER: US 08/732,181
PRIOR APPLICATION NUMBER: US 60/020,840
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-10-17
PRIOR FILING DATE: 1995-12-04
PRIOR PILING DATE: 1995-10-17
PRIOR PILING DATE: 1995-10-17
PRIOR PILING DATE: 1995-10-17
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
LEMOTH: 17
TUDE: NUMBER OF SEQ ID NOS: 45
LEMOTH: 17
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Pred. No. 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
| LOCATION: (9)..(9)
| OTHER INFORMATION: n is a, c,
US-10-782-002-40
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64.3%;
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Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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schultz1-727.rnpb

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Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribbozyme Pharmaceuticals, Inc.
APPLICANT: Ribbozyme Pharmaceuticals, Inc.
APPLICANT: Baccobedo, Jam
APPLICANT: Becobedo, Jam
APPLICANT: Becobedo, Jam
APPLICANT: Brobedo, Jame
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFUGANTION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Backsiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Scobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
NUMBER OF SEO ID NOS: 2082-
SOFTWARE: Patentin version 3.0
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                                                 DB 1; Length 17;
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                                               50.9%; Score 11.2; DB 1; Length 1
81.2%; Pred. No. 49;
cive 0; Mismatches 3; Indels
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                                            Query Match
Best Local Similarity 81.21
Matches 13; Conservative
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Matches 13; Conservative
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mus musculus
US-10-138-674-2873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
CORGANISM: Mus musculus
US-10-287-949A-2873
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US-10-287-949A-2873/c
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US-10-138-674-2873/c
    US-10-297-068-1196
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LENGTH: 17
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| Sequence 788, Application US/10230006
| Publication No. US2030191077A1
| Grentian No. US2030191077A1
| Grentan Information
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Fornaugh, Kathy
| APPLICANT: McSwiggen, Jim
| TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDITION
| FILE REFERENCE: 400/056 (MeHB01-1110)
| FRIOR APPLICATION NUMBER: US 60/315,315
| PRIOR FILING DATE: 2001-08-28
| NUMBER OF SEQ ID NOS: 2678
| SOFTWARE: Patent In version 3.0
| SEQ ID NO 788
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Publication NO. US2030228585A1
GENERAL INFORMATION:
MAPLICANT: INFORTA, Taeko
APPLICANT: ICHIHARA, Taeko
APPLICANT: MAGITA, Taeko
APPLICANT: MAGITA, Takuo
APPLICANT: MAGITA, Shogo
APPLICANT: MISHIDA, Mila
FILE REFERRICE: 13140PLI74
CURRENT APPLICATION NUMBER: US/10/297,068
CURRENT FILING DATE: 2002-11-27
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 1298
SOFTWARE: Patentin Ver. 2.1
LENGTH: 17
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:capture
                                                                                                                                                                                           DB 1; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 17;
                                                                                                                                                                                                                                        3; Indels
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81.2%; Pred. No. 49;
tive 0; Mismatches
                                                                                                                                                                                      Query Match 50.9%; Score 11.2; D. Best Local Similarity 81.2%; Pred. No. 49; Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                  730 CAGGAGAAACAGAACA 745
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NUMBER OF SEQ ID NOS: 4666
SOFTWARE: Patentin version 3.0
SEQ ID NO 133
LENGTH: 17
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                            ) TYPE: RNA
) ORGANISM: Homo sapiens
US-10-238-700-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-788
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US-10-297-068-1196
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US-10-230-006-788
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Gaps
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                                    DB 1; Length 15;
                                                                        Indels
                                                                        2
                                                                                                                                                                                                                                                                                                                                           McSwiggen, James
TITLE OF INVENTION: RIBGAZMB TREATMENT OF
DISEASE OR CONDITIONS
RELATED TO LEVELS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Comparible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-Jan-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
RAPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
                                  49.1%; Score 10.8; I 85.7%; Pred. No. 52; cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-10-056-414-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 833 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                            Sequence 10, Application US/10056414 Publication No. US20030003469A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     APPLICANT: Stinchcomb, Dan T. Draper, Kenneth G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION NAME: Warburg, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                               735 GAAACAGAACACCG 748
                                                                                                                                                 15 GAPACAGTACACTG 2
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                                    Query Match
Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                          RESULT 55
US-10-056-414-10/c
US-09-274-553D-653
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Sequence 653, Application US/09274553D

Sequence 653, Application US/09274553D

Sequence 653, Application US/09274553D

SERVERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Dames
APPLICANT: Roberts, Dames
APPLICANT: Roberts, Dames
APPLICANT: Roberts, Dames
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
TITLE OF INVENTION WHERE: US/09/274,553D
CURRENT FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: Patentin version 3.0
SEQ ID NO 653
                                                              FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.1%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 52; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      735 GAAACAGAACACCG 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 54
US-09-274-553D-653/c
                                                            US-09-504-231A-653/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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; LOCATION: (1302700)...(1302715)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1513 US-10-339-674-1160
                                                                                                                          ConnectronObjectNumber
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                                                                                                                                                                                                                                               Gaps
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: nucleotide motif sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Feldmann, Richard J., Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION UNBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
SOFTWARE: Proprietary
SEQ ID NOS: 3537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.1%; Score 10.8; DB 1; Length 16; 85.7%; Pred. No. 54; vative 0; Mismatches 2; Indels
                                                                                                                                                                                                  DB 1; Length 16;
                                                                                                                                                                                                                                               2; Indels
                     TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655 complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655 complete genome.
                                                                                                                          Strand = positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PHILLIPS, JONATHAN
APPLICANT: PHILLIPS, SATHISH
APPLICANT: PUTHIGAE, SATHISH
APPLICANT: POTHIGAE, SATHISH
APPLICANT: FOROTER, RICHARD S.
APPLICANT: FORSTER, RICHARD S.
APPLICANT: PORSTER, RICHARD S.
APPLICANT: PARSTER, RICHARD S.
APPLICANT: PARSTER, RICHARD S.
APPLICANT: PARSTER, RICHARD S.
APPLICANT: PARSTER, RICHARD S.
FILE REFERRICE: 044463-0264
CURRENT APPLICATION NUMBER: US/10/717,897
CURRENT FILING DATE: 2003-11-21
PRIOR PILING DATE: 2003-11-22
NUMBER OF SED ID NOS: 86
SOFTWARE: PATENTIN VET: 3.2
                                                                                                                                                                                            Score 10.8; DE
Pred. No. 54;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1160, Application US/10339674
Publication No. US20030204318A1
GENERAL INFORMATION:
                                                                     FEATURE: (616577)...(616592)
COTHEN INFORMATION: Chromosome = 1 US-10-339-674-558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 78, Application US/10717897
Publication No. US20040163146A1
GENERAL INFORMATION:
                                                                                                                                                                                            Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                 735 GAAACAGAACACCG 748
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Best Local Similarity 85.73
Matches 12, Conservative
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US-10-339-674-1160/c
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LENGTH: 16
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                                                                             Sequence 11, Application US/10116993

Publication No. US20030044947A1

Publication No. US20030044947A1

Publication No. US20030044947A1

APPLICANT INFORMATION:

APPLICANT THE BOARD OXIDASE 1 REGULATORY NUCLEOTIDE SEQUENCES FOR HETEROLOGOUTITLE OF INVENTION: AERRESSION IN YEAST

TITLE OF INVENTION: BERRESSION IN YEAST

FILE REFERENCE: UNL 3071.1

CURRENT APPLICATION NUMBER: US 60/281,861

PRIOR APPLICATION NUMBER: US 60/281,861

PRIOR APPLICATION NUMBER: 2001-04-05

NUMBER OF SEQ ID NOS: 26

SOFTWARE PATENT PLANTAL PATENT NOS: 26

NUMBER OF SEQ ID NOS: 26

LENGTH: 15
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Sequence 11. Application US/10743163

SEQUENCE 11. Application No. US20040137591A1

GENERAL INFORMATION:

PAPPLICANT: The Board of Regents of the University of Nebraska and ALCOHOL OXIDASE 1 REGULATORY NUCLECTIDE SEQUENCES FOR TITLE OF INVENTION: HETEROLOGOUS GENE EXPRESSION IN YEAST TITLE OF INVENTION: HETEROLOGOUS GENE EXPRESSION IN YEAST TITLE OF INVENTION: US/10.1.1

CURRENT APPLICATION NUMBER: US/10/743,163

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PATENTIN VEFSION 3.1

SEQ ID NO 11.
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Publication No. US2003204318A1
Publication No. US20030204318A1
Publication No. US20030204318A1
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
TITLE OF INVENTION: DESCHERICHIA COLI K-12 MG1655 COMPLECATION UNMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
SOFTWARE: PROPRIETATION UNMBER: US/10/339,674
SEQ ID NO 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
49.1%; Score 10.8; D
Best Local Similarity 85.7%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.1%; Score 10.8; Ilarity 85.7%; Pred. No. 52; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: methylotrophic yeast US-10-116-993-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA; CRGANISM: methylotrophic yeast US-10-743-163-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      728 GCCAGGAGAACAG 741
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Best Local Similarity
Matches 12; Conserv
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                                                                  US-10-116-993-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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US-00-877-478-6035, Application US/0987478

Sequence 6035, Application US/0987478

Publication No US20030068301A1

GENERAL INPREMATION

APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth

APPLICANT: Draper, Kenneth

APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Wolfer: US 09/53,385

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 1994-02-07

PRIOR FILING DATE: US 08/434,504

PRIOR FILING DATE: 1995-05-04

PRIOR FILING DATE: 1995-
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Sequence 6035, Application US/10342902

Publication No. US20040054156A1

GENERAL INPORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Mcswiggen, Jim

APPLICANT: Worksen, US/10/342,902

CURRENT FILING DATE: 2003-61-15

PRIOR APPLICATION NUMBER: US 09/636,385

PRIOR FILING DATE: 2000-03-00

PRIOR PLING DATE: 2000-03-00

PRIOR APPLICATION NUMBER: US 09/636,385

PRIOR APPLICATION NUMBER: US 09/636,347

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR PILING DATE: 2000-010-07

PRIOR PILING DATE: 2000-010-07
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Pred. No. 60;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Hepatitis B virus US-09-877-478-6035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     728 GCCAGGAGAAC 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Ancisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.3%; Score 10.4; DB 1; Length 14; 91.7%; Pred. No. 57; ive 0; Mismatches 1; Indels
                                                          47.3%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 51; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 400 Seventh St. N.W.
CTTY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/10/146,058
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICALL.

ATTING DATE: 13...
ATTORNEY/AGENT INFORMATION.
ATTORNEY/AGENT INFORMATION.
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/F58418
TELEPHONE: (202) 393-5350
TELEPAX: (202) 393-5350
TELEPAX: (202) 393-5350
TELEPAX: RCA 24853 IDEA UR
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TELENGTH: 14 base pairs
TELENGTH: 14 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: PRIAYER, WILLIAM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 125, Application US/10146058 Publication No. US20030040499A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
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                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                       GGAGAAACAAAA 12
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Best Local Similarity
Matches 11; Conserva
                                                                 Query Match
Best Local Similarity
Matches 11; Conserv
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ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-146-058-125
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US-10-717-897-78
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                                  Indels
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                                                                                                                                                                                                                                                                                                               MCSWiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
NF-KB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
PAPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOS 5.0
               Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.3%; Score 10.4; D
91.7%; Pred. No. 60;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32, 327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: December 7, 1992
                                                                                                                                                                            RESULT 66
US-10-056-414-11/C
is aguence 11, Application US/10056414
publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
Draper, Kenneth G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                          736 AAACAGAACACC 747
          Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731 AGGAGAAACAGA 742
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Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                               13 AAACAGCACACC 2
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US-10-339-674-1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655 complete genome.
PEATURE:
LDCATION: (4276408)...(4276422)
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 4240
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TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3537
SEQ ID NO 1179
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3197, Application US/10339674
Publication No. US20030204318A1
Publication No. US20030204318A1
Publication No. US20030204318A1
APPLICANT: Foldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
TITLE REPERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3537
SEQ ID NO 3197
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.3%; Score 10.4; DB 1; Length 15;
                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655 complete genome.
                                                                                                                                                                                                                                                        Score 10.4; DE
Pred. No. 60;
0; Mismatches
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1179, Application US/10339674; Publication No. US20030204318A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                    ch 47.3%;
il Similarity 91.7%;
11; Conservative
                                                                                                                                                                     TYPE: RNA
CRGANISM: Hepatitis B virus
US-10-342-902-6035
                                                                                                                                                                                                                                                                                                                                         728 GCCAGGAGAAC 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              736 AAACAGAACACC 747
                                                                                                                                                                                                                                                                                                                                                                              12 GCCAAGAGAAC 1
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                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 11, Conserv
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                                                                                                                              SEQ ID NO 6035
                                                                                                                                                      LENGTH: 15
                                                                                                                                                                                                                                                      Query Match
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US-09-504-231A-715/c

i Sequence 715, Application US/09504231A

patent No. US20020013458A1

GENERAL INFORMATION:

APPLICANT: Blatt, Laweence

APPLICANT: Roberts, Beth

APPLICANT: Roberts, Beth

APPLICANT: Pacco, Panela

APPLICANT: NUMBER: 06/100, 842

PRIOR PILING DATE: 1998-09-18

PRIOR APPLICANT: NUMBER: 60/100, 842

PRIOR APPLICANT: Pacco, Panela

APPLICANT: Pacco, Pacco, Panela

APPLICANT: Pacco, Pacco, Panela

APPLICANT: Pacco, Pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 716, Application US/09504231A
Patent No. US20020013458A1
Patent No. US20020013458A1
Patent No. US20020013458A1
APPLICANT: Blatt, Lawrence
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Deth
APPLICANT: Paveo, Memala
APPLICANT: Paveo, Pennis
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATER
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE REPERENCE: Pp. 247/282
CURRENT APPLICATION NUMBER: US/09/504,231A
CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INPORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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; LENGTH: 16; TYPE: DNA; OKGANISM: Artificial Sequence; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-997-326-2
                                                                                                                                                                                                                                                                           Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

46.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                           Score 10.4; DE Pred. No. 62; 0; Mismatches
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GGGAAACAGAA 5
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US-09-504-231A-715/c
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US-09-504-231A-716/c
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Paratice, Lee
APPLICANT: Rennech, Draper
TITLE OF INVENTION: UNING REPLICATION
TITLE OF INVENTION: UNING REPLICATION
TITLE OF INVENTION: UNING REPLICATION
TITLE OF THE REPRENCE: 400/0428 (MRHB02-249-8)
CURRENT PALLICATION NUMBER: US/10/669,841
CURRENT PALLICATION NUMBER: PCT/0502/09187
PRIOR PILLING DATE: 2001-06-08
PRIOR PILLING DATE: 2001-06-08
PRIOR PILLING DATE: 2001-10-24
PRIOR PILLING DATE: 2001-10-24
PRIOR PILLING DATE: 2001-10-24
PRIOR PILLING DATE: 2001-06-08
PRIOR PILLING DATE: 2001-03-26
PRIOR PILLING DATE: 2001-03-26
PRIOR PILLING DATE: 2002-03-11
PRIOR PILLING DATE: 2002-03-11
PRIOR PILLING DATE: 2002-03-12
PRIOR PILLING DATE: 2002-03-12
PRIOR PILLING DATE: 2002-03-12
PRIOR PILLING DATE: 2002-03-12
PRIOR PILLING DATE: 2002-03-14
PRIOR PILLING DATE: 2000-02-16
PRIOR PILLING DATE: 2000-02-16
PRIOR PILLING DATE: 2000-02-15
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Pred. No. 60;
0; Mismatches
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APPLICANT: Barbara Wendy SNOWDEN
APPLICANT: Chantelle Louise WARD
FILE REFERENCE: PG4334US
CURRENT APPLICATION NUMBER: US/09/997,326
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: GB 0029270.6
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
                                Sequence 2438, Application US/10669841
Publication No. US20040127446A1
GENERAL INFORMATION:
                                                                                                                                                        APPLICANT: Sirna Therapeutics, Inc. APPLICANT: Lawrence, Blatt APPLICANT: Dennis, Macejak APPLICANT: James, McWiggen APPLICANT: David, Morrissey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09997326
Patent No. US20020142294A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Hepatitis B Virus
US-10-669-841-2438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           728 GCCAGGAGAAC 739
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US-09-997-326-2/c
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AFFLICANT: ARACO, Family TITLE OF INVENTIORS NEGATIONS RELATED TITLE OF INVENTION: BEATTICANT: APPLICANT: APPLICANT: ARACO, PAGE AND TITLE OF INVENTION: BEATTIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED TITLE OF INVENTION: HEAPATTICS C VIRUS INFECTION FILL SEFERANCE: Toj 247/282
CURRENT APPLICATION NUMBER: US/09/274,553D
PRIOR PILING DATE: 1999-03-24
PRIOR PILING DATE: 1999-02-24
PRIOR PILING DATE: 1999-02-24
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: PALENTING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: PALENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-716
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APPLICANT: DONNELLY, JOHN J.

APPLICANT: DONNELLY, JOHN J.

LIU, MARGARET A.

MONTGOMERY, DONNA L.

PARKER, SUEZANNE E.

SHIVER, JOHN W.

TITLE OF INFUENCE: O'CH W.

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
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STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/835,694
FILING DATE: 16-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/461,268
FILING DATE: 05-June-1995
PPLICATION NUMBER: PCT/US94/02751
PILING DATE: 14-March-1994
APPLICATION NUMBER: 08/089,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
46.4%; Score 10.2; D
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches
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APPLICATION NUMBER: 08/032,383
FILING DATE: 18-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/09835694
Publication No. US20040087521A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
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                                               Pamela
                       Roberts, Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: RAHWAY STATE: NJ
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PRICANT BLACK, LAWERS

APPLICANT: ROBERTS, Beth

APPLICANT: Pavco, Pamela

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

FILE REFERENCE: rpi 247/282

CURRENT APPLICATION NUMBER: US/09/274,553D

CURRENT FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-24

PRIOR FILING DATE: 1998-09-18

PRIOR FILING DATE: 1998-09-18

PRIOR FILING DATE: 1998-09-18

WINDER OF SEQ ID NOS: 3148

SOFTWARE: PatentIN VERSION 3.0

SEQ ID NO 715
                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target US-09-504-231A-716
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80.0%; Pred. No. 64;
Live 0; Mismatches
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46.4%; Score 10.2; 1
Best Local Similarity 80.0%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches
             PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3242
SGOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 716
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 715, Application US/09274553D Patent No. US20020082225A1
PRIOR APPLICATION NUMBER: 09/274,553
PRIOR FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  728 GCCAGGAGAACAGA 742
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Best Local Similarity 80.0
Matches 12; Conservative
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US-09-274-553D-716/c
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US-U9-504-2134-71/c

US-U9-504-2134-71/c

Sequence 717, Application US/09504231A

Parent No. US20020013458A1

GENERAL INFORMATION:

APPLICANT: Blatt, Lawrence

APPLICANT: Roberts, Beth

APPLICANT: Roberts, Beth

APPLICANT: Roberts, Beth

APPLICANT: Bacco, Pannis

ITILE OF INVENTION: HEATITIS C VIRUS INFECTION

ITILE OF INVENTION: HEATITIS C VIRUS INFECTION

FILE REPERBUCE: rpi 247/282

CURRENT APPLICATION NUMBER: US/09/504,231A

CURRENT APPLICATION NUMBER: US/09/274,553

PRIOR PILING DATE: 1999-03-23

PRIOR PLING DATE: 1999-03-24

PRIOR PLING DATE: 1999-09-18

PRIOR PLING DATE: 1999-09-19

PRIOR PLING DATE: 1999-09-19

PRIOR PLING DATE: 1999-09-19

PRIOR PLING DATE: 1999-09-19

PRIOR DATE: 1999-09-19

PRIOR DATE: 1999-09-19

PRIOR DATE: 1999-09-1
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                                                                                                                                                                                           552
                           i LENGTH: 15

YYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655 complete genome.
FEATURE:
COATION: (435971)...(435985)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = US-10-339-674-421
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45.5%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 10; Conservative 0; Mismatches 0; Indels
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Patent No. US2002008225A1
GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Macejak, Dennis
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity 80.0
Matches 12; Conservative
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SEQ ID NO 421
                                                                                                                                                                                                                                                                                            Query Match
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = US-10-339-674-420
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Publication No. US2030204318A1
GENERAL INFORMATION:
APPLICANT: Feldaman, Richard J.; Global Determinants, Inc.
APPLICANT: Feldaman, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ. ID NOS: 3537
SOFTWARE: Proprietary
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78-56quence 420, Application US/10339674
Publication No. US2003024318A1
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: Escherichia coli K-12 MG455 complete genome.
TITLE OF INVENTION: Escherichia coli K-12 MG455 complete genome.
TITLE OF INVENTION: 2003-06-06
CURRENT APPLICATION NUMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3537
SEQ ID NO 420
LENGTH: 15
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ORGANISM: Escherichia coli K-12 MG1655 complete genome
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                    NAME: HAND, J. MRRK
REGISTRATION NUMBER: 36,545
REGISTRATION NUMBER: 36,545
REFERENCE FOCKET NUMBER: 18972PCA
TELECOMMUNICATION INFORMATION:
TELEPRA: 732-594-4720
TELEPRA: 732-594-4720
TELEPRA: 732-594-4720
TELEPRA: 732-594-4720
TELEPRA: 732-594-4720
TELEPRA: 732-594-4720
TELERA: CURRACTERISTICS:
LENGTH: 15 base pairs
TYPE: NUCleic acid
STREE: NUCLEIC acid
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80.0%; Pred. No. 64;
tive 0; Mismatches
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FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-835-694-19
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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Best Local Similarity 80.v.
Best Local 2; Conservative
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Matches 12; Conservative
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APPLICANT: MCSWiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Pavco, Pamela
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE REFERENCE: Tpl 247/282
CURRENT FILING DATE: 1999-02-24
CURRENT FILING DATE: 1999-02-24
FRICR PAPPLICATION NUMBER: 60/100,842
FRICR PAPPLICATION NUMBER: 60/083,217
FRICR PAPLICATION NUMBER: 60/083,217
FRICR PAPLICATION NUMBER: 60/083,217
FRICR PAPLICATION NUMBER: 00/083,217
FRICR PAPLI
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APPLICANT: Schlingensiepen, Malfgang
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Kamar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Acobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target US-09-274-553D-1341
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84.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Jacobson, Price, Holman & Stern CITY: Washington D.C COUNTRY: U.S.A. ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 126, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              732 GGAGAACAGAAC 744
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Sequence 1341, Application US/09504231A

Patent No. US20020013458A1

GENERAL INFORMATION:

APPLICANT: Blatt, Lawrence

APPLICANT: Blatt, Lawrence

APPLICANT: Roberts, Beth

APPLICANT: Roberts, Beth

APPLICANT: Pavoo, Eamel

APPLICANT: Pavoo, Eamel

APPLICANT: Pavoo, Eamel

APPLICANT: Pavoo, Eamel

FILE REFERENCE: TPI 247/282

CURRENT FILING DATE: 2000-02-15

PRIOR PILING DATE: 1999-03-23

PRIOR PLING DATE: 1999-03-23

PRIOR PLING DATE: 1999-02-24

PRIOR PLING DATE: 1998-02-24

PRIOR PLING DATE: 1998-04-27

PRIOR PLING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3242

SEC ID NO 1341

LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target US-09-274-553D-717
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44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.5%; Score 10; DB 1; Length 15; 100.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
CURRENT APPLICATION NUMBER: US/09/274,553D
CURRENT FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-04-18
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: PATENTIN VETSION 3.0
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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; Sequence 1341, Application US/09274553D
; Patent No. US20020082225A1
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Matches 10; Conservative
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MESULT 83
US-09-504-231A-654/C
is Sequence 654, Application US/09504231A
APPLICANT: Blatt, Lawrence
APPLICANT: Moseyak James
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE REFERENCE: Tpi 247/282
CURRENT FILING DATE: 1999-02-15
PRIOR APPLICATION NUMBER: 09/274,553
PRIOR PELING DATE: 1999-03-23
PRIOR PELING DATE: 1999-03-24
PRIOR PELING DATE: 1998-09-18
PRIOR PELING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3242
SEQ ID NO 654
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APPLICANT: Macejak, Dennis
TITLE OF INVENTION: ENZYMATITIS C VIGUS INFECTION
TITLE OF INVENTION: HEPATITIS C VIGUS INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                 Description of Artificial Sequence:Predicted Thermodynamic Parameters.
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84.6%; Pred. No. 71;
tive 0; Mismatches 2; Indels
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44.5%; Score 9.8; DB 1;
Best Local Similarity. 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2.
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                                                                                       TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
CHER INFORMATION: Description
COTHER INFORMATION: Thermodynam
US-10-324-409B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    734 AGAAACAGAACAC 746
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 14
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Matches 11; Conserva
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US-09-274-553D-654/c
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Sequence 9, Application US/20030165876A1

GENERAL INFORMATION

APPLICANT: AVENUTS PHARMA SA

APPLICANT: CAMENON, Beartince

TITLE OF INVENUTON: SEQUENCES BY TRIPLE HELIX INTERACTION

FILE REFERENCE: O3806.0546

CURRENT APPLICATION NUMBER: US/10/104,025

CURRENT PILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: RS 0103953

PRIOR APPLICATION NUMBER: RS 0103953

PRIOR FILING DATE: 2001-04-23

PRIOR PILING DATE: 2001-03-23

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Version 3.0

SEQUENCE: SEQ ID NOS: 16

SEQ ID NOS 9
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Publication No. US20040086880A1
GREERAL INFORMATION:
APPLICANT: Sampson, et al.
TITLE OF INVENTION: Method of Producing Nucleic Acid Molecules with Reduced TITLE OF INVENTION: Secondary Structure
FILE REFERENCE: 2003309-0028
CURRENT APPLICATION NUMBER: US/10/324,409B
CURRENT FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 33
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44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 14;
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                 ALIGNATION NUMBER: 31,409
REGISTRATION NUMBER: 31,409
REGISTRATION NUMBER: 31,409
REGISTRATION NUMBER: 31,409
RELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-666
TELEPHONE: (202) 833-550
TELEPA: RCA 24859 IDEA UR
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
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Best Local Similarity 84.6%;
Matches 11; Conservative
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 728 GCCAGGAGAACA 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-146-058-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-324-409B-21
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Tina Anderson Hollerup
TITLE OF INVENTION: Novel Process For The Detection of Mycobacteria
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                       44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/544,934B
FILING DATE: 07-Apr-2000
PRIOR APPLICATION DATA:
                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: ASCXI
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/028,392
FILING DATE: 12-0ct-96
APPLICATION NUMBER: 60/029,595
FILING DATE: 23-0ct-96
FILING DATE: 08-May-97
APPLICATION NUMBER: 60/045,962
FILING DATE: 08-May-97
APPLICATION NUMBER: 60/943,777
) TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-10-347-510A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid basepairs STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 45,958
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: FINNEGAN, HENDERE
STREET: 1300 I ST. NW
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                   Sequence 95, Application US/09544934B Publication Wo. US20020137035A1 GENERAL INFORMATION: APPLICANT: Henrik Stender
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 3-Oct-97
ATTORNEY/AGENT INFORMATION:
NAME: Anthony C. Tridico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 95
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                            730 CAGGAGAAACAGA 742
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                                                                                  Query Match
Best Local Similarity 84.64
Matches 11, Conservative
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Best Local Similarity
Matches 11; Conserv
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US-10-339-674-1871/c
                                                                                                                                                                                                                                                                                             RESULT 86
US-09-544-934B-95/c
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Tina Anderson Hollerup
TITLE OF INVENTION: No. US20040063110Alel Process For The Detection of Mycobact
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT, & DUNNER
STREET: 1300 I ST. NW
                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: ASCXI
SOFFWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/347,510A
FRILNG DATE: 21-Jan-2003
PRIOR APPLICATION DATA:
  FILE REFERENCE: rpi 247/282
CURRENT APPLICATION WUMBER: US/09/274,553D
CURRENT FILING DATE: 1999-03-23
FRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: Patentin version 3.0
SEQ ID NO 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/028,392
FILING DATE: 15-0ct-96
FILING DATE: 23-0ct-96
FILING DATE: 23-0ct-96
APPLICATION NUMBER: 60/045,962
FILING DATE: 08-May-97
APPLICATION NUMBER: 60/943,777
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TYPE: nucleic acid basepairs
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
STATE: District of Columbia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 45,958 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-347-510A-95/c
; Sequence 95, Application US/10347510A
; Publication No. US20040063110A1
; GENERAL INFORMATION:
APPLICANT: Henrik Stender
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Anthony C. Tridico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  408-4400
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INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732 GGAGAAACAGAAC 744
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Best Local Similarity
Matches 11; Conserv
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Sequence 6, Application US/10073377

Bublication No. US2003099670A1

GENERAL INPORMATION:

APPLICANT: Hobom, Gert

APPLICANT: Hobom, Gert

TITLE OF INVENTION: Influence with Enhanced Transcriptional and

TITLE OF INVENTION: Influence Viruses with Enhanced and

TITLE OF INVENTION: Replicative Capacities

FILE REFERENCE: 010293us/JH/ml

CURRENT APPLICATION NUMBER: US/10/073,377

CURRENT FILING DATE: 2002-02-08

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MS-010-073-377-5/c

Sequence 5, Application US/10073377

Publication No. USCO030099670A1

GENERAL INFORMATION:
APPLICANT: Hobom, Gert
APPLICANT: Hobom, Gert
TITLE OF INVENTION: Replicative Capacities
TITLE OF INVENTION: Replicative Capacities
FILE REPRENCE: 010293us/JH/ml
CURRENT APPLICANT: 10023us/JH/ml
CURRENT FILING DATE: 2002-02-08

NUMBER: OF SEQ ID NOS: 47

CURRENT FILING DATE: 2012-02-08

NUMBER: PatentIN Ver. 2.1

SEQ ID NO 5

LENGTH: 12

TYPE: RNA
OTHER NATIFICIAL Sequence
FEATURE:
CURRENTINE: OTHER INFORMATION: Influenza A 3'-sequence
US-10-073-377-5
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                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Caspase-8; OTHER INFORMATION: substrate recognition sequence US-10-100-957A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
CRGANISM: Artificial Sequence
FETURE:
COHER INFORMATION: Description of Artificial Sequence: Modified
COTHER INFORMATION: influenza A 3'-sequence
US-10-073-377-6
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                                                                                                                                                                                                                                                   Length 12;
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42.7%; Score 9.4; DB 1;
Best Local Similarity 90.9%; Pred. No. 73;
Matches 10; Conservative 0; Mismatches 1;
                                                                             TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 12
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Best Local Similarity 90.9
Matches 10; Conservative
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2480
US-10-339-674-1871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-450-797-1219/c
; Sequence 119, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE RERERENCE: HEMR.-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT PILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR PILING DATE: 2001-10-20
; PRIOR PILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 1435
; SEQ ID NOS: 1435
; SEQ ID NO 1219
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Sequence 1871, Application US/10339674
Publication No. US20030204318A1
Publication No. US20030204318A1
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REPERRINCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3537
SSG ID NO 1871
LENGTH: 15
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44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 74;
Matches 11; Conservative 0; Mismatches 2; Indels
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US-10-100-957A-73

Sequence 73, Application US/10100957A

Publication No. US20030096322A1

GENERAL INFORMATION:

APPLICANT: Giuliano, Kenneth A.

TITLE OF INVENTION: A System for Cell Based Screening;
FILE REFERENCE: 97-022-L1A

CURRENT APPLICATION NUMBER: US/10/100,957A

CURRENT FILING DATE: 2002-03-19

NUMBER OF SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655 complete genome.
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Best Local Similarity 90.9%;
Matches 10; Conservative
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ORGANISM: Homo sapiens
US-10-450-797-1219
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Sequence 35, Application US/10146058
Publication No. US20030040499A1
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, deorg-Ferdinand
APPLICANT: Schlingensiepen, Rarl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
APPLICANT: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (7)
CORRESPONDENCE ADDRESS:
ADDRESSES: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                    APPLICANT: Oligos Etc., Inc.
APPLICANT: DALE, Roderic M. K.
APPLICANT: DALE, Roderic M. K.
APPLICANT: ARROW, AM.
APPLICANT: THOMBON, Terry
TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
FILE REPERENCE: 58400-5019
CURRENT PERFERENCE: 58400-5019
CURRENT PILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,820
PRIOR FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin version 3.1
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Pred. No. 81;
0; Mismatches 1; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Jacobson, Price, Holman & Stern
400 Seventh St. N.W.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: ASM oligonucleotide US-10-191-997-1
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                                                                                                                                                         Sequence 1, Application US/10191997; Publication No. US20030207834A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Y: U.S.A.
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14 AGTAGAAACAG
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                                                                                                            RESULT 94
US-10-191-997-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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LENGTH: 14
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Sequence 19, Application US/10073377

Sequence 19, Application US/10073377

Publication No. US20030099670A1

GENERAL INFORMATION:
APPLICANT: Menke, Annette

TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and
TITLE OF INVENTION: Replicative Capacities
FILE REFERENCE: 0.10293us/JH/ml

CURRENT APPLICATION NUMBER: US/10/073,377

CURRENT FILING DATE: 2002-02-08

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 19
                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Arrow, Amy
APPLICANT: Arrow, Amy
APPLICANT: Thompson, Terry
TILLE OF INVENTION: Antisense Phosphodiesterase Inhibitors
TILLE OF INVENTION: Antisense Phosphodiesterase Inhibitors
TILLE REFERENCE: OLIG-003CIP
CURRENT APPLICATION NUMBER: US,10/076,597
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/364,626
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1998-07-29
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 51
SOUTHWRE: FASESEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 81; tive 0; Mismatches 1; Indels
                                 DB 1; Length 12;
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42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Synthesized Oligonucleotide US-10-076-597-32
                              Query Match
42.7%; Score 9.4; DB
Best Local Similarity 90.9%; Pred. No. 73;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                           US-10-076-597-32
) Sequence 32, Application US/10076597
) Sequence 32, Application US/10076597
) Publication No. US20030045490A1
) GENERAL INFORMATION:
APPLICANT: Dale, Roderic M. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence /
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Best Local Similarity
Matches 10; Conserva
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40.9%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 80; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                               Query Match 40.9%; Score 9; DB 1;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 9; Conservative 0; Mismatches
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: Patentin version 3.0
SEQ ID NO 1921
LENGTH: 10
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                        TYPE: DNA CRGANISM: Homo sapiens US-10-033-145-1921
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US-10-450-797-167
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| Publication No. US200201515A1
| GENERAL INFORMATION:
| APPLICANT: GENZYME CORPORATION
| APPLICANT: ROBERTS, BRUCE
| APPLICANT: ROBERTS, BRINIVAS
| TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
| TITLE OF INVENTION: PREPARATION NUMBER: US/10/033,145
| CURRENT APPLICATION NUMBER: US/10/033,145
| CURRENT FILING DATE: 2001-11-05
| PRIOR PILING DATE: 1999-06-18
| PRIOR PILING DATE: 1999-06-18
| NOWHERE OF SEQ ID NOS: 2137
| SOFTWARE: PATENTIN VETSION 3.0
| SEQ ID NO 1787
| LENGTH: 10
| TYPE: DNA
| ORGANISM: Homo sapiens
| US-10-033-145-1787
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Sequence 1921, Application US/10033145
Publication No. US20020151515A1
GENDRAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPREATION ADD USE OF SUPERIOR VACCINES
FILE REFERENCE: GA0201C
CURRENT APPLICATION UNMERE: US/10/033,145
CUBRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 14;
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Pred. No. 87;
0; Mismatches 3;
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APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPHONE: (202) 393-5350
TELEPHONE: (202) 393-5350
TELEPHONE: (202) 393-5350
TELEPHONE: (202) 393-5350
TELERA: RCA 248593 IDEA UR
INFORMATION POR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDMISS: unknown
MOLGLOGY: unknown
MOLGCULE TYPE: DNA (Genomic)
MATI-SENSE: YES
US-10-146-058-35
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40.9%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 75;
Matches 9; Conservative 0; Mismatches
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Best Local Similarity 78.6%;
Matches 11; Conservative
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US-10-033-145-1787
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US-09-263-959-843/c
US-09-263-959-843/c
Sequence 843, Application US/09263959
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: Seed and Berry Lip
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: Mashington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 167, Application US/10450797

Publication No. US20040142335A1

GENERAL INFORMATION:

APPLICANT: Petersohn, Dirk

APPLICANT: Petersohn, Marcus

APPLICANT: Hofmann, KAy

TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

CURRENT APPLICATION NUMBER: US/10/450,797

CURRENT PELING DATE: 2003-12-04

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-01-03

NUMBER OF SEQ ID NOS: 1435

SOFTWARE: PATENTIN VERSION 3.2

LENGTH: 11
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MESON. 104
US-09-981-803-47/C

Sequence 47, Application US/09981803

Publication No. US20030032092A1

GENERAL INFORMATION:
APPLICANT: Daniel SCHERMAN

APPLICANT: Daniel SCHERMAN

APPLICANT: Pierre WILS

APPLICANT: Anne-Marie DARQUET

TITLE OF INVENTION: DN MOLECULES, PREPARATION AND USE IN GENE THERAPY

TITLE OF INVENTION: UNMBER: US/09/981,803

CURRENT APPLICATION NUMBER: US/09/981,803

CURRENT FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Crouzet, Joel
APPLICANT: Scherman, Daniel
APPLICANT: Scherman, Daniel
APPLICANT: Scherman, Daniel
APPLICANT: Willia, Pierre
APPLICANT: Willia, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURPLICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: IMMOBILIZED CLICONUCLECTIDE
FILE REFERENCE: 0888 0138-02
FILE REFERENCE: 0888 0138-02
FILE REPERENCE: 009-64-07
FRIOR APPLICATION NUMBER: 09/580,923
FRIOR APPLICATION NUMBER: 09/580,923
FRIOR APPLICATION NUMBER: 08/860,038
FRIOR PILING DATE: 1997-06-09
FRIOR PILING DATE: 1995-1-08
FRIOR FILING DATE: 1995-1-08
FRIOR FILING DATE: 1995-1-08
                                                                                                                                                                                                                                                   Gaps
                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-8; OTHER INFORMATION: substrate recognition sequence
US-10-100-957A-75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of the artificial sequence: OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                 Length 12;
                                                                                                                                                                                              Query Match
40.9%; Score 9; DB 1;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial sequence
                          TYPE: DNA ORGANISM: Artificial Sequence
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Matches 10; Conserv
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  LENGTH: 12
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US-10-100-957A-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 75, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giulianon:
; TITLE OF INVENTION: A System for Cell Based Screening; FILE REPERENCE: 97-022-11A
; CURRENT APPLICATION NUMBER: US/10/100,957A
; UNDRES OF SEQ ID NOS: 180
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

40.9%; Score 9; DB 1;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches
                                                                                       ATTORNEY AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPAN: (206) 622-4900
TELEPAN: (206) 622-4900
TELEPAN: (206) 622-4900
INFORMATION FOR SEQ ID NO: 843:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.9%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILLING DATE: 05-MAR-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              737 AACAGAACA 745
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US-10-100-957A-75
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                                                                               Score 8.8; DB 1; Length 12;
Pred. No. 91;
0; Mismatches 2; Indels
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Pred. No. 91;
0; Mismatches 2
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Patent No. US2002068708A1
GENERAL INFORMATION
JEDGEMENT NELSER
APPLICANT: WENGEL, USSPER
APPLICANT: WENGEL, USSPER
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165 (71394)
CURRENT APPLICATION NUMBER: US/09/152,059
CURRENT APPLICATION NUMBER: 60/058,541
PRIOR APPLICATION NUMBER: 60/058,541
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-01-12
PRIOR FILING DATE: 1997-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-28
PRIOR FILING DATE: 1998-04-29
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83.3%;
                                                                                        Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
; ORGANISM: Escherichia coli
US-10-684-830-34
                                                                                                                                                                                                         731 AGGAGAAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Escherichia coli
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Best Local Similarity 83.3
Matches 10, Conservative
                                                                                                                                                                                                                                                                12 AGGAAAAAAAGA 1
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US-10-684-830-37/c
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US-09-152-059-3/c
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| US-10-10-14/Ca
| Sequence 34, Application US/10684830
| Publication No. US20040142452A1
| GENERAL INFORMATION:
| APPLICANT: Gencell S. A. Aventis Pharmaceuticals, Inc.
| APPLICANT: Gencell S. Aventis Pharmaceuticals, Inc.
| APPLICANT: Goubrier, Fabienne
| TITLE OF INVENTION: Circular DNA Molecule with Conditional Origin of Replication, Met
| TITLE OF INVENTION: Circular DNA Molecule with Conditional Origin of Replication, Met
| TITLE OF INVENTION: Preparing Same, and Use Thereof in Gene Therapy
| FILE REFERENCE: 8888.0132-02
| CURRENT APPLICATION NUMBER: US/268,948
| PRIOR FILING DATE: 1098-03-13
| PRIOR FILING DATE: 1998-03-13
| PRIOR FILING DATE: 1998-09-13
| PRIOR PRIOR FILING DATE: 1998-09-13
| PRIOR PRIOR FILING DATE: 1998-09-13
| PRIOR FILING DATE: 1998-09-13
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Publication No. US20030190617A1

GENERAL INFORMATION:

APPLICANT: RAYMOND, VINCENT

APPLICANT: RAYMOND, VINCENT

APPLICANT: BY

TITLE OF INVENTION: OPTINEURIN NUCLBIC ACID MOLECULES AND USES THEREOF

TILE REFERENCE: 13587.338

CURRENT APPLICATION NUMBER: US/10/091,281

CURRENT APPLICATION NUMBER: US/10/091,281

CURRENT PILING DATE: 2002-03-06

NUMBER OF SEQ ID NOS: 463

SOSTWARE: Patentin Ver. 2.1

SEQ ID NO 393

LENGTH: 12
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                                                                                                                                                                           ) OTHER INFORMATION: Description of Artificial Sequence:
, OTHER INFORMATION: oligonucleotide
US-10-275-071-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Putative SORY/SRY.01 motifus-10-091-281-393
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Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
      SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                             731 AGGAGAAACAGA 742
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserva
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US-10-684-830-34/c
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SEQ ID NO 5
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NAME/KRY: modified base
LOCATION: (6)..(9)
OTHER INFORMATION: LNA monomer
OTHER INFORMATION: Description of Artificial Sequence: LNA modified
OTHER INFORMATION: oligonuclectide
                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-152-059-3
                                                                                                                                                                                                                                                  Score 8.8; DB 1; Length 13;
Pred. No. 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLECTIDE ANALOGUES
FILE REFERNCE: 49165 (71994)
FURRENT APPLICATION NUMBER: U$/09/152,059
CURRENT FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR FILING DATE: 1998-01-06
PRIOR FILING DATE: 1998-01-03
PRIOR APPLICATION NUMBER: 60/088,309
PRIOR APPLICATION NUMBER: 60/088,309
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/094,355
PRIOR FILING DATE: 1998-07-28
PRIOR FILING DATE: 1998-07-28
PRIOR FILING DATE: 1998-07-28
PRIOR FILING DATE: 1998-07-28
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Patent No. US20020068708Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09152059
Patent No. US20020006B708A1
GENERAL INFORMATION:
APPLICANT: WENGEL, JESPER
                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 13
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TITLE OF TYNEWRINGS (CALCANUCEOTIDE ANALOGUES)
FILLE REFERENCE: 43.56 (CALCANUCEOTIDE ANALOGUES)
FORTERTY PARTICATION WOMERS: (0)(55,41)
FRIOR APPLICATION WOMERS: (0)(55,41)
FRIOR APPLICATION WOMERS: (0)(75,541)
FRIOR APPLICATION WOMERS: (0)(75,541)
FRIOR APPLICATION WOMERS: (0)(70,591)
FRATURE: INFORMATION: OLIGORICATION APPLICATION WOMERS: (0)(70,591)
FRATURE: INFORMATION: OLIGORICATION APPLICATION WOMERS: (0)(70,591)
FRATURE: INFORMATION: OLIGORICATION WOMERS: (0)(70,591)
FRATURE: INFORMATION WOMERS: (0)(70,591)
FRATURE: INFORMATION WOMERS: (0)(70,591)
FRATURE: PRINCE APPLICATION WOMERS: (0)(70,591)
FRATURE: PRI
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PRIOR FILING DATE: 1997-09-12
PRIOR PLILING DATE: 1997-09-12
PRIOR PLILING DATE: 1997-12-19
PRIOR PLILING DATE: 1997-12-19
PRIOR PLILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR PLILING DATE: 1998-04-29
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 13
TYPE: DAA
TYPE: DAA
ORGANISM: Artificial Sequence
FATURE:
NAME/KEY:
NA
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| Sequence 9, Application US/09152059
| Patent No. US20020068708A1
| GENERAL INFORMATION:
| APPLICANT: WIRGEL. VEOUR
| TITLE OF INVENTION: DIGORUCLEOTIDE ANALOGUES
| FILE REFERENCE: 49165 (71994)
| CURRENT FILING DATE: 1998-09-11
| PRIOR FILING DATE: 1998-09-11
| PRIOR PILING DATE: 1998-01-16
| PRIOR PILING DATE: 1998-04-29
| PRIOR PILING DATE: 1998-04-29
| PRIOR PILING DATE: 1998-04-29
| PRIOR PILING DATE: 1998-06-05
| PRIOR APPLICATION NUMBER: 60/084,309
| PRIOR PILING DATE: 1998-06-05
| PRIOR APPLICATION NUMBER: 60/084,309
| PRIOR FILING DATE: 1998-06-05
| PRIOR APPLICATION NUMBER: 60/084,309
| PRIOR PILING DATE: 1998-06-05
| PRIOR APPLICATION NUMBER: 60/084,309
| PRIOR PILING DATE: 1998-06-05
| PRIOR PILING DATE: 1998-06-05
| PRIOR FILING DATE: 1098-06-05
| PRIOR PILING DATE: 1008-06-05
| PRIOR PILING DATE: 1008
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collection of Artificial Sequence: LNA modified
collectio
           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: oligonucleotide
US-09-152-059-6
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                              Query Match
40.0%; Score 8.8; DB 1; Length 13.
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
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US-09-152-059-7/C

Sequence 7, Application US/09152059
Patent No. US20020068708A1
GENERAL INFORMATION:
APPLICANT: WENELSEN, POUL
TITLE OF INVENTION: OLIGONUCLECTIDE ANALOGUES
FILE REPRENCE: 49165 (71994)
CURRENT APPLICATION NUMBER: US/09/152,059
CURRENT PILING DATE: 1998-09-11
PRIOR PILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-13
PRIOR FILING DATE: 1997-09-13
PRIOR FILING DATE: 1998-01-16
PRIOR PRILING DATE: 1998-01-16
PRIOR PRILING DATE: 1998-01-16
PRIOR PRILING DATE: 1998-01-05
PRIOR PILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOSE: 146
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GENERAL INFORMATION:
APPLICANT: WENGEL, JESPER
APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165 (71994); CURRENT APPLICATION NUMBER: US/09/152,059; CURRENT FILING DATE: 1998-09-11; PRIOR APPLICATION NUMBER: 60/058,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     736 AAACAGAACACC 747
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US-09-152-059-8/c
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LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: modified base
LOCATION: (1)...(12)
OTHER INFORMATION: LNA monomer
COTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-152-059-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified base
LOCTGATION: (12)
OCHER INFORMATION: LNA monomer
OTHER INFORMATION: Description of Artificial Sequence: Probe
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NIELSEN, POUL
APPLICANT: NIELSEN, POUL
APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165 (71994)
CURRENT APPLICATION NUMBER: US/99/152,059
CURRENT APPLICATION NUMBER: 06/058,541
PRIOR APPLICATION NUMBER: 66/058,541
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-12-19
PRIOR PLICATION NUMBER: 66/068,293
PRIOR PLICATION NUMBER: 66/071,682
PRIOR PLICATION NUMBER: 66/071,682
PRIOR PLICATION NUMBER: 66/071,682
PRIOR PLICATION NUMBER: 66/076,591
PRIOR PLICATION NUMBER: 66/076,591
PRIOR APPLICATION NUMBER: 66/083,507
PRIOR PLICATION NUMBER: 66/083,507
PRIOR PLILING DATE: 1998-04-29
PRIOR PLILING DATE: 1998-04-29
PRIOR PLILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 66/083,309
PRIOR PLILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 66/084,355
PRIOR PLILING DATE: 1998-06-05
PRIOR PLILING DATE: 1998-07-28
PRIOR FILING DATE: 1998-03-03
PRIOR PAPLICATION NUMBER: 60/083,507
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/094,355
PRIOR APPLICATION NUMBER: 60/094,355
PRIOR PILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-152-059-30/c
; Sequence 30, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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SEQ ID NO 30
LENGTH: 13
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                  DB 1; Length 13;
                                                                                                                        2; Indels
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1/S-09-152-059-29/C

Sequence 29, Application US/09152059
Fatent No. US20200068708A1
FAPPLICANT: WENGEL, JESPER
FILLE REFERENCE: 49165 (71394)
CURRENT APPLICATION NUMBER: US/09/152,059
CURRENT FILLNG DATE: 1998-09-11
FRIOR APPLICATION NUMBER: 60/058,541
FRIOR APPLICATION NUMBER: 60/058,541
FRIOR APPLICATION NUMBER: 60/058,541
FRIOR APPLICATION NUMBER: 60/058,541
FRIOR FILLING DATE: 1997-09-12
FRIOR FILLING DATE: 1997-09-12
FRIOR FILLING DATE: 1997-09-12
FRIOR FILLING DATE: 1997-09-12
FRIOR FILLING DATE: 1998-09-11
FRIOR FILLING DATE: 1998-01-16
FRIOR FILLING DATE: 1998-01-16
FRIOR FILLING DATE: 1998-01-16
FRIOR FILLING DATE: 1998-01-16
                                                               Query Match
40.0%; Score 8.8; DB
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REPERENCE: 49165 (71994)
CURRENT APPLICATION NUMBER: US/09/152,059
CURRENT FILING DATE: 1998-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1998-09-11
PRICE PRINCE APPLICATION NUMBER: 60/058,541
PRICE PILING DATE: 1997-09-12
PRICE PILING DATE: 1997-09-12
PRICE FILING DATE: 1999-01-19
PRICE PILING DATE: 1998-01-16
PRICE APPLICATION NUMBER: 60/076,591
PRICE APPLICATION NUMBER: 60/076,591
PRICE PILING DATE: 1998-01-03
PRICE PILING DATE: 1998-01-03
PRICE PILING DATE: 1998-04-29
PRICE PILING DATE: 1998-06-05
PRICE PILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO SEQ ID NOS: 146
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application US/09152059
Patent No. US20020068708A1
GENERAL INFORMATION:
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            US-09-152-059-9
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ORGANISM: Artificial Sequence
FRATURE:
NAME/KEY: modified base
LOCATION: (6)..(9)
OTHER INFORMATION: LNA monomer
OTHER INFORMATION: Description of Artificial Sequence: LNA modified
SOTHER INFORMATION: Oligonucleotide
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; PRATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; LOCATION: (1)...(12)
; LOCATION: LINA monomer
US-09-152-059-32
                                                                                                                                                                                                                                                                                                                                     Query Match 40.0%; Score 8.8; DB 1; Length 13; Best Local Similarity 83.3%; Pred. No. 95; Matches 10; Conservative 0; Mismatches 2; Indels
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/09152059
Patent No. US20020068708A1
| GENERAL INFORMATION:
APPLICANT: WIELSEN, POUL
| TITLE OF INVENTION: OLICONUCLEOTIDE ANALOGUES
| TITLE OF INVENTION: OLICONUCLEOTIDE ANALOGUES
| FILE REFERENCE: 49165 (71994)
| CURRENT APPLICATION NUMBER: US/09/152,059
| CURRENT APPLICATION NUMBER: 60/058,541
| PRIOR APPLICATION NUMBER: 60/058,541
| PRIOR FILING DATE: 1998-09-12
| PRIOR FILING DATE: 1997-12-19
| PRIOR FILING DATE: 1998-01-16
| PRIOR FILING DATE: 1998-01-29
| PRIOR FILING DATE: 1998-01-29
| PRIOR FILING DATE: 1998-01-29
| PRIOR FILING DATE: 1998-01-28
| NUMBER OF SEQ ID NOS: 146
| SOFTWARE: PARENTIN VEY: 2.1
| INVERT OF IN NOS: 146
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; Sequence 44, Application US/09152059
; Patent No. US20020068708A1
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                               APPLICANT: WRENEEL, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE SPERRENCE: 49165 (71994)
CURRENT APPLICATION OULGONUCLEOTIDE ANALOGUES
FILE SPERRENCE: 49165 (71994)
CURRENT FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/056,541
PRIOR FILING DATE: 1997-19-19
PRIOR FILING DATE: 1997-10-19
PRIOR FILING DATE: 1997-10-19
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR APPLICATION NUMBER: 60/083,507
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084,355
PRIOR PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PATCHIN VOWER: 09/094,355
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
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Patent No. US2002068708A1
GENERAL INFORMATION:
APPLICANT: WIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REPERENCE: 49165 (71994)
CURRENT FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 06/059,541
PRIOR PELING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-28
                                                                                                                                     Sequence 31, Application US/09152059
Patent No. US20020068708A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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     12 AAACAAACCACC:1
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US-09-152-059-32/c
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. OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-152-059-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                               DB 1; Length 13;
                                                                                                                                                                                                    Indels
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APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165 (71994)
CURRENT APPLICATION NUMBER: US/09/152,059
CURRENT FILING DATE: 1998-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WENGEL, JESPER
APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLICONUCLECTIDE ANALOGUES
FILE REFERENCE: 49165 (71994)
CURRENT APPLICATION NUMBER: US/09/152,059
CURRENT FILING DATE: 1998-09-11
                                                                                                                 Best Local Similarity 83.3%; Pred. No. 95; Matches 10; Conservative 0; Miemra.
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PRIOR FILING DATE: 1997-09-12
PRIOR PAPLICATION NUMBER: 60/068,541
PRIOR PAPLICATION NUMBER: 60/068,293
PRIOR PILING DATE: 1997-12-19
PRIOR PAPLICATION NUMBER: 60/071,682
PRIOR FILING DATE: 1998-01-16
PRIOR PILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
NUMBER OF SEQ ID NOS: 146
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PRIOR APPLICATION NUMBER: 60/058,541
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; Sequence 47, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
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US-09-152-059-48/c

) Sequence 48, Application US/09152059

; Partent No. US20020068708A1

; GENERAL INFORMATION:
TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                          736 AAACAGAACACC 747
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ORGANISM: Artificial Sequence
FEATURE:
.OTHER INFORMATION: Description of Artificial Sequence: Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-152-059-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.0%; Score 8.8; DB 1; Length 13; illarity 83.3%; Pred. No. 95; Conservative 0; Mismatches 2; Indels
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US-09-152-099-46/C

Patent No. US20020068708A1

GENERAL INPORMATION:
APPLICANT: WIELSEN, POUL

TITLE OF INVENTION: OLIGONUCLECTIDE ANALOGUES
FILE SPERENCE: 49165 (71994)
CURRENT APPLICATION NUMBER: US/09/152,059
CURRENT APPLICATION NUMBER: US/09/152,059
CURRENT APPLICATION NUMBER: 60/086,241

PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-07-28
NUMBER: OF SEQ ID NOS: 146

SOFTWARE: PATCHTIN VET. 2.1
                                APPLICANT: WENGEL, JESPER
APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLIGONULLEOTIDE ANALOGUES
FILE REPERENCE: 49.65 (71994)
CURRENT APPLICATION NUMBER: US/09/152,059
CURRENT FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-13
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SSEQ ID NO SEQ ID NOS: 146
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Best Local Similarity
Matches 10; Conserv
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified base
LOCATION: (6)..(9)
OTHER INFORMATION: LNA monomer
OTHER INFORMATION: Description of Artificial Sequence: LNA modified
US-09-152-059-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                            sequence 74, Application US/09152059
sequence 74, Application US/09152059
sequence 74, Application US/09152059
setent No. US200200680A1
GENERAL INFORMATION:
APPLICANT: WEBSEL, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165 (71994)
CURRENT FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/058,541
PRIOR APPLICATION NUMBER: 60/058,541
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR FILING DATE: 1998-01-16
PRIOR PELLING DATE: 1998-01-16
PRIOR PELLING DATE: 1998-01-16
PRIOR PELLING DATE: 1998-01-18
PRIOR PELLING DATE: 1998-01-28
PRIOR PELLING DATE: 1998-01-28
PRIOR PELLING DATE: 1998-01-28
PRIOR FILING DATE: 1998-01-28
PRIOR PELLING DATE: 1998-01-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 74
PURCHALLING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 74
PURCHALLING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 74
PURCHALLING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 74
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US-09-152-059-77/C

Sequence 77, Application US/09152059
Patent No. US20020068708A1
GENERAL INFORMATION:
APPLICANT: WEMCEL, USEPER
APPLICANT: WIELER, FOUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165 (71994)
CURRENT APPLICATION NUMBER: US/9/152,059
CURRENT FILING DATE: 1998-09-11
PRIOR FILING DATE: 1997-09-12
PRIOR PELICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/01,682
PRIOR APPLICATION NUMBER: 60/01,682
PRIOR PRILING DATE: 1998-01-16
PRIOR PLING DATE: 1998-01-16
PRIOR PLING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR PLING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR APPLICATION NUMBER: 60/076,591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 95;
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patent No. US20020068708A1

GENERAL INFORMATION:

APPLICANT: WENGEL, JESPER

APPLICANT: WENGEL, JESPER

TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

FILE REFERENCE: 49165 (71994)

CURRENT APPLICATION NUMBER: US/09/152,059

CURRENT FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR FILING DATE: 1997-09-12

PRIOR PILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-01-16

PRIOR APPLICATION NUMBER: 60/071,682

PRIOR PILING DATE: 1998-03-03

PRIOR PILING DATE: 1998-04-29

PRIOR PILING DATE: 1998-04-29

PRIOR PILING DATE: 1998-04-29

PRIOR PILING DATE: 1998-04-29

PRIOR PILING DATE: 1998-07-28

PRIOR APPLICATION NUMBER: 60/083,507

PRIOR PILING DATE: 1998-07-28

PRIOR PILING DATE: 1998-07-28

NUMBER: OF SEQ ID NOS: 146

SOFTWARE: PATENTIN VET: 2.1

FRANCE APPLICATION NUMBER: 0/094,355

PRIOR PILING DATE: 1998-07-28

NUMBER: OF SEQ ID NOS: 146

SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-03-03
PRIOR PILING DATE: 1998-03-03
PRIOR PILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/083,507
PRIOR APPLICATION NUMBER: 60/083,309
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 48
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 10, Conservative
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US-09-152-059-71/c
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736 AAACAGAACACC 747

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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASESEQ for Windows Version 4.0
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83.3%; Pred. No. 95;
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83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-177279
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 177279
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Sequence 23, Application US/09781811

Fatent No. US20020151463A1

GENERAL INFORMATION:
APPLICANT: WOYCHIK, RICHARD P.
APPLICANT: WOYCHIK, RICHARD P.
APPLICANT: BULTMAN, SCOTT J.
APPLICANT: BULTMAN, SCOTT J.
APPLICANT: MICHAUD, EDWARD J.
TITLE OF INVENTION: AGGOTTI POLYNUCLEOTIDE COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4310.001682
CURRENT APPLICATION NUMBER: US/09/781,811
CURRENT APPLICATION NUMBER: 09/034,088
PRIOR FILING DATE: 1998-03-03

PRIOR FILING DATE: 1998-03-03

PRIOR FILING DATE: 1993-05-21

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 23

LENGTHANE: PatentIN Ver. 2.1

LENGTHANE: PATENTIN VER. 2.1
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                                                                                                                                                                                                                                               NAME/KEY: modified base
LOCATION: (1)...(13)
OTHER INFORMATION: Description of Artificial Sequence: LNA modified
OTHER INFORMATION: Digonucleotide
OTHER INFORMATION: 0ligonucleotide
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Sequence 177279, Application US/10027632

PUBLICATION NO. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPRENCE: 108927.123

CURRENT APPLICATION NUMBER: US/10/027,632
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US-09-781-811-23
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
PRIOR APPLICATION NUMBER: 60/088,309
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/094,355
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 77
                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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Matches 10; Conservative
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US-09-152-059-77
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GENERAL IN CHARATION:

APPLICANT:
Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERBORE: 10857.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2002-04-20

PRIOR PELING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/199,676

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR PLING DATE: 1999-10-34

PRIOR FILING DATE: 1999-10-34

PRIOR FILING DATE: 1999-10-34

PRIOR FILING DATE: 1999-09-28

PRIOR PRIOR DATE: 1999-09-28

PRIOR DATE: 1999-09-28

PRIOR PRIOR DATE: 1999-09-28

PRIOR PRIOR DATE: 1999-09-28

PRIOR DATE: 1999-09-28
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Pred. No. 95;
0; Mismatches 2; Indels
DB 1; Length 13;
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Gaps
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                                                                                                                                                                                                      TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: LNA modified
COTHER INFORMATION: Oligonucleotide
NAME/KEY: modified_base
LOCATION: (6)..(9)
COTHER INFORMATION: LNA monomer
US-10-008-029-4
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OTHER INFORMATION: oligonucleotide
NAME/KEX: modified base
LOCATION: (1)...(12)
OTHER INFORMATION: LNA monomer
US-10-008-029-5
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Pred. No. 95;
0; Mismatches 2; Indels
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APPLICANT: WIELSEN, POUL
TITLE OF INVENTION: OLFOWOULLECTIDE ANALOGUES
FILE OF INVENTION OWNER: US/10/008,029
CURRENT APPLICATION NUMBER: 09/152,059
PRIOR FILING DATE: 1998-09-12
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/071,682
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR APPLICATION NUMBER: 60/084,355
PRIOR FILING DATE: 1998-01-28
PRIOR FILING DATE: 1998-07-28
NUMBER: OF SEQ ID NOS: 146
SOFTWARE: PATENTING DATE: 1998-07-28
NUMBER: OF SEQ ID NOS: 146
SOFTWARE: DATE: 1998-07-28
TYPE: DATE: TRANTIFIED AND SET OF SEQ ID NOS: 146
PREATHER FILING DATE: 1998-07-28
NUMBER: OF SEQ ID NOS: 146
PROMINENT: 13
PRIOR PRIOR FILING DATE: 1998-07-28
NUMBER: OF SEQ ID NOS: 146
PROMINENT: 13
PROM
PRIOR APPLICATION NUMBER: 60/094,355
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 4
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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US-10-008-029-5/c
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                                                                                          US-10-008-025-3/C
US-10-008-025-3/C
Publication No. US20030134808A1
GENERAL INFORMATION:
APPLICANT: NIELSEN, POUL
TITLE OF INVENDING: LOCONUCLECTIDE ANALOGUES
FILE REPERENDE: 4001-10.
TITLE OF INVENDING: 0.10-000001.
CURRENT APPLICATION NUMBER: US/10/008,029
CURRENT APPLICATION NUMBER: US/10/008,029
CURRENT APPLICATION NUMBER: 09/152,059
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR PRILING DATE: 1998-01-16
PRIOR PRILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-28
PRIOR FILING DATE: 1998-07-28
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SCOTWARE: PATENTIN VOR: 2.1
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Publication No. US20030134808A1
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
JITLE OF INVENTION:
JITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/008,029
CURRENT APPLICATION NUMBER: US/10/008,029
CURRENT APPLICATION NUMBER: 05/15,059
PRIOR APPLICATION NUMBER: 06/15,059
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-03
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
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ORGANISM: Artificial Sequence
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                                       RESULT 130
US-10-008-029-3/c
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                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence ORGANISM: Artificial Sequence: LNA modified OTHER INFORMATION: Description of Artificial Sequence: LNA modified OTHER INFORMATION: oligonucleotide NAME/KEY: modified_base
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OTHER INFORMATION: Description of Artificial Sequence: LNA modified
OTHER INFORMATION: Oligonucleotide
NAME/KEY: modified base
LOCATION: (6)..(9)
COTHER INFORMATION: LNA monomer
US-10-008-029-8
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
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Publication No. US2003013480841
GENERAL INFORMATION USEDER
APPLICANT: WIELEN, JESPER
APPLICANT: WIELEN, POUL
ITILE OF INVENTION: OLICONUCLECTIDE ANALOGUES
FILE SPERENCE: 49165-C2 (71994)
CURRENT APPLICATION NUMBER: 09/152,059
RRIOR APPLICATION NUMBER: 09/152,059
RRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-06
PRIOR FILING DATE: 1998-01-08
PRIOR PRIOR PLICATION NUMBER: 60/084,355
PRIOR PLICATION NUMBER: 60/084,355
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 8
ILENGTH: 13
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Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION WUMBER: 60/094,355
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin Ver. 2.1
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (7)
; OTHER INFORMATION: LNA monomer US-10-008-029-7
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ORGANISM: Artificial Sequence
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                 Sequence 6, Application US/10008029
Publication No. US20030134808A1
GENERAL INFORMATION:
APPLICANT: WIRDEL, NESPER
APPLICANT: WIRDEL, POUL
ITILE OF INVENTION: OLIFONUCLEOTIDE ANALOGUES
FILE REFERENCE: 491.65-C2 (71994)
CURRENT FILING DATE: 2001-11-05
FRIOR APPLICATION NUMBER: 09/152,059
FRIOR FILING DATE: 1998-09-11
FRIOR FILING DATE: 1997-09-12
FRIOR FILING DATE: 1997-09-12
FRIOR APPLICATION NUMBER: 60/068,293
FRIOR FILING DATE: 1997-09-12
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-28
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US-10-008-029-7/C

Sequence 7, Application US/10008029

Publication No. US2003134808A1

GENERAL INFORMATION:

APPLICANT: WENGEL, JESPER

APPLICANT: WENGEL, JESPER

TITLE OF INVENTION: OLIGONUCLECTIDE ANALOGUES

FILE REFERENCE: 49165-02/(71994)

CURRENT APPLICATION NUMBER: US/10/008,029

CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: 09/152,059

PRIOR PILING DATE: 1999-09-11

PRIOR APPLICATION NUMBER: 60/058,541

PRIOR PILING DATE: 1997-09-12

PRIOR PILING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR APPLICATION NUMBER: 60/076,591

PRIOR APPLICATION NUMBER: 60/076,591

PRIOR APPLICATION NUMBER: 60/076,591

PRIOR APPLICATION NUMBER: 60/076,591

PRIOR APPLICATION NUMBER: 60/076,591
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/089,309
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APPLICATION NUMBER: 60/088,309
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ö ; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Probe NAME/KBY: modified base LOCATION: (1)..(12) OTHER INFORMATION: LNA monomer ; OTHER INFORMATION: Description of Artificial Seguence: Probe US-10-008-029-28 Length 13; DB 1; Length 13; Indels Indels Query Match
40.0%; Score 8.8; DB 1;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Sequence 29, Application US/10008029
Publication No. US20030134808A1
GENERAL INFORMATION:
APPLICANT: WENGEL, USEPER
APPLICANT: WIELSEN, POUL
ITILE OF INVENTION: OLIFORNOLIZEDIDE ANALOGUES
FILE REFERENCE: 49165-C2 (71994)
CURRENT FILING DATE: 2001-11-05
FRIOR APPLICATION NUMBER: 09/152,059
FRIOR FILING DATE: 1998-09-11
FRIOR FILING DATE: 1998-09-11
FRIOR FILING DATE: 1997-09-12
FRIOR FILING DATE: 1997-09-12
FRIOR PRILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-05
FRIOR FILING DA Query Match 40.0%; Score 8.8; DB Best Local Similarity 83.3%; Pred. No. 95; Matches 10; Conservative 0; Mismatches PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: 60/083,507
PRIOR FILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 28
LENGTH: 13 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: TYPE: DNA ORGANISM: Artificial Sequence 736 AAACAGAACACC 747 736 AAACAGAACACC 747 12 AAACAAACCACC 1 12 AAACAAACCACC 1 US-10-008-029-29/c US-10-008-029-29 දි ö Gaps OTHER INFORMATION: Description of Artificial Sequence: LNA modified
COTHER INFORMATION: oligonucleotide
NAME/KEY: modified base
LOCATION: 10...(12)
COTHER INFORMATION: LNA monomer
US-10-008-029-9 ö Ouery Match
40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels Geguence 9, Application US/10008029; Squence 9, Application US/10008029; Publication No. US20030134808A1
GENERAL INFORMATION:
APPLICANT: WENGEL, JESPER
APPLICANT: NIELSEN, POUL
TITLE OF INVANITON: OLIGONUCLEOTIDE ANALOGUES
FILE SEFERENCE: 49165-C2(71994); CURRENT PILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: 09/152,059
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-12
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR FILING DATE: 1998-01-6
PRIOR FILING DATE: 1998-01-6
PRIOR FILING DATE: 1998-01-6
PRIOR FILING DATE: 1998-01-6
PRIOR FILING DATE: 1998-03-03
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-07-28
PRIOR PILING DATE: 1998-07-28 RESULT 137
US-10-08-029-28/C

US-10-008-029-28/C

Sequence 28, Application US/10008029

Publication No. US20030134808A1

GENERAL INFORMATION:

APPLICANT: WENGEL, USEPER

APPLICANT: WIELSEN, POUL

TITLE OF INVENTION: OLICONUCLEOTIDE ANALOGUES

FILE REFERENCE: 4916-C2(1994)

CURRENT APPLICATION NUMBER: US/10/008,029

CURRENT FILING DATE: 2001-11-05

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: 60/068,541

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR FILING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/01,682

PRIOR FILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-16 TYPE: DNA ORGANISM: Artificial Sequence 736 AAACAGAACACC 747 12 AAACAAACCACC 1 12 AAACAAACCACC 1 RESULT 136 US-10-008-029-9/c g ò

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                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-008-029-31
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
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APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165-C2 (7194)
CURRENT APPLICATION NUMBER: U5/10/008,029
CURRENT PILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 06/152,059
PRIOR APPLICATION NUMBER: 60/058,541
PRIOR FILING DATE: 1999-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR PILING DATE: 1998-01-03
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40.0%; Score 8.8; DB
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/088,309
PRIOR PILING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR PILING DATE: 1998-07-28
NUMBER: OF SEQ ID NOS: 146
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32, Application US/10008029
Publication No. US20030134808A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   736 AAACAGAACACC 747
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SEQ ID NO 32
LENGTH: 13
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COTHER INFORMATION: Description of Artificial Sequence: Probe NAMENSTRY: modified base
LOCATION: (1)..(12)
COTHER INFORMATION: LNA monomer
US-10-008-029-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                   APPLICANT: WINGEL, JOSPER
APPLICANT: WINGEL, JOSPER
APPLICANT: WIELSEN, POUL
ITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165-C2 (71994)
CURRENT APPLICATION NUMBER: US/10/006,029
CURRENT APPLICATION NUMBER: 09/152,059
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR PILING DATE: 1998-01-16
PRIOR PILING DATE: 1998-01-16
PRIOR PILING DATE: 1998-01-01
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 30
LENGTH: 13
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US-10-008-022-31/C
Publication No US20030134808A1
GENERAL INFORMATION:
APPLICANT: WHENEX.
APPLICANT: WHENEX.
APPLICANT: WHENEX.
POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REPRENCE: 49165-C2 (71994)
CURRENT APPLICATION NUMBER: US/10/008,029
CURRENT APPLICATION NUMBER: 09/112,059
PRIOR APPLICATION NUMBER: 60/058,541
PRIOR FILING DATE: 1997-09-12
PRIOR FLILING DATE: 1997-09-12
PRIOR FLILING DATE: 1997-09-12
PRIOR FLILING DATE: 1997-09-12
PRIOR FLILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-03-03
                                                                                                             Sequence 30, Application US/10008029; Publication No. US20030134808A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              736 AAACAGAACACC 747
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                                                          RESULT 139
US-10-008-029-30/c
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
NAME/KEY: modified base
DOCATION: (6)..(9)
COTHER INFORMATION: LNA monomer
US-10-008-029-46
                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-10-008-029-44
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-008-029-46/C

US-10-008-029-46/C

Sequence 46, Application US/10008029

Publication No. US2030134808A1

Sequence 46, Application US/10008029

Publication No. US2030134808A1

APPLICANT: WENGEL, USERER

APPLICANT: WENGEL, POUL

TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

FILE REFERENCE: 49165-C2 (71994)

CURRENT APPLICATION NUMBER: US/10/008,029

CURRENT APPLICATION NUMBER: US/10/008,029

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR PILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-03-03

PRIOR APPLICATION NUMBER: 60/008,309

PRIOR APPLICATION NUMBER: 60/088,309

PRIOR FILING DATE: 1998-04-29

PRIOR FILING DATE: 1998-04-29

PRIOR FILING DATE: 1998-04-29

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-04-28

NUMBER OF SEQ ID NOS: 146

SEQ ID NO 46

LENGTH: 13
PRIOR APPLICATION NUMBER: 60/088,309
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/094,355
PRIOR APPLICATION NUMBER: 60/094,355
PRIOR PILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 44
LENGTH: 13
TYPE: DNA
CREANISM: Artificial Sequence
FEATURE:
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GENERAL INCORMATION:

GENERAL INCORMATION:

GENERAL INCORMATION:

GENERAL INCORMATION:

APPLICANT: WIELSEN, FOUL

TITLE OF INCORTION: OLIGONUCLECTIDE ANALOGUES

FILE SPERENCE: 49165-C2 (71994)

CURRENT APPLICATION NUMBER: US/10/008,029

CURRENT ALLING DATE: 1998-09-11

PRIOR FILING DATE: 1997-05-12

PRIOR FILING DATE: 1997-05-12

PRIOR FILING DATE: 1997-03-12

PRIOR FILING DATE: 1997-03-12

PRIOR FILING DATE: 1998-04-13

PRIOR FILING DATE: 1998-04-29

PRIOR FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 146

SEQ ID NO 43

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                    ) FEATURE:
) OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-008-029-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
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| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: WIELSEN, POUL
| TITLE OF INVENTION:
| TITL
PRIOR APPLICATION NUMBER: 60/094,355
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74, Application US/10008029; Publication No. US20030134808A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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US-10-008-029-71/c
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US-10-008-029-74/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 13;
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                                                                                                                                                                   APPLICANT: WENGEL, JESPER
APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE SEFERENCE: 49165-C2 (71994)
CURRENT APPLICATION NUMBER: US/10/008,029
CURRENT FILING DATE: 2001-11-05
FRICE APPLICATION NUMBER: 09/152,059
FRICE FILING DATE: 1998-09-11
FRICE FILING DATE: 1997-09-12
FRICE FILING DATE: 1997-09-12
FRICE RILING DATE: 1997-01-15
FRICE RILING DATE: 1998-09-11
FRICE APPLICATION NUMBER: 60/006,591
FRICE RILING DATE: 1998-01-16
FRICE APPLICATION NUMBER: 60/076,591
FRICE APPLICATION NUMBER: 60/096,591
FRICE APPLICATION NUMBER: 60/096,591
FRICE APPLICATION NUMBER: 60/098,309
FRICE FILING DATE: 1998-03-03
FRICE FILING DATE: 1998-04-29
FRICE FILING DATE: 1998-04-28
FRICE APPLICATION NUMBER: 60/094,355
FRICE APPLICATION 
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Sequence 48, Application US/10008029

Publication No. US20030134808A1

GENERAL INFORMATION:

APPLICANT: NIELESEN, POUL

TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

FILE REFERENCE: 49165-C2(71994)

CURRENT APPLICATION NUMBER: US/10/008,029

CURRENT FILING DATE: 1098-09-11

PRIOR APPLICATION NUMBER: 60/058,541

PRIOR APPLICATION NUMBER: 60/058,541

PRIOR FILING DATE: 1999-09-12

PRIOR PILING DATE: 1999-012

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR PILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-16

PRIOR APPLICATION NUMBER: 60/065,591

PRIOR APPLICATION NUMBER: 60/065,591

PRIOR APPLICATION NUMBER: 60/065,591

PRIOR APPLICATION NUMBER: 60/083,507

PRIOR APPLICATION NUMBER: 60/083,507

PRIOR APPLICATION NUMBER: 60/088,309

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/088,309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
40.0%; Score 8.8; DE
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
                                                Sequence 47, Application US/10008029
Publication No. US20030134808A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                      GENERAL INFORMATION:
         US-10-008-029-47/c
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                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
CORGANISM: Artificial Sequence
COTHER INFORMATION: Discription of Artificial Sequence: LNA modified
COTHER INFORMATION: Oligonucleotide
NAME/KEY: modified base
LOCATION: (1)..(12)
COTHER INFORMATION: LNA monomer
US-10-008-029-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; JOHER INFORMATION: Oligonucleotide
US-10-208-650-3
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Pred. No. 95;
0; Mismatches 2; Indels
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PUBLICATION NO. US20030144231A1
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
JITTLE OF INVENTION: OLIGOMUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165-C2 (71994)
CURRENT APPLICATION NUMBER: US/10/008,029
FRIOR REPLICATION NUMBER: 09/152,059
FRIOR FILING DATE: 2001-11-05
FRIOR FILING DATE: 1998-09-11
FRIOR FILING DATE: 1998-09-11
FRIOR FILING DATE: 1997-12-19
FRIOR FILING DATE: 1997-01-12
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-28
FRIOR FILING DATE: 1998
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40.0%; Score 8.8; DE
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
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Best Local Similarity 83.3%;
Matches 10; Conservative
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 77
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                736 AAACAGAACACC 747
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US-10-208-650-3/c
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US-10-208-650-4/c
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CTHER INFORMATION: oligonucleotide
NAME/KEY: modified base
LOCATION: (6). (9)
COTHER INFORMATION: LNA monomer
US-10-008-029-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 13;
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                   APPLICANT: MERGEN, OUGGENTERS, APPLICANT: MERGEN, DOUL
FILE OF INVENTION: OLIGONUCLECTIDE ANALOGUES
FILE REFERENCE: 49165-C2 (71994)
CURRENT APPLICATION NUMBER: US/10/008,029
CURRENT FILING DATE: 2001-11-05
FRIOR FILING DATE: 1994-09-11
FRIOR APPLICATION NUMBER: 06/058,541
FRIOR APPLICATION NUMBER: 06/058,541
FRIOR APPLICATION NUMBER: 60/068,293
FRIOR APPLICATION NUMBER: 60/068,293
FRIOR FILING DATE: 1997-12-19
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-03-03
FRIOR FILING DATE: 1998-04-29
FRIOR FILING DATE: 1998-04-29
FRIOR FILING DATE: 1998-04-29
FRIOR FILING DATE: 1998-04-29
FRIOR FILING DATE: 1998-07-28
FRIOR APPLICATION NUMBER: 60/083,507
FRIOR FILING DATE: 1998-07-28
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 10; Conservative
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: LNA modified
OTHER INFORMATION: oligonucleotide
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Sequence 6, Application US/10208650
Sequence 6, Application US/10208650
Sequence 6, Application US/10208650
SEQUENCE ON NO. USCO 30144231A1
SEPERAL INFORMATION
TITLE OF INVENTION OLIGONUCLECTIDE ANALOGUES
FILE REFERENCE: 49165-C2 (71994)
CURRENT APPLICATION NUMBER: US/10/008, 029
PRIOR APPLICATION NUMBER: US/10/008, 029
PRIOR APPLICATION NUMBER: 09/15, 059
PRIOR PELING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR PELICATION NUMBER: 60/068, 293
PRIOR PELICATION NUMBER: 60/068, 293
PRIOR PELICATION NUMBER: 60/076, 591
PRIOR PELICATION NUMBER: 60/076, 591
PRIOR PELICATION NUMBER: 60/089, 309
PRIOR PELICATION NUMBER: 60/089, 309
PRIOR PELING DATE: 1998-01-05
PRIOR PELING DATE: 1998-01-05
PRIOR PELING DATE: 1998-05-05
PRIOR PELING DATE: 1998-06-05
PRIOR PELING DATE: 1998-07-28
NUMBER: OF SEQ ID NOS: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
40.0%; Score 8.8; DB
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
      PRIOR FILING DATE: 1998-03-03
PRIOR PELING DATE: 1998-03-03
PRIOR PELING DATE: 1998-04-29
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088,309
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/094,355
PRIOR FILING DATE: 1998-07-28
NUMBER: OF SEQ ID NOS: 146
SOFTWARE: PATCHILN VET. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEATURE:
NAME/KEY: modified base
LOCATION: (1)...(12)
OTHER INFORMATION: LNA monomer
US-10-208-650-5
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
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LENGTH: 13
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Sequence 4, Application US/10208650
Publication No. US20030144231A1
SAPELICANT: WORSEL, JESPER
APPLICANT: WIELSEN, JOUL
TITLE OF INVENTION: OLISONUCLECTIDE ANALOGUES
FILE REFERENCE: 49165-C2(71994)
CURRENT APPLICATION NUMBER: US/10/208,650
CURRENT APPLICATION NUMBER: US/10/008,029
PRIOR APPLICATION NUMBER: US/10/008,029
PRIOR PILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 09/152,059
PRIOR PILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/068,291
PRIOR APPLICATION NUMBER: 60/068,291
PRIOR APPLICATION NUMBER: 60/068,291
PRIOR APPLICATION NUMBER: 60/068,291
PRIOR PILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/071,682
PRIOR APPLICATION NUMBER: 60/068,309
PRIOR PILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/088,309
PRIOR PILING DATE: 1998-01-28
PRIOR APPLICATION NUMBER: 60/088,309
PRIOR FILING DATE: 1998-01-28
NUMBER OF SEQ ID NOS: 146
SEPTOR APPLICATION NUMBER: 60/098,305
PRIOR APPLICATION NUMBER: 60/098,305
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PUBLICATION NO. US20030144231A1
GENERAL INFORMATION:
APPLICANT: WESCEL, USEPER
APPLICANT: WIELSEN, POUL
ITILE OF INVENTION: OLIGOMUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165-C2 (71994)
CURRENT FILING DATE: 2002-07-29
FRIOR APPLICATION NUMBER: US/15/008,029
FRIOR FILING DATE: 2001-11-05
FRIOR FILING DATE: 2001-11-05
FRIOR FILING DATE: 1998-09-11
FRIOR APPLICATION NUMBER: 06/058,541
FRIOR FILING DATE: 1997-09-12
FRIOR FILING DATE: 1997-09-12
FRIOR FILING DATE: 1997-12-19
FRIOR FILING DATE: 1997-12-16
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-16
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Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: modified base
LOCATION: (6) .. (9)
CHER INFORMATION: LNA monomer
US-10-208-650-4
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ORGANISM: Artificial Sequence
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        PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-09-12

PRIOR PLILING DATE: 1997-09-12

PRIOR PLILING DATE: 1997-12-19

PRIOR PLILING DATE: 1997-12-19

PRIOR PLILING DATE: 1997-12-19

PRIOR PLILING DATE: 1998-01-16

PRIOR PLILING DATE: 1998-01-16

PRIOR PLILING DATE: 1998-03-03

PRIOR PLILING DATE: 1998-04-29

PRIOR PLILING DATE: 1998-04-29

PRIOR PLILING DATE: 1998-06-05

PRIOR PLING DATE: 1998-06-05

PRIOR PLING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/094,355

PRIOR PLING DATE: 1998-06-05

PRIOR PLING DATE: 1998-06-05

PRIOR PLING DATE: 1998-06-05

PRIOR APPLICATION OF SECULOUSE

SOFTWARE: PARATHES:

OTHER INFORMATION: Oligonucleotide

PRATIRE:

OTHER INFORMATION: Oligonucleotide
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Pred. No. 95;
0; Mismatches 2; Indels
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Sequence 9, Application US/10208650
Sequence 9, Application US/10208650
Publication No. US20030144231A1
Publication No. US20030144231A1
Publication No. US20030144231A1
APPLICANT: WENGEL, JESPER
APPLICANT: WINCERN, POUL
TITLE OF INVENTION: OLICONUCLECTIDE ANALOGUES
FILE REPERENCE: 49165-02(71994)
CURRENT APPLICATION NUMBER: US/10/008,029
PRIOR PLILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 09/152,059
PRIOR FILING DATE: 1998-09-11
PRIOR PLILING DATE: 1998-09-12
PRIOR PLILING DATE: 1997-09-12
PRIOR PLILING DATE: 1997-09-12
PRIOR PLILING DATE: 1998-01-16
PRIOR PLILING DATE: 1998-01-16
PRIOR PLILING DATE: 1998-01-16
PRIOR PLILING DATE: 1998-01-06
PRIOR PLILING DATE: 1998-01-08
PRIOR PLILING DATE: 1998-01-08
PRIOR PLILING DATE: 1998-01-08
PRIOR PLILING DATE: 1998-01-08
PRIOR PLILING DATE: 1998-01-28
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 9
LENGTH: 13
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NAME/KEY: modified base
LOCATION: (6)..(9)
CTHER INFORMATION: LNA monomer
US-10-208-650-8
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Best Local Similarity 83.3%;
Matches 10; Conservative
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OTHER INFORMATION: oligonucleotide
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  Indels
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73
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APPLICANT: WIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLECTIDE ANALOGUES
FILE REFERENCE: 43165-C2 (71934)
CURRENT APPLICATION: OLIGONUCLECTIDE ANALOGUES
FILE REFERENCE: 43165-C2 (71934)
CURRENT APPLICATION NUMBER: US/10/08, 029
PRIOR APPLICATION NUMBER: US/10/08, 029
PRIOR FILING DATE: 1930-09-11
PRIOR FILING DATE: 1930-09-11
PRIOR FILING DATE: 1930-09-11
PRIOR FILING DATE: 1930-09-12
PRIOR FILING DATE: 1930-12-19
PRIOR PLICATION NUMBER: 60/068, 293
PRIOR PLICATION NUMBER: 60/068, 293
PRIOR PLICATION NUMBER: 60/068, 293
PRIOR PLILING DATE: 1938-01-16
PRIOR PLILING DATE: 1938-01-16
PRIOR PLILING DATE: 1938-01-05
PRIOR PLILING DATE: 1938-06-05
PRIOR PLILING DATE: 1938-06-05
PRIOR PLILING DATE: 1938-07-28
NUMBER OF SEQ ID NOS: 146
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APPLICANT: WIELSEN, DESPER; APPLICANT: WIELSEN, POUL; TITLE OF INVENTION: OLIGONUCLECTIDE ANALOGUES; FILE REPERENCE: 49165-C2 (71994); CURRENT APPLICATION NUMBER: US/10/208,650; CURRENT APPLICATION NUMBER: US/10/008,029; PRIOR FILING DATE: 2002-07-29; PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8.8; DB
Pred. No. 95;
0; Mismatches
  0; Mismatches
                                                                                                                                                                                                                                            Sequence 7, Application US/10208650; Publication No. US20030144231A1; GENERAL INFORMATION:
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; OTHER INFORMATION: LNA monomer
US-10-208-650-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                    736 AAACAGAACACC 747
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10; Conservative
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US-10-208-650-8/c
                                                                                                                                                                                                                       US-10-208-650-7/c
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US-10-208-650-30/c
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Matches
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                                                                         OTHER INFORMATION: Description of Artificial Sequence: LNA modified OTHER INFORMATION: oligonucleotide FEATURE: NAME/KEY: modified_base
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                                                                                                                                                                                                                                                                                   Query Match
40.0%; Score 8.8; DB
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REPERENCE: 49165-C2(71994)
CURRENT APPLICATION NUMBER: US/10/208,650
CURRENT FILING DATE: 2002-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: US/10/008,029

PRIOR FILING DATE: 2001-11-05

PRIOR FILING DATE: 1996-09-11

PRIOR PELING DATE: 1998-09-11

PRIOR PILING DATE: 1998-09-11

PRIOR PELING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR PILING DATE: 1997-09-12

PRIOR FILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-04-29

PRIOR FILING DATE: 1998-04-29

PRIOR PILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 146

SEQ ID NOS: 146

SEQ ID NOS: 10 NOS: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-10-208-650-28/c
Sequence 28, Application US/10208650
Publication No. US/2030144231A1
APPLICANT: WENGEL, JESPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 158
US-10-208-650-29/c
, Sequence 29, Application US/10208650
, Publication No. US20030144231A1
, GENERAL INFORMATION:
                                                                                                                                                                                 LOCATION: (1)..(12)
; CTHER INFORMATION: LNA monomer
US-10-208-650-9
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Seguence
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OTHER INFORMATION: Description of Artificial Sequence: Probe
FEATURE:
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APPLICANT: MEMCEN, COULTILLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165-C2 (71994)
CURRENT APPLICATION NUMBER: US/10/208,650
CURRENT PILING DATE: 2002-07-29
FRICR FILING DATE: 2001-11-05
FRICR FILING DATE: 1996-09-11
FRICR FILING DATE: 1996-09-11
FRICR FILING DATE: 1996-09-11
FRICR FILING DATE: 1996-09-12
FRICR FILING DATE: 1997-09-12
FRICR FILING DATE: 1997-09-13
FRICR FILING DATE: 1996-01-16
FRICR FILING DATE: 1996-01-16
FRICR FILING DATE: 1996-01-05
FRICR FILING DATE: 1996-04-29
FRICR FILING DATE: 1996-05-05
FRICR FILING DATE: 1996-05-05
FRICR FILING DATE: 1996-05-05
FRICR FILING DATE: 1996-05-05
FRICR FILING DATE: 1996-07-28
NUMBER OF SEQ ID NOS: 146
FOR THE NOS: 146
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0; Mismatches
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83.3%; Pred. No. 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)..(12); OTHER INFORMATION: LNA monomer US-10-208-650-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      736 AAACAGAACACC 747
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les 10; Conservative
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ORGANISM: Artificial Sequence
PERATURE:
OTHER INFORMATION: Description of Artificial Sequence: Probe
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Pred. No. 95;
0; Mismatches 2; Indels
                                                                                            Delication No. US20030144231A1

GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
JITLE OF INVENTION:
FILE OF INVENTION: OLIGONICLEOTIDE ANALOGUES
FILE OF INVENTION: OLIGONICLEOTIDE ANALOGUES
FILE OF INTENTION OLIGONICLEOTIDE ANALOGUES
FILE OF INTENTION: OLIGONICLEOTIDE ANALOGUES
FILE OF INTENTION: OLIGONICLEOTIDE ANALOGUES
FILE OF INTENTION: OLIGONICLEOTIDE ANALOGUES
FRICK APPLICATION NUMBER: US/10/008,029
FRICK FILING DATE: 1998-09-11
FRICK FILING DATE: 1997-12-19
FRICK FILING DATE: 1997-12-19
FRICK FILING DATE: 1998-01-16
FRICK FILING DATE: 1998-01-16
FRICK FILING DATE: 1998-01-16
FRICK APPLICATION NUMBER: 60/076,591
FRICK APPLICATION NUMBER: 60/083,507
FRICK FILING DATE: 1998-04-29
FRICK APPLICATION NUMBER: 60/084,355
FRICK APPLICATION NUMBER: 60/094,355
FRICK FILING DATE: 1998-04-29
FRICK FILING DATE: 1998-04-29
FRICK FILING DATE: 1998-04-29
FRICK APPLICATION NUMBER: 60/094,355
FRICK FILING DATE: 1998-04-29
FRICK FILING DATE: 1998-04
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Publication No. US20030144231A1
GENERAL INFORMATION:
APPLICANT: WIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165-C2(71994)
CURRENT APPLICATION NUMBER: US/10/008,029
FRIOR APPLICATION NUMBER: 09/152,059
FRIOR FILING DATE: 2001-11-05
FRIOR PLILING DATE: 1998-09-11
FRIOR FILING DATE: 1998-09-11
FRIOR FILING DATE: 1997-09-12
FRIOR FILING DATE: 1997-12-19
FRIOR APPLICATION NUMBER: 60/068,293
FRIOR FILING DATE: 1997-12-19
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LOCATION: (1)...(12)

OTHER INFORMATION: LNA monomer

US-10-208-650-32
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Best Local Similarity 83.3'
Matches 10; Conservative
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US-10-208-650-43/c
                                                                             JS-10-208-650-32/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 13;
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Sequence 31, Application US/10208650
Publication No. US20030144231A1
GENERAL INFORMATION:
TILLE OF INVENTION: DESPER
APPLICANT: WENCEL, JESPER
APPLICANT: WIELSEN, POUL
TILLE OF INVENTION: OLIGONUCLECTIDE ANALOGUES
FILE REPRENCE: 4916.-C2 (71994)
CURRENT APPLICATION NUMBER: US/10/208,650
CURRENT FILING DATE: 2001-10-29
FRIOR FILING DATE: 1998-09-11
FRIOR FILING DATE: 1998-09-11
FRIOR FILING DATE: 1998-09-11
FRIOR FILING DATE: 1998-09-11
FRIOR APPLICATION NUMBER: 60/068,541
FRIOR APPLICATION NUMBER: 60/068,541
FRIOR APPLICATION NUMBER: 60/068,541
FRIOR APPLICATION NUMBER: 60/068,541
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-01-16
FRIOR FILING DATE: 1998-03-03
FRIOR FILING DATE: 1998-03-03
FRIOR FILING DATE: 1998-03-03
FRIOR FILING DATE: 1998-04-29
FRIOR APPLICATION NUMBER: 60/083,507
FRIOR APPLICATION NUMBER: 60/083,507
FRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 31
FRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 31
FRINGE DATENTING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 31
FRINGE DATENTING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 31
FRINGE DATENTING DATE: 1998-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3%; Pred, No. 95;
Matches 10; Conservative 0; Mismatches
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION UNDER: 60/094,355
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO ELENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified base

LOCATION: (1)...(12)

CTHER INFERMATION: LNA monomer

US-10-208-650-30
                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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                                   2; Indels
                                                                                                                                                                                                                                                                                                   US-10-208-650-46/C

Sequence 46, Application US/10208650

Publication No. US20030144231A1

Sequence 46, Application US/10208650

Publication No. US20030144231A1

SAPPLICANT: WENGEL, JESPER

APPLICANT: WENGEL, JESPER

APPLICANT: WIELSEN, POUL

TITLE OF INVENTION: OLIGONUCLEDTIDE ANALOGUES

FILE FREERENCE: 49165-C2 (71994)

CURRENT FILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: US/10/008,029

PRIOR APPLICATION NUMBER: 09/152,059

PRIOR APPLICATION NUMBER: 60/058,541

PRIOR FILING DATE: 1997-01-19

PRIOR FILING DATE: 1997-01-16

PRIOR FILING DATE: 1998-00-11

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR FILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-16

PRIOR PILING DATE: 1998-01-16

PRIOR FILING DATE: 1998-01-28

PRIOR FILING DATE: 1998-01-28
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APPLICANT: WIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
TITLE REPERENCE: 49165-C2 (71394)
CURRENT APPLICATION NUMBER: US/10/208,650
CURRENT FILING DATE: 2002-07-29
PRIOR PILING DATE: 2001-11-05
   Pred. No. 95;
0; Mismatches
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Sequence 47, Application US/10208650
Publication No. US20030144231A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10, Conservative
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
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GREEKAL AND MELSEN, POUL
TITLE OF INVENTION: OLICEATIDE ANALOGUES
FILE REFERENCE: 49165-C2 (71994)
CURRENT APPLICATION NUMBER: US/10/208,650
CURRENT APPLICATION NUMBER: US/10/008,029
PRIOR APPLICATION NUMBER: 09/15,059
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-16
PRIOR PELING DATE: 1998-01-16
PRIOR PELING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-05
PRIOR PRILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
PRIOR PRILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
PRIOR 
PRIOR FILING DATE: 1998-01-16
PRIOR PAPLICATION NUMBER: 60/076,591
PRIOR PILING DATE: 1998-03-03
PRIOR PILING DATE: 1998-04-03
PRIOR PLING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/088,309
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PATENTIN VET. 2.1
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         736 AAACAGAACACC 747
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-71
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                                              FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-208-650-48
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Pred. No. 95;
0; Mismatches 2; Indels
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred, No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 167
US-10-208-650-71/C
Sequence 71, Application US/10208650
Fublication No. US20300144231A1
GENERAL INFORMATION:
APPLICANT: WENGEL, JESPER
TITLE OF INVENTION: OLIGONUCLEDTIDE ANALOGUES
FILE REFERENCE: 49165-C2(71994)
CURRENT APPLICATION NUMBER: US/10/006,029
PRIOR PILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US/10/006,029
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/068,233
PRIOR APPLICATION NUMBER: 60/068,233
PRIOR PILING DATE: 1998-01-16
PRIOR PILING DATE: 1998-01-29
PRIOR PILING DATE: 1998-01-29
PRIOR PILING DATE: 1998-01-28
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iSequence 74, Application US/10208650
iPublication No. US2030144231A1
iGENERAL INFORMATION:
APPLICANT: WENGEL, JESPER
i APPLICANT: WIELSEN, POUL,
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
iFILE REFERENCE: 49165-C2 (71994)
iCURRENT APPLICATION NUMBER: US/10/208,650
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Best Local Similarity 83.3%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
                 ORGANISM: Artificial Sequence
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APPLICANT: WENCELL, USSTERN,
FILE REPRENCE: 49166-C2 (71994)
CURRENT APPLICATION UNMERR: US/10/208,650
CURRENT APPLICATION NUMBER: US/10/208,650
CURRENT APPLICATION NUMBER: US/10/008,029
FRIOR PILING DATE: 2001-11-05
FRIOR APPLICATION NUMBER: 05/152,059
FRIOR FILING DATE: 1998-03-11
FRIOR FILING DATE: 1998-03-11
FRIOR FILING DATE: 1997-03-12
FRIOR FILING DATE: 1997-03-12
FRIOR FILING DATE: 1997-03-12
FRIOR FILING DATE: 1998-03-03
FRIOR FILING DATE: 1998-04-04
FRIOR FILING DATE: 1998-04-05
FRIOR FILING DATE: 1998-04-03
FRIOR FILING DATE: 1998-07-28
FRIOR FILING DATE: 1908-07-28
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Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 09/152,059
PRIOR PILING DATE: 1998-09-11
PRIOR PELLING NUMBER: 60/058,541
PRIOR PELLING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR APPLICATION NUMBER: 60/071,682
PRIOR APPLICATION NUMBER: 60/071,682
PRIOR PILING DATE: 1998-01-05
PRIOR PILING DATE: 1998-01-05
PRIOR PILING DATE: 1998-03-03
PRIOR PELLING DATE: 1998-04-29
PRIOR PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PATENTIN VOWER: 60/094,355
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 47
FENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-208-650-48/c
; Sequence 48, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION;
APPLICANT: WENGEL, JESPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: modified_base; LOCATION: (6); OTHER INFORMATION: LNA monomer US-10-208-650-47
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ORGANISM: Artificial Sequence
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US-10-194-882-5/c

Sequence 5, Application US/10194882

Sequence 5, Application US/10194882

Sequence 5, Application US/204001442A1

Sequence 5, Application

Publication

GENERAL INFORMATION:

APPLICANT: UJ, Jingyue

TITLE OF INVENTION: Mass Spectrometry

FILE REFERENCE: 0575/66833/JPW/ADM

CURRENT APPLICATION NUMBER: US/10/194,882

CURRENT FILING DATE: 2002-07-12

NUMBER OF SEQ ID NOS: 14

SOTTWARE: Patentin version 3.1
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US-10-091-281-199
Sequence 199, Application US/10091281
Publication No. US20030190617A1
GENERAL INFORMATION:
APPLICANT: RAYMOND, VINCENT
APPLICANT: SI, ERWINDON, VINCENT
APPLICANT: SI, ERWINTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
TITLE REFERENCE: 13587-338
CURRENT APPLICATION NUMBER: US/10/091,281
CURRENT FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 463
SOFTWARE: Patentin Ver. 2.1
                                                                                     TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OCTHER INFORMATION: Description of Artificial Sequence: LNA modified OTHER INFORMATION: oligonucleotide
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Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches 2; Indels
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40.0%; Score 8.8; DB
Best Local Similarity 83.3%; Pred. No. 95;
Matches 10; Conservative 0; Mismatches
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                                                                                                                                                                                                                                           NAME/KEY: modified base COLORION: (1)..(12) COTHER INFORMATION: LNA monomer US-10-208-650-77
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 77
LENGTH: 13
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LENGTH: 13
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LENGTH: 13
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Sequence 77, Application US/10208650

Sequence 77, Application US/10208650

Publication No. US2030144231A1

GENERAL INFORMATION

APPLICANT: WENGEL, JESPER

APPLICANT: WIELSEN, POUL

TITLE OF INVENTION OLICONUCLECTIDE ANALOGUES

FILE REFRENCE: 49165-C2 (71994)

CURRENT APPLICATION NUMBER: US/10/208,650

CURRENT APPLICATION NUMBER: US/10/008,029

PRIOR FILING DATE: 2001-11-05

PRIOR PILING DATE: 1998-09-11

PRIOR PLING DATE: 1997-012,19

PRIOR PLING DATE: 1997-012,19

PRIOR PLING DATE: 1997-12-19

PRIOR PLING DATE: 1997-12-19

PRIOR PLING DATE: 1998-01-16

PRIOR PLING DATE: 1998-04-29

PRIOR PLING DATE: 1998-04-29

PRIOR PLING DATE: 1998-04-29

PRIOR PLING DATE: 1998-04-29

PRIOR PLING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088,309

PRIOR PLING DATE: 1998-06-05

PRIOR PLING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/084,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.0%; Score 8.8; DE Best Local Similarity 83.3%; Pred. No. 95; Matches 10; Conservative 0; Mismatches
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CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US/10/008,029
PRIOR FILING DATE: 2001-11-05
PRIOR PELLOR NUMBER: 09/152,059
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/068,541
PRIOR APPLICATION NUMBER: 60/068,293
PRIOR FILING DATE: 1997-09-12
PRIOR PELLOR DATE: 1997-09-12
PRIOR FILING DATE: 1998-01-16
PRIOR PELLORATION NUMBER: 60/076,591
PRIOR PILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/083,507
PRIOR PILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR PLING DATE: 1998-07-08
PRIOR PILING DATE: 1998-07-08
PRIOR PILING DATE: 1998-07-08
PRIOR PILING DATE: 1998-07-28
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NAME/KEY: modified base
LOCATION: (6)...(9)
COTHER INFORMATION: LNA MONOMER
US-10-208-650-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Gaps
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                                                                                                                                                          Sequence 331, Application US/10033145
Publication No. US2002015155A1
| GENERAL INFORMATION
| APPLICANT: GENZYME CORPORATION
| APPLICANT: ROBERTS, BRUCE
| APPLICANT: SHANKRAA, SRINIVAS
| TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
| TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
| TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
| TITLE OF INVENTION UNMERR: US/10/033,145
| CURRENT APPLICATION NUMBER: PCT/US99/13800
| PRIOR FILING DATE: 1999-06-18
| NUMBER OF SEQ ID NOS: 2137
| SOFTWARE: PATENTIN VERSION 3.0
| SEQ ID NO 331
| LENGTH: 10
| TYPE: DNA
| ORGANISM: Homo sapiens
| US-10-033-145-331
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Sequence 1175, Application US/10033145

PUBLICALION NO. US20020151518A1

GENERAL INFORATION: BENZYME CORPORATION

APPLICANT: ROBERTS, BRUCE

APPLICANT: SHANKARA, SRINUVAS

TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

FILE REFERENCE: GA0201C

CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: US/10/033,145

CURRENT FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 2137

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1175

LENGTH: 10

TYPE: DNA

TYPE: DNA

ORGANISM: Home sapiens
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Publication No. US20020151515A
GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 38.2
Best Local Similarity 90.0
Matches 9; Conservative
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735 GAAACAGAAC 744
                                              1 GAAACTGAAC 10
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                                                                                                                                          -10-033-145-331/c
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                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10073377
Publication NorUS20030099670A1
| Publication NorUS20030099670A1
| GENERAL INFORMATION:
| APPLICANT: Hobom, Gert
| CURRENT FILING DATE: 1000: 47
| SEQ ID NOS: 47
| SEQ ID NOS: 47
| SEQ ID NOS: 47
| LIBUTH: 13
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Pred. No. 1e+02;
2; Mismatches 1; Indels
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                                                DB 1; Length 13;
                                                                                                 2; Indels
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Sequence 102, Application US/10257021
Sequence 102, Application US/10257021
Sequence 102, Application US/10257021
Sequence 102, DS20030211498A1
GENERAL INFORMATION:
APPLICANT: Sherman Baust, Cheryl A.
APPLICANT: Pizer, Blins S.
APPLICANT: Hough, Colleen D.
TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
FILE REFERENCE: 14014.036912
CURRENT APPLICATION NUMBER: US/10/257,021
CURRENT APPLICATION NUMBER: US/10/257,021
PRIOR APPLICATION NUMBER: DCT/US01/10947
PRIOR FILING DATE: 2002-04-03
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 102
LENGTH: 10
                                              Score 8.8; DB
Pred. No. 95;
0; Mismatches
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; OTHER INFORMATION: n = any nucleotide
US-10-073-377-8
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                                              40.0%;
83.3%;
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ORGANISM: Influenza B virus
                                                                                                                                          734 AGAAACAGAACA 745
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Best Local Similarity 72.7%
"...rhes 8; Conservative
                                           Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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1 AGUAGWAACAR 11
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CRGANISM: Homo sapiens
US-10-257-021-102
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US-10-194-882-5
                                                                                                                                                                                                                                                                RESULT 172
US-10-073-377-8
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Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Matches 9; Conservative
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LENGTH: 10
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Publication No. US20030170713A1

GENERAL INPORMATION:

APPLICANT: SRIVASTAVA, SHIV

APPLICANT: SEGWA, TAKEHKO

TITLE OF INVENTION: POYNCLEOTIDE ARRAY

TITLE OF INVENTION: POYNCLEOTIDE ARRAY

TITLE OF INVENTION: POYNCLEOTIDE ARRAY

FILE REFERENCE: 04995.0057-00000

CURRENT APPLICATION NUMBER: US/10/390,045

PRIOR APPLICATION NUMBER: 06/179,482

PRIOR PILING DATE: 2003-03-18

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 67

SEC ID NO 47

LEWARD APPLICATION VET. 2.1
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APPLICANT: SHAWKAA, SRINUAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REPREPARED: GA02010.
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT PILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOGTWARE: Patentin version 3.0
SEQ ID NO 1215
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38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Publication No. US20030175771A1
GENERAL INFORMATION:
APPLICANT: Velculescu, Victor E.
APPLICANT: Kinzler, Kenneth W
APPLICANT: Vogelstein, Bert
                                                                                                                                                                                                                                                                                                                                                                    38.2%;
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ORGANISM: Artificial Sequence
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; ORGANISM: Homo sapiens
US-10-033-145-1215
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Best Local Similarity
Matches 9; Conserva
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US-10-390-045-47/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1293, Application US/10330627
Fublication No. US20030175771A1
GENERAL INFORMATION:
APPLICANT: Velculescu, Victor E.
APPLICANT: Velculescu, Victor E.
APPLICANT: Velculescu, Nert
TITLE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
FRIOR APPLICATION NUMBER: US 09/448,480
FRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1293
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Sequence 1363, Application US/10330627

Publication No. US2003017571A1

SEDERAL INFORMATION:
APPLICANT: Velculescu, Victor E.
APPLICANT: Velculescu, Victor E.
APPLICANT: Vogelstein, Bert
ITLE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 001107.00319

CURRENT APPLICATION NUMBER: US/10/330,627

CURRENT APPLICATION NUMBER: US/10/330,627

CURRENT FILING DATE: 2002-12-30

PRIOR FILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 1564

SOFTHARE: RESERRED FOR Windows Version 4.0
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FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
FRIOR PEPLICADION NUMBER: US 09/448,480
FRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SEQ ID NO 834
LENGTH: 10
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; ORGANISM: Homo sapiens
US-10-450-797-47
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; Sequence 47, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Conradt, Marcus
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT APPLICATION NUMBER: PCT/FP01/15178
; PRIOR APPLICATION NUMBER: PCT/FP01/15178
; PRIOR PFLING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 47
; TYPE: DNA
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                                                                                                                                                                                                                                                                                                               Sequence 47, Application US/10434479

Sequence 47, Application US/10434479

Publication No. US20040092469A1

GENERAL INFORMATION:

APPLICANT: SILVASTAVA, SHIV

APPLICANT: KU, LINDA L.

TITLE OF INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND POLYPEPTIDES

FILE REFERENCE: 04995.0057-02000

CURRENT APPLICATION NUMBER: US/10/434,479

FURRENT PLING DATE: 2003-05-09

PRIOR PILING DATE: 2003-05-09

PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/178,72

PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-01-31

SEQ ID NO 47

LENGTH: 10

LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
OTHER INFORMATION: Oligonucleotide
105-10-434-479-47
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                                                                Score 8.4; DB 1; Length 10;
Pred. No. 93;
0; Mismatches 1; Indels
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38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                     Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                     733 GAGAAACAGA 742
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; ORGANISM: Homo sapiens
US-10-330-627-1363
                                                                                                                                                                                                                 10 GATAAACAGA 1
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US-10-434-479-47/c
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US-10-450-797-47/c
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RESULT 183
US-10-450-797-532/c

i Gequence 532, Application US/10450797

publication No. US20040142335Al

GENERAL INFORMATION:
APPLICANT: Conradt, Marcus
APPLICANT: Hofmann, Kay

ITILE OF INVENTION: NETHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
FILE REPERENCE: HENK-0041

CURRENT APPLICATION NUMBER: US/10/450,797

CURRENT FILING DATE: 2001-12-204

PRIOR FILING DATE: 2001-12-204

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 1435

SOFTWARE: Patentin Version 3.2

LENGTH: 11

LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 184
US-10-450-797-537
Sequence 537, Application US/10450797
Publication No. US20040142335A1
GENERAL INFORMATION:
APPLICANT: Peterson, Dirk
APPLICANT: Conradt, Marcus
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
FILE REFERENCE: HENK-0041
CURRENT APPLICATION NUMBER: US/10/450,797
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: PCT/EP01/15178
PRIOR APPLICATION NUMBER: PCT/EP01/15178
PRIOR APPLICATION NUMBER: DE 101 00 121.5
PRIOR APPLICATION NUMBER: DE 101 00 121.5
SOFTWARE: PatentIn Version 3.2
SOFTWARE: PatentIn Version 3.2
LENGTH: 11
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Score 8.4; DB 1; Length 11;
Pred. No. 99;
0; Mismatches 1; Indels
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  Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                       733 GAGAAACAGA 742
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                                                                                                                               10 GATAAACAGA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Homo sapiens
US-10-450-797-532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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Gaps
                                                           APPLICANT: Hubert K ster
David M. Lough
Guobing Xiang
TITLE OF INVENTION: DAN DIAGNOSTICS BASED ON MASS SPECTROMETRY
NUMBER OF SEQUENCES: 320
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/931,792

APPLICATION NUMBER: 08/933,792

FILING DATE: 08-050-97

APPLICATION NUMBER: 08/787,639

FILING DATE: 23-40a-97

APPLICATION NUMBER: 08/786,988

FILING DATE: 23-40a-97

APPLICATION NUMBER: 08/746,055

FILING DATE: 06-No. US20020042112A1-96

APPLICATION NUMBER: 08/744,590

FILING DATE: 06-No. US20020042112A1-96

APPLICATION NUMBER: 08/744,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2004B
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/179,536B
FILING DATE: 26-Oct-1998
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US97/20444 ELLING DATE: 06-NOV-1997 APPLICATION NUMBER: 08/947,801 FILING DATE: 08-Oct-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 81:
US-09-179-536B-81
Sequence 81, Application US/09179536B Patent No. US20020042112A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 858-587-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 81
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <Unknown>
                                                                                                                                                                                                                                                                                                                  ZIP: 92037
COMPUTER READABLE FORM:
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Best Local Similarity 90.0
Matches 9; Conservative
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                            STATE: CA
                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                 Sequence 613, Application US/10450797

Publication No. US20040142335A1

GENERAL INFORMATION:

APPLICANT: Petersohn, Dirk

APPLICANT: Conradt, Marcus

APPLICANT: Petersohn, Dirk

APPLICANT: Petersohn, Dirk

APPLICANT: Hofmann, KAy

ITILE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

FILE REFERENCE: HENK-0041

CURRENT APPLICATION NUMBER: PCT/EP01/15178

PRIOR PILING DATE: 2003-12-20

PRIOR PILING DATE: 2001-12-20

PRIOR PILING DATE: 2001-01-03

NUMBER OF SEQ ID NOS: 1435

SOFTHARE: Patentin version 3.2

SEQ ID NO 613

LENGTH: 11
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APPLICANT: Hofmann, Kay
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
FILE REFERENCE: HENK-0041
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Pred. No. 99;
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CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: PCT/EP01/15178
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: DE 101 00 121.5
PRIOR FILING DATE: 2001-01-03
NUMBER OF SEQ ID NOS: 1435
SOFTWARE: Patentin version 3.2
LENGTH: 11
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Publication No. US20040142335A1
GAPLICANT: Petersohn, Dirk
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90.0%;
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Best Local Similarity 90.0
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Best Local Similarity 90.v-
       739 CAGAACACCG 748
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; ORGANISM: Homo sapiens
US-10-450-797-741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-450-797-613
                                                                                                                                            US-10-450-797-613/c
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US-09-179-536B-81
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RESULT 188 US-09-179-536B-86

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Sequence 86, Application US/09179536B
Sequence 0.0520020042112A1
Sequence 0.0520020042112A1
GENERAL INFORMATION:
GENERAL INFORMATION:
David M. Lough
Guobing Xiang
TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
NUMBER OF SEQUENCES: 320
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor

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RESULT 189

US-09-263-959-477/c

US-09-263-959-477/c

Sequence 477, Application US/09263959

Patent No. US20020156891A1

GENERAL INFORMATION:
APPLICANT: Rowen, Leroy B.
APPLICANT: Rowen, Lee

APPLICANT: Rowen, Lee

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP

ADDRESSEE: Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. le+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                             CANDERSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STATE: Washington
CONNTRY: US
ZIP: 98104-7092
COMPUTER: EDAPABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.25
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICALON DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 3,963
REGISTRATION NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 477:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.2%;
Best Local Similarity 90.0%;
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-09-263-959-477
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COUNTER: UGA

CONTRER: BLANCHEE

COMPUTER READBABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: ASCII

CLASSIFICATION DATA:

APPLICATION NUMBER: US/09/179,536B

FILING DATE: 06-NOV-1997

APPLICATION NUMBER: PCT/US97/20444

FILING DATE: 06-NOV-1997

APPLICATION NUMBER: 08/947,801

FILING DATE: 06-NOV-1997

APPLICATION NUMBER: 08/947,801

FILING DATE: 19-Sep-97

APPLICATION NUMBER: 08/93,792

FILING DATE: 23-Jan-97

APPLICATION NUMBER: 08/746,039

FILING DATE: 23-Jan-97

APPLICATION NUMBER: 08/746,036

FILING DATE: 23-Jan-97

APPLICATION NUMBER: 08/746,036

FILING DATE: 06-NO. US20020042112A1-96

APPLICATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 33,779

TELLEPAN: SES-587-5360

736 AAACAGAACA 745 ઠે

Sequence 492, Application US/09263959
Facent No. US20020150831A1
Facent No. US20020150831A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
STREET: Seed and Berry LLP
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: Seat.Le
CITY: Seat.Le
STATE: Washington
COUNTRY: US US-09-263-959-492/c

ZIP: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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38.2%; Score 8.4; DB 1; Length 12; llarity 90.0%; Pred. No. 1e+02; Conservative 0; Mismatches 1; Indels

Query Match Best Local Similarity Matches 9; Conserva

728 GCCAGGAGAA 737

| TOPOLOGY: unknown | TOPOLOGY: unknown | MOLECULE TYPE: cDNA | HYPOTHETICAL: NO | ANTI-SENSE: NO | FRAGMENT TYPE: cUnknown | ORIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO: 86: US-09-179-536B-86

TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

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Sequence 4, Application US/09845938A
Sequence 4, Application US/09845938A
Sequence 4, Application US/09845938A
GENERAL INFORMATION:
APPLICANT: Kabanov, Alexander V
APPLICANT: Lonieux, Pierre
APPLICANT: Vullevich, Vergey V.
APPLICANT: Vullevich, Sergey V.
APPLICANT: Vinogradov, Sergey V.
PITLE OF INVENTION: Compositions and Methods for Inducing Activation of Dendritic Cell
CURRENT APPLICATION NUMBER: US/09/845,938A
CURRENT APPLICATION NUMBER: US/09/845,938A
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                   APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTIONS DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
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                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: US/09/263,959 FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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H
    Pred. No. 1e+02;
0; Mismatches
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NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 850, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
    90.08;
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
    Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
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                                                           736 AAACAGAACA 745
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washingt
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                               US-09-263-959-850/c
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Patent No. US20020150891A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hood, Lery E.
APPLICANT: Kowen, Lee
APPLICANT: Kowen, Ben F.
TITLE OF INVENTION: BIR F.
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 492:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104-7092
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 755
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                             LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           736 AAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AAACAAAACA 2
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CITY: Seattle
STATE: Washingt
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US-09-263-959-755/c
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RESULT 196
US-09-297-576A-86
is Sequence 86, Application US/09297576A
j Publication No. US20030129589A1
general information:
APPLICANT: KOSTER, Hubert
j APPLICANT: LOUGH, David M.
APPLICANT: LOUGH, David M.
APPLICANT: TANG, Guobing
APPLICANT: VAN DEN BOOM, Dirk
APPLICANT: VAN DEN BOOM, Dirk
APPLICANT: VAN DEN BOOM, Dirk
APPLICANT: WAN DEN BOOM, Dirk
APPLICANT: RUPERET, Andreas
ITTLB OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
NUMBER OF SEQUENCES: 320
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Emman White & MCAuliffe
STREET: 4250 Executive Square, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 18+02; tive 0; Mismatches 1; Indels
APPLICATION NUMBER: US/09/297,576A
FILING DATE: 07-Jun-2000
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 08/933,792
FILING DATE: 08-Oct-97 977,639
APPLICATION NUMBER: 08/787,639
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/786,988
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/746,055
FILING DATE: 06-No. US20030129589A1-96
APPLICATION NUMBER: 08/744,481
FILING DATE: 06-No. US20030129589A1-96
APPLICATION NUMBER: 08/744,481
FILING DATE: 06-No. US20030129589A1-96
APPLICATION NUMBER: 24736-2004
FILING DATE: 06-No. US20030129589A1-96
ATTORNEY/AGBRT INFORMATION:
NAME: Seidman, Stephanie L
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
TELEPHONE: 858-450-8400
INFORMATION FOR SEQ ID NO: 81:
FIRINGTH: 12 base pairs
TYPE: DATE of aingle
TYPE: DATE of aingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: Sing:
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       La Jolla
: CA
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FRAGMENT TYPE: <
ORIGINAL SOURCE:
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US-09-845-918A-7/C

US-09-845-918A-7/C

Sequence 7, Application US/09845938A

Publication No. US20330118550A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lenieux, Pierre
APPLICANT: Vinogradov, Sergey V.
APPLICANT: Vinogradov, Sergey V.
TITLE OF INVENTION: Compositions and Methods for Inducing Activation of Dendritic Cell
FILE REFERENCE: 3874-129 US
FURENT APPLICATION UNDERF: US/09/845,938A

CURRENT FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3:1

SEQ ID NO 7

LENGTH: 12
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US-09-297-576A-81

i Sequence 81, Application US/09297576A

publication No. US20030129589A1

GENERAL INFORMATION:

APPLICANT: KOSTER, Hubert

APPLICANT: LITTLE, Daniel P.

APPLICANT: LITTLE, Daniel P.

APPLICANT: LOUGH, David M.

APPLICANT: VAN DEN BOOM, Dirk

APPLICANT: VAN DEN BOOM, Dirk

APPLICANT: WIRINKE, Christian

APPLICANT: WIRINKE, Christian

APPLICANT: WURINKE, Andreas

ITILE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY

NUMBER OF SEQUENCES: 320

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McAuliffe

STATE: CA

COMPUTER: DA JOLIA

STATE: CA

COMPUTER: DA COMPUTER: DISACETE

COMPUTER: DA COMPATION: DNA COMPATION:

MEDIUM TYPE: LA JOLIA

SOFTWARE: ARCTT

COMPUTER: DA COMPATION: DNA COMPATION:

SOFTWARE: ARCTT
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                                                                                                                                                                                           Query Match 38.2%; Score 8.4; DB 1; Length 12; Best Local Similarity 90.0%; Pred. No. 1e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.2%; Score 8.4; DB 1; Length 12; Best Local Similarity 90.0%; Pred. No. 1e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Herpes Simplex Virus type 1
                                                                                         TYPE: DNA ORGANISM: herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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                                  ; SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.2%; Score 8.4; DB 1; Length 12; Best Local Similarity 90.0%; Pred. No. 1e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dhallan, Ravinder S.
TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
TITLE OF INVENTION: DISORDERS
FILE REPERENCE: 543312000420
CURRENT APPLICATION NUMBER: US/10/661,165
CURRENT FILING DATE: 2003-09-11
PRIOR PLICATION NUMBER: PCT/US03/06198
PRIOR PLING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Kabanov, Alexander V.
APPLICANT: Alakov, Valery Y.
APPLICANT: Alakov, Valery Y.
APPLICANT: Alakov, Sergey V.
TITLE OF INVENTION: Polymuclectide Compositions
FILE REPERENCE: 3874.118.1.2.1.US
CURRENT APPLICATION NUMBER: US/10/164,875C
CURRENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 09/320,640
PRIOR APPLICATION NUMBER: 09/320,640
PRIOR APPLICATION NUMBER: 09/320,640
PRIOR PILING DATE: 1998-07-30
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1994-01-18
NUMBER OF SEG ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 12
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PRIOR FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 10/093,618
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/360,232
PRIOR FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 433, Application US/10661165
Publication No. US20040137470A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10164875C Publication No. US20030198678A1
                                                                                                 ; TYPE: DNA
; ORGANISM: Herpes Simplex Virus 1
US-10-164-875C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Herpes Simplex Virus 1
                                                                                                                                                                                   Ouery Match
Best Local Similarity 90.0'
                                                                                                                                                                                                                                                                                               730 CAGGAGAAAC 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INCOMPATION:
APPLICANT: Kabanov, Alexander V.
APPLICANT: Alaxov, Valery Y.
APPLICANT: Alaxov, Valery Y.
APPLICANT: Alaxov, Valery Y.
TITLE OF INVENTION: Polynucleotide Compositions
FILE REFERENCE: 3874.1181.2.1.US
CURRENT APPLICATION NUMBER: US/10/164,875C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8.4; DB 1;
Pred. No. 1e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/746,056
PILING DATE: 08-0-00 US20030129589A1-96
PILING DATE: 06-00 US20030129589A1-96
APPLICATION NUMBER: 08/746,036
APPLICATION NUMBER: 08/744,590
FILING DATE: 06-No. US20030129589A1-96
APPLICATION NUMBER: 08/744,481
FILING DATE: 06-No. US20030129589A1-96
APPLICATION NUMBER: 08/744,481
FILING DATE: 06-No. US20030129589A1-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2004
TELECOMONICATION INFORMATION:
                            OPEKALL...
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/297,576A
APPLICATION NUMBER: US/09/297,576A
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PRIOR APPLICATION NUMBER: 09/320,640
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: 09/124,943
PRIOR FILING DATE: 1998-07-30
PRIOR PLILING DATE: 1998-07-30
PRIOR PLILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: 08/912,968
PRIOR PLILING DATE: 1997-08-01
PRIOR PLILING DATE: 1994-11-18
                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/947,801
FILING DATE: 08-0ct-97
APPLICATION NUMBER: 08/933,792
FILING DATE: 19-Sep-97
APPLICATION NUMBER: 08/787,639
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/786,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10164875C Publication No. US20030198678A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.2%;
Best Local Similarity 90.0%;
Matches 9; Conservative
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 858-450-8499
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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ORIGINAL SOURCE:
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Gaps ; 0

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US-10-033-145-537

Sequence 537, Application US/10033145

Publication No. US2002015155A1

GENERAL INFORMATION:

APPLICANT: GENZYME CORPORATION

APPLICANT: GENERYS, BRUCE

APPLICANT: SHANKARA, SRINIVAS

TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

CURRENT APPLICATION NUMBER: US/10/033,145

CURRENT FILING DATE: 2001-11-05

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 2137

SOFTWARE: ParentIn version 3.0

LENGTH: 10

LENGTH: 10

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                 Query Match

36.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indele
          ; TYPE: DNA
; CRGANIEM: Homo sapiens
; FEATURE:
; COMPARE INFORMATION: Putative AREB/AREB6.04 motif
US-10-091-281-222
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US-10-293-222-96/C
US-10-293-222-96/C
Sequence 96, Application US/10293222
Publication No. US20040033932A1
GENERAL INFORMATION:
APPLICANT: Verteegy, Rogier
APPLICANT: Garon, Hubertus N.
TITLE OF INVENTION: MXC targets
FILE REFRENCE: 2183-5580US
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US/10/293,222
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: EP 00201698.8
PRIOR FILING DATE: 2000-05-11
PRIOR FILING DATE: 2000-05-11
PRIOR FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 455
SOFTWARE: Patentin Ver. 2.1
SENGTH: 10
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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| Sequence 2.22, Application US/10091281
| Publication No. US20030190617A1
| GENERAL INFORMATION:
| APPLICANT: RAYMOND, VINCENT
| APPLICANT: RAYMOND, VINCENT
| APPLICANT: BI, ERREPTE, JEAN
| TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
| FILE REPERENCE: 15587.38
| CURRENT APPLICATION NUMBER: US/10/091,281
| CURRENT FILING DATE: 2002-03-06
| NUMBER OF SEQ ID NOS: 463
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 222
| LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-667-891-32

/ Sequence 32, Application US/10667891

/ Dublication No. US20040171024A1

/ Dublication No. US20040171024A1

/ Dublication No. US20040171024A1

/ APPLICANT: ROTH, CHARLES W.

/ APPLICANT: BOTH, CHARLES W.

/ APPLICANT: BOLM, INGE

/ APPLICANT: ROLM, INGE

/ APPLICANT: ROLM, INGE

/ APPLICANT: RAINENS WARINE

/ APPLICANT: RAINESWARINE

/ TITLE OF INVENTION: MULTIDENG RESISTANCE PROTEINS IN DROSOPHILA AND

/ TITLE OF INVENTION: ANOPHELSS

/ TITLE OF INVENTION: ANOPHELSS

/ TITLE OF INVENTION: US-10/667,891

/ CURRENT FILING DATE: 2003-09-26

/ NUMBER OF SEQ ID NOS: 76

/ SOFTWARE: Patentin Ver. 3.2

/ LENGTH: 12
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Pred. No. 1e+02;
0; Mismatches 1; Indels
PRIOR APPLICATION NUMBER: PCT/US03/27308
PRIOR FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 10/376,770
PRIOR FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 628
SSCPWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 433
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-667-891-32
                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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US-10-091-281-222/c
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36.4%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 0; Indels
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Publication No. US20030175771A1
GENERAL INFORMATION:
APPLICANT: Volculescu, Victor E.
APPLICANT: Vogelstein, Bert
TILLE REFERENCE: 001107.00319
CURRENT APPLICATION: Human Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT FILING DATE: 2002-12-30
PRIOR PILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SEQ ID NO 77
SEQ ID NO 77
                                                                                                                                                                         APPLICANT: Velculescu, Victor E. APPLICANT: Velculescu, Victor E. APPLICANT: Velculescu, Kenneth W. APPLICANT: Vogelstein, Bart TITLE OF INVENTION: Human Transcriptomes FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 09/448,480
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                           US-10-330-627-26

"Sequence 26, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
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US-10-330-627-77
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US-10-330-627-26
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2 GGAGAAAC 9
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Best Local Similarity
Matches 8; Conserv
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US-10-330-627-79
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LENGTH: 10
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                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MALTITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MALTITLE OF INVENTION: FUSION
FILE REPERBACE: 27373/37928A
CURRENT APPLICATION NUMBER: US/10/329,465
CURRENT APPLICATION NUMBER: US 60/343,826
PRIOR FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 315
SOFTWARE: PATENTIN VEYSION 3.1
SEO ID NO 139
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| Sequence 2, Application US/1035820
| Publication No. US2030166282A1
| GENERAL INFORMATION:
| APPLICANT: BROWN, DAVID
| APPLICANT: PALOTTA, VICH
| APPLICANT: AMBRITAN
| TITLE OF INVENTION: HIGH POTENCY SIRNAS FOR REDUCING THE EXPRESSION OF
| TITLE OF INVENTION: TARGET GENES
| TITLE OF INVENTION NUMBER: 0S/10/35
| CURRENT PILING DATE: 2003-01-31
| PRIOR APPLICATION NUMBER: 60/353,332
| PRIOR FILING DATE: 2002-02-01
| NUMBER OF SEQ ID NOS: 34
| SEQ ID NO 2
| LENGTH: 10
Gaps
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
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36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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, OTHER INFORMATION: Synthetic oligonucleotide US-10-329-465-139
Mismatches
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Publication No. US20030165949A1
GENERAL INFORMATION:
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8; Conservative
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                                                741 GAACACCG 748
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                                                                                           1 GAACACCG 8
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Matches
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Sequence 8, Application US/09828211A
Publication No. US20010034029A1
Publication No. US20010034029A1
GENERAL INFORMATION:
APPLICANT: FULTIWAKE, Hideshi
TITLE OF INVENTION: Method of Detecting Mutation in Base Sequence of Nucleic Acid
FILE REFERENCE: NOG-0009
CURRENT APPLICATION NUMBER: US/09/828,211A
CURRENT FILING DATE: 2001-04-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE PATENTH Version 3.1
SEQ ID NO 8
LENGTH: 11
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                                                       Query Match 36.4%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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    , ORGANISM: Homo sapiens US-10-330-627-1321
                                                                                                                                          728 GCCAGGAG 735
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US-09-828-211A-8/c
                                                                                                                                                                                                                                         RESULT 211
US-10-302-547-55/c
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36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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US-10-330-627-1321/c
Sequence 1221, Application US/10330627
Sequence 1221, Application US/10330627
Sequence 1221, Application US/10330627
SENERAL INFORMATION:
APPLICANT: Velculescu, Victor E.
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Human Transcriptomes
TITLE OF INVENTION: Human Transcriptomes
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: PastEBEQ for Windows Version 4.0
SEQ ID NO 1321
LENGTH: 10
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 85, Application US/10330627; Publication No. US20030175771A1
GENERAL INFORMATION: V0220030175771A1
GENERAL INFORMATION: Volculescu, Victor E.; APPLICANT: Valculescu, Victor E.; APPLICANT: Vogelstein, Bert TILE OF INVORTION: Human Transcriptomes; FILE REFERENCE: 001107.00319; CURRENT FILING DATE: 2002-12-30; CURRENT FILING DATE: 1999-11-24; NUMBER OF SEQ ID NOS: 1564; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 85
TITLE OF INVENTION: Human Transcriptomes FILE REFERENCE: 001107.00319; CURRENT APPLICATION NUMBER: US/10/330,627; CURRENT FILING DATE: 2002-12-30; PRIOR APPLICATION NUMBER: US 09/448,480; PRIOR FILING DATE: 1990-11-24; NUMBER OF SEQ ID NOS: 1564; SOFTWARE: PRESEQ FOR WINDOWS Version 4.0; SEQ ID NOS: 1004
                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Homo sapiens
US-10-330-627-79
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US-10-330-627-85
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US-10-330-627-85
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JUBER 138 PROTICE OF APPLICATION US/10266138B

PUBLICATION NO. US20030152964A1

FUBLICANT: INFORMATION:

APPLICANT: IOBST, Kurt M

APPLICANT: SCHILLING, Kurt M

APPLICANT: BCYD, CHARLES

APPLICANT: WRSCHITZ, Johann

TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE

TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE

TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE

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TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE

TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE

TITLE OF INVENTION NUMBER: G0/338,272

PRIOR APPLICATION NUMBER: G0/338,272

PRIOR APPLICATION NUMBER: G0/338,272

PRIOR APPLICATION NUMBER: G0/338,272

FRIOR FILING DATE: 2001-11-08

NUMBER OF SEQ ID NOS: 34

SOFTWARE PATENTIN VOF: 2.1

SEQ ID NO 6

LENGTH: 11
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US-09-918-715-65/c

i Sequence 65. Application US/09918715

i Publication No. US20030017157A1

i GENERAL INFORMATION:

APPLICANT: Brad St. Croix

APPLICANT: Reneth Kinzler

ITILE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

PILE REPERENCE: 1107.00134

CURRENT APPLICATION NUMBER: US/09/918,715

CURRENT FILING DATE: 2000-08-02

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR PILING DATE: 2000-08-02

PRIOR PILING DATE: 2000-08-04

PRIOR FILING DATE: 2000-08-04

NUMBER: OF SEQ ID NOS: 358

SOFTWARE: EastSEQ for Windows Version 3.0

LENGTH: ...
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CORGANISM: Homo sapiens
US-09-918-715-65
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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OTHER INFORMATION: Description of Artificial Sequence: Seq.# 56 of
CTHER INFORMATION: Table I
US-10-265-509B-6
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; Bublication No. US2030170739A1
; Bublication No. US2030170739A1
; Bublication No. US2030170739A1
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: USCHITZ, Johann
; TILLE OF INVENTION: GENE EXPRESSION FOR ANALYZING PHOTODAMAGE
; TILE REFERENCE: J6663US(ED.PEP/UYF) Seqlis13Sep' 02;51-84
; CURRENT FILLING DATE: 2003-03-03-03
; PRIOR PLILING DATE: 2003-03-03-03
; PRIOR PLILING DATE: 2001-10-08
; NUMBER OF SEQ ID NOS: 34
; SOFTHARE: PatentIN Ver. 2.1
; SEQ ID NO 6
LENTH: 11
                                                                                                      APPLICANT: van der Kuyl, Antoinette C.
APPLICANT: van der Kuyl, Antoinette C.
APPLICANT: Cornelissen, Marion
TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
FILE REFERENCE: 5.24440 (REN/PS51900000)
CURRENT APPLICATION NUMBER: 05/126,728
CURRENT APPLICATION NUMBER: 60/325,728
FRIOR APPLICATION NUMBER: 60/325,722
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: EP 01200228.3
PRIOR APPLICATION NUMBER: EP 156
NUMBER: OF SEQ ID NOS: 156
SOFTWARE: patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: TAG sequence Hs23579
US-10-055-728-27
                           Sequence 27, Application US/10055728 Publication No. US20030170720A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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-10-055-728-27
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LENGTH: 11
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RESULT 217

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Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative 0
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Matches 8; Conservative
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US-10-450-797-1387
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CORGANISM: Homo sapiens
US-10-450-797-714
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| Sequence 452, Application US/10450797 |
| Publication No. US20040142335A1 |
| GENERAL INFORMATION: |
| APPLICANT: Conradt, Marcus |
| APPLICANT: Conradt, Marcus |
| APPLICANT: HORMATION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO |
| TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO |
| FILE REFERENCE: HENK-0041 |
| CURRENT APPLICATION NUMBER: US/10/450,797 |
| CURRENT PAPLICATION NUMBER: PCT/ED01/15178 |
| PRIOR FILING DATE: 2001-12-20 |
| PRIOR FILING DATE: 2001-12-20 |
| PRIOR FILING DATE: 2001-01-03 |
| NUMBER OF SEQ ID NOS: 1435 |
| SEQ ID NO 452 |
| LENTH: 11 |
| LENTH: 11
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Sequence 27, Application US/10310677

Publication No. US20030219772A1

GENERAL INFORMATION:

APPLICANT: Kuyl v.d., Antoinette C.

APPLICANT: Cornelissen, Marion

TITLE OF INVENTION:

FILE REFERENCE: P55190US10

CURRENT APPLICATION NUMBER: US/10/310,677

CURRENT FILING DATE: 2002-12-05

PRIOR APPLICATION NUMBER: EP 0120328.3

PRIOR PILING DATE: 2001-09-28

PRIOR PILING DATE: 2001-09-28

PRIOR PILING DATE: 2001-09-28

NUMBER OF SEQ ID NOS: 165

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 27

LENGTH: 11
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Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
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, NAME/KEY: misc_feature

; LOCATION: (1). (11)

US-10-310-677-27
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CORGANISM: Homo sapiens
US-10-450-797-452
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US-10-450-797-452/c
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RESULT 219

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Sequence 6, Application US/10620514

Publication No US20040068762A1

GENERAL INFORMATION:

APPLICANT: Actar', Ricardo M.

APPLICANT: Bol, David K.

APPLICANT: Bol, David K.

APPLICANT: Gortardis, Marco

APPLICANT: Rowley, Ronald B.

APPLICANT: Rowley, Ronald B.

APPLICANT: OF INVENTION: TRANSCENIC NON-HUMAN MAMMALS EXPRESSING A REPORTER NUCLEIC ACID

TITLE OF INVENTION: UNDER THE RECULATION OF ANDROGEN RESPONSE ELEMENTS

TITLE OF INVENTION NUMBER: US/10/620,514

CURRENT FILING DATE: 2003-07-16

PRIOR FILING DATE: 2002-07-17

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.2
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
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APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
APPLICANT: Brat Vogelstein
APPLICANT: Bent Vogelstein
APPLICANT: Bent Vogelstein
TILLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPRENENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
SPRIOR FILING DATE: 2000-08-11
FRIOR PILING DATE: 2000-08-11
SPRIOR FILING DATE: 2000-08-11
FRIOR FILING DATE: 2000-08-11
SPRIOR FILING DATE: 2000-08-11
SPRIOR FILING DATE: 2000-04-11
SPRIOR PILING DATE: 2000-04-11
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           EARLIER FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 73
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-918-715-49
; Sequence 49, Application US/09918715
; Publication No. US20030017157A1
                                                                                                                                                                                                                                                                       35.5%;
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Best Local Similarity 81.00,
Conservative
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US-09-249-155-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-918-715-49
                                                                                                                                                        TYPE: DNA
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Publication No. US20030022165A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Mutations in a No. US20030022165A1e1 Photoreceptor-pineal gene 17
TITLE OF INVENTION: leber congenital amaurosis (LCA4)
TITLE OF INVENTION NUMBER: US/09/765,061B
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
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NAME/KEY: mutation
LOCATION: (4)...(4)
UCHION: (4)...(4)
US-09-765-061B-30
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Sequence 73, Application US/09249155

Sequence 73, Application US/09249155

Publication No. USC000037345A1

GENERAL INFORMATION:

APPLICANT: Heber-Katz, Ellen

TITLE OF INVENTION: Compositions and Methods for Wound

TITLE OF INVENTION: Healing

FILE REFERENCE: 00486.78503

CURRENT FILING DATE: 1999-02-15

EARLIER APPLICATION NUMBER: 60/074,737

EARLIER APPLICATION NUMBER: 60/097,937

EARLIER APPLICATION NUMBER: 60/097,937

EARLIER FILING DATE: 1998-08-26

EARLIER FILING DATE: 1998-08-26

EARLIER FILING DATE: 1998-08-26

EARLIER FILING DATE: 1998-08-26
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100.0%; Pred. No. 1.1
tive 0; Mismatches
FILE OF INVENTION: Gene
FILE REFERENCE: VARD-0798
CURRENT APPLICATION NUMBER: US/10/723,940
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 08/956,518
PRIOR APPLICATION NUMBER: 08/956,518
FILOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
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US-09-765-061B-30/c
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LENGTH: 11
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TYPE: DNA
CORGANISM: Homo sapiens
US-10-450-797-1044
; TYPE: DNA; ORGANISM: Homo sapiens
US-10-450-797-297
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                                                                                                                                              Score 7.8; DB 1; Length 11;
Pred. No. 1.2e+02;
0; Mismatches 2; Indels
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Sequence 73, Application US/10314322
Publication No. US20030229911A1
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
FILE REFERENCE: 00046.0016
CURRENT APPLICATION NUMBER: US/10/314,322
CURRENT APPLICATION NUMBER: US 60/097,373
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-8
PRIOR FILING DATE: 1998-03-86
SPRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
SPRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
SPRIOR FILING DATE: 1998-03-18
SPRIOR FILING DATE: 1998-03-18
SPRIOR FILING DATE: 1998-03-18
SEQ ID NO 73
LENGTHALL DATE: 1998-03-18
SEQ ID NO 73
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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                                                                                            ; OTHER INFORMATION: DR-1
US-10-620-514-6
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CORGANISM: Mus musculus
US-10-314-322-73
 ; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
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Best Local Similarity
Matches 9; Conserva
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US-10-456-797-1044/C

US-10-456-797-1044/C

Sequence 1044, Application US/10450797

Publication No. US20040142335al

GENERAL INPORMATION:

APPLICANT: Petersohn, Dirk

APPLICANT: Conradt, Marcus

APPLICANT: Conradt, Marcus

APPLICANT: Conradt, Marcus

APPLICANT: Delarsohn, Kay

TILLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

FILE REFERENCE: HENK-0041

CURRENT APPLICATION NUMBER: US/10/450,797

CURRENT FILING DATE: 2001-12-20

PRIOR PLILING DATE: 2001-12-20

PRIOR PLILING DATE: 2001-01-03

NUMBER OF SEQ ID NOS: 1435

SEQ ID NO 1044

LENGTH: 11

LENGTH: 11

LENGTH: 11
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US-09-21

US-09-21

Sequence 21, Application US/09365029

Patent No. US20010021772A1

GENERAL INFORMATION:
APPLICANT: UHLMANN, Bugen
APPLICANT: PETWAN, Anuschirwan
APPLICANT: PITCHANT: PITCHANT: PAPLICANT: POSSNER Richard D.
TITLE OF INVENTION: SHORT CLIGONUCLECTIDES FOR THE INHIBITION OF VEGF
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 2608/3208
CURRENT APPLICATION NUMBER: US/09/365,029
CURRENT APPLICATION NUMBER: EP 98114853.9
EARLIER PILING DATE: 1998-08-02
SEALIER PILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PATENTIN OF 21
LENGTH: APPLICATION NUMBER: PATENTING DATE: LIBRICA DATE: DATE
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: VEGF antisense
OTHER INFORMATION: oligonucleotide
US-09-365-029-21
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    Length 11;
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Score 7.8; DB 1; Length 11
Pred. No. 1.2e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative (
         Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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35.5%; Score 7.8; DB 1;
81.8%; Pred. No. 1.3e+02;
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Publication No. US20030099670A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Influenza C virus
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Best Local Similarity 81.8
Matches 9; Conservative
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| Patent No. US20020058287A1
| Patent No. US20020058287A1
| GENERAL INFORMATION:
| APPLICANT: de draaf, David
| APPLICANT: Lander, Eric S.
| TITLE OF INVENTION: No. US20020058287A1e1 Small Nuclear RNA Vectors and Uses
| TITLE OF INVENTION: Therefor
| TITLE OF INVENTION: US/09/804,481
| CURRENT APPLICATION NUMBER: US/09/804,481
| CURRENT APPLICATION NUMBER: 60/188,304
| PRIOR APPLICATION NUMBER: 60/188,304
| PRIOR APPLICATION NUMBER: 60/188,304
| PRIOR APPLICATION NUMBER: 0100-03-10
| SOFTWARE PESCO ID NOS: 11
| SOFTWARE PESCO ID NOS: 11
| SEQ ID NO 9
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US-09-828-034-24
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Score 7.8; DB 1; Length 12;
Pred. No. 1.3e+02;
0; Mismatches 2; Indels
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Patent No. US20020064771A1
GENERAL INFORMATION:
APPLICANT: Thong, Weidong
APPLICANT: Anng, Zhi
APPLICANT: Hong, Zhi
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION UNMBER: US. 60/195,852
PRIOR APPLICATION UNMBER: US. 60/195,852
PRIOR APPLICATION UNMBER: US. 60/195,852
NUMBER OF SEC ID NOS: 33
SOFTWARE: PATENTING DATE: 2000-04-06
NUMBER OF SEC ID NOS: 33
SOFTWARE: PATENTING DATE: 2000-04-06
NUMBER OF SEC ID NOS: 33
SOFTWARE: PATENTING DATE: 2010 04-06
NUMBER OF SEC ID NOS: 33
SOFTWARE: PATENTING DATE: 2010
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Query Match 35.5%;
Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                  728 GCCAGGAGAA 738
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Hobom, Gert
APPLICANT: Hobom, Gert
TILLE OF INVENTION: Influence with Enhanced Transcriptional and
TITLE OF INVENTION: Influence viruses with Enhanced Transcriptional and
TITLE OF INVENTION: Replicative Capacities
FILE REFERENCE: 010293us/JH/ml
CURRENT APPLICATION NUMBER: US/10/073,377
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 47
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Sequence 4, Application US/10073377

Publication No. US20030099670A1

Publication No. US20030099670A1

APPLICANT: Hobom, Gert

APPLICANT: Menke, Annette

APPLICANT: Menke, Annette

TITLE OF INVENTION: Influenza Viruses with Enhanced Transcriptional and TITLE OF INVENTION: Replicative Capacities

FILE REPERENCE: 010291Us/JH/ml

CURRENT APPLICATION NUMBER: US/10/073,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Caspase-6; OTHER INFORMATION: substrate recognition sequence US-10-100-957A-65
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Sequence 65, Application US/10100957A
Fublication No. US2030096322A1
GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-LiA
CURRENT APPLICATION NUMBER: US/10/100,957A
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEG ID NOS: 180
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TYPE: RNA

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scnuttzi-///.rnpp

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RESULT 237

1 US-10-427-14

1 Sequence 14, Application US/10427629

2 Publication No. US20040078834A1

2 GENERAL INFORMATION:

3 APPLICATION: Croce, Carlo M.

3 TITLE OF INVENTION: Human Chronic Lymphocytic Leukemia Modeled In Mouse By Targeted

3 TITLE OF INVENTION: TCLI Expression

4 TITLE OF INVENTION: TCLI Expression

5 TITLE OF INVENTION: UNBER: US/10/427,629

6 CURRENT APPLICATION NUMBER: 05/376,464

7 PRIOR APPLICATION NUMBER: 60/376,464

7 PRIOR PELING DATE: 2002-04-29

7 SOFTWARE: PatentIn Version 3.2

7 SEQ ID NO 14

7 LENGTH: 12
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UG-10-455-101-13

Square 13, Application US/10455101

Publication No. US20040038405A1

GENERAL INFORMATION:

APPLICANT: Liu, Dakai

APPLICANT: Liu, Dakai

APPLICANT: Rabbani, Blazar

TITLE OF INVENTION: VECTORS AND VIRAL VECTORS, AND PACKAGING CELL LINES FOR TITLE OF INVENTION: PROPOGATING SAME

FILE REFERENCE: Enz.-56 (D2) SquanceListing051199

CURRENT FILING DATE: 2003-06-04

FRICK RAPLICATION NUMBER: US/10/455,101

PRIOR FILING DATE: ERRLIER FILING DATE: 1998-03-24

PRIOR FILING DATE: BARLIER FILING DATE: 1997-03-21

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 13

LENGTH: 9
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Pred. No. 1.36+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                 FEATURE:
, OTHER INFORMATION: recognition sequence US-10-273-334-41
PRIOR APPLICATION NUMBER: US 60/069,677
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 41
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 35.5%;
Best Local Similarity 81.8%;
Matches 9; Conservative (
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Best Local Similarity 81.8%;
Matches 9; Conservative (
                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Mus musculus US-10-427-629-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
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Sequence 359, Application US/10211088

Publication No. US2003104479A1

SEQUENCE S
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US-10-273-334-41/c

Sequence 41, Application US/10273334

Publication No. US20030129631A1

GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Rodkol, Shrihari S.
APPLICANT: Rodkol, Shrihari S.
TILE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
FILE REFERENCE: 03178.0076

CURRENT APPLICATION NUMBER: US/09/591,500

PRIOR PILING DATE: 2000-1-06

PRIOR FILING DATE: 2000-1-06

PRIOR FILING DATE: PCT/US98/26433

PRIOR FILING DATE: PCT/US98/26433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                    FEATURE:
COTER INFORMATION: Description of Artificial Sequence: Modified
COTER INFORMATION: influenca A 3'-sequence
US-10-073-377-4
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 1.3e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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       CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                              TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 81.8
Matches 9; Conservative
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APPLICANT: Schwelzer, Markus
APPLICANT: Schwelzer, Markus
APPLICANT: Anderson, Richard R.
APPLICANT: Aneller, Jochen
APPLICANT: Fiechtner, Michael
APPLICANT: Renle, Stefan
APPLICANT: Kienle, Stefan
APPLICANT: Raddatz, Stefan
APPLICANT: Pignot, Marc
APPLICANT: Raddatz, Stefan
APPLICANT: Raddatz, Stefan
APPLICANT: Mindhab, No. US20030175702Albert
TITLE OF INVENTION: Binding and Immobilization System for Nucleic Acids Using Syntheti
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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                                                                                                                  OTHER INPORMATION: Synthetic binding system; NAME/KEY: modified base; LOCATION: (1)..(10); COTHER INFORMATION: pyranosyl RNA US-09-910-469-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic binding system NAME/KEY: modified base Location: (1) ... (10) ... (10) OTHER INFORMATION: pyranosyl RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 264/217 Nanogen Recognomics CURRENT APPLICATION NUMBER: US/09/910,469 CURRENT FILING DATE: 2001-07-19 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 212, Application US/10293222
Publication No. US2004003393A1
GENERAL INFORMATION:
APPLICANT: Caron, Hubertus N.
TITLE OF INVENTION: MYC targets
FILE REFRENCE: 213-5560US
CURRENT APPLICATION NUMBER: US/10/293,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-910-469-56; Application US/09910469; Publication No. US20030175702A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  33.6%;
88.9%;
SEQ ID NO 55
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity 88.2
Best Local Similarity
Best Local Similarity
Best Local Similarity
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                  FEATURE:
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APPLICANT: Pignot, Marc
APPLICANT: Pignot, Marc
APPLICANT: Raddatz, Stefan
APPLICANT: Raddatz, Stefan
APPLICANT: Raddatz, Scheibard
APPLICANT: Schneider, Eberhard
APPLICANT: Windhab, No. US20030175702Albert
TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthet
TITLE OF INVENTION: Binding System Secognomics
FILE REFERENCE: 264/217 Nanogen Recognomics
CURRENT APPLICATION NUMBER: US/09/910,469
CURRENT FILING DATE: 2001-07-19
NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.1
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:nucleic acid,
; OTHER INFORMATION: double stranded, linear topology
US-10-455-101-13
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                                                                                                                    Score 7.4; DB 1; Length 9;
Pred. No. 8.3e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Battersby, Bronwyn J.
APPLICANT: Miller, Christopher R.
APPLICANT: Miller, Christopher R.
APPLICANT: Trau, Matthias
APPLICANT: Trau, Matthias
APPLICANT: Way, Jeffery C.
APPLICANT: Way, Jeffery C.
APPLICANT: Way, Jeffery C.
APPLICANT: Wolnston, Angus
TITLE OF INVENTION: Synthesis of Chemical Libraries
TILE OF INVENTION: Synthesis of Chemical Libraries
TILE REFERENCE: 50277/003002
CURRENT APPLICATION NUMBER: US/10/283,741
CURRENT APPLICATION NUMBER: US 60/330,759
PRIOR FILING DATE: 2001-10-30
PRIOR PLING DATE: 2001-10-30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 14, Application US/10283741; Publication No. US20030182068A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 55, Application US/09910469
Publication No. US20030175702A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schweitzer, Markus
APPLICANT: Anderson, Richard R.
APPLICANT: Mueller, Jochen
APPLICANT: Fiechtner, Michael
APPLICANT: Riucher, Christoph
APPLICANT: Kienle, Stefan
                                                                                                                       33.6%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic US-10-283-741-14
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Best Local Similarity 88.2.
Best Local 8; Conservative
                                                                                                                  Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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US-10-283-741-14/c
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RESULT 246

US-10-033-145-339/C

US-10-033-145-339/C

Sequence 339, Application US/10033145

Publication No. 2820020151515A1

GENERAL INFORMATION:

APPLICANT: GENERAL ORPORATION

APPLICANT: GENERAL SERICANS, BRIGARAS, BRILLANT SHANKARA, SRINIVAS

TILLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

TILLE OF INVENTION PREPARATION AND USE OF SUPERIOR VACCINES

CURRENT APPLICATION NUMBER: US/10/033,145

CURRENT PLING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: PCT/US99/13800

PRIOR SEQ ID NOS: 2137

SOFTWARE OF SEQ ID NOS: 2137

LENGTH: 10

LENGTH: 10

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                        US-110-033-145-245,

US-210-033-145-245,

Sequence 236, Application US/10033145

Publication No. US2002015155A1

GENERAL INFORMATION:

APPLICANT: GENZYME CORPORATION

APPLICANT: SHANKARA, SRINIVAS

ITLLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

FILE REPERENCE: GAO201C

CURRENT APPLICATION NUMBER: US/10/033,145

CURRENT PILING DATE: 1999-06-18

FRIOR PILING DATE: 1999-06-18

FRIOR FILING DATE: 1999-06-18

WHWHER OF SEQ ID NOS: 2137

SOFTWARE: Patentin version 3.0

LENGTH: 10

LENGTH: 10

LENGTH: 10

TYPE: DNA

ORGANISM: Homo sapiens

US-10-033-145-236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.38+02;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                     Query Match 33.6%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 1.38+02; Matches 8; Conservative 0; Mismatches 1; Indels
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CORGANISM: Homo sapiens
US-10-033-145-339
               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-196
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US-10-033-145-236/c
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j Sequence 196, Application US/10033145

j Publication No. US200215155A1

GENERAL INFORMATION:

APPLICANT: GENERAL SERUCE

APPLICANT: SHANKARA, SRINIVAS

j TILLE OF INVENTION: PREPRARATION AND USE OF SUPERIOR VACCINES

FILE REFERENCE: GA0201C

CURRENT APPLICATION NUMBER: US/10/033,145

CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: PCT/US99/13800

PRIOR APPLICATION NUMBER: PCT/US99/13800

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 2137

SOFTWARE: Patentin version 3.0

LENGTH: 10

LENGTH: 10
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US-10-033-145-75
Sequence 75, Application US/10033145
Sequence 75, Application US/10033145
Sequence 75, Application US/10033145
SEGUENCE 100 US 002002015155A1
GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: ROBERTS, BRUCE
STILLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
CURRENT PELING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US/10/033,145
CURRENT PILING DATE: 1999-06-18
SHOR FILING DATE: 1999-06-18
NUMBER FOR SEQ ID NOS: 2137
SOFTWARE: Patentin Version 3.0
SEQ ID NOS: 2137
                                                                                                                                                                                                                                                                                                                                                                                     33.6%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.3e+02; Attive 0; Mismatches 1; Indels
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CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: PCT/ML01/00361
PRIOR FILING DATE: 2001-05-11
PRIOR PILING DATE: 2001-05-11
PRIOR PILING DATE: 2000-05-11
PRIOR PILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: EP 00202284.6
NUMBER OF SEQ ID NOS: 455
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 212
LENGTH: 10
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Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-212
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CORGANISM: Homo sapiens
US-10-033-145-75
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US-10-033-145-196
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                                                                                                                                                                                                   ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-033-145-780
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; ORGANISM: Homo sapiens
US-10-033-145-794
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TYPE: DNA
ORGANISM: Homo sapiens
FILE REFERENCE: GA0201C
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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US-10-033-145-813/c
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                                                                         Sequence 373, Application US/10033145

Publication No. US2002015155A1

GENERAL INFORMATION:
APPLICANT: GENEXTWE CORPORATION
APPLICANT: ROBERTS, BRUCE
FILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/033,145

CURRENT FILING DATE: 2001-11-05
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: PATENTIN VERSION 3:0
SOFTWARE: PATENTIN VERSION 3:0
SOFTWARE: PATENTIN VERSION 3:0
SOFTWARE: PATENTIN VERSION 3:0
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| Publication No. US20020151515A1
| Publication No. US20020151515A1
| Publication No. US20020151515A1
| APPLICANT: GENERAL INFORMATION:
| APPLICANT: ROBERTS, BRUCE
| APPLICANT: RAHNKARA, SRINIVAS
| TITLE OF INVENTION: PERPARATION AND USE OF SUPERIOR VACCINES
| TITLE OF INVENTION: UNMBER: US/10/033,145
| CURRENT APPLICATION NUMBER: US/10/033,145
| CURRENT FILING DATE: 2001-11-05
| PRIOR APPLICATION NUMBER: PCT/US99/13800
| PRIOR FILING DATE: 1999-06-18
| NUMBER OF SEQ ID NOS: 2137
| SOFTWARE: PatentIn version 3.0
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Sequence 780, Application US/10033145
Publication No. US20020151515A1
GENERAL INFORMATION:
APPLICANT: GENZYME CCRPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHAMKARA, SRIVE
APPLICANT: SHAMKARA, SRIVINAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
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Best Local Similarity 88.9
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-10-033-145-595
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US-10-033-145-373
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                                        RESULT 247
US-10-033-145-373/c
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LENGTH: 10
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Sequence 794, Application US/10033145

Sequence 794, Application US/10033108

SEQUENCE SET SERVERS CORPORATION

APPLICANT: SHANTARA, SRINIVAS

TILLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

TILLE REFERENCE: GA0201C

CURRENT APPLICATION NUMBER: US/10/033,145

CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: PCT/US99/13800

PRIOR PILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 2137

SOFTWARE: PatentIn Version 3.0

LENGTH: 10

LENGTH: 10
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APPLICANT: ROBERTS, BRUCE
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SININAS,
ITILE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REPERENCE: GA0201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
FRIOR APPLICATION NUMBER: PCT/US99/13800
FRIOR PAPLICATION NUMBER: PCT/US99/13800
FRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: Patentin version 3.0
SEQ ID NO 813
LENGTH: 10
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CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: Patentin version 3.0
LENGTH: 10
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Publication No. US20020151515A1
GENERAL INFORMATION:
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Gaps
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RESULT 254
US-10-033-145-1396
is equence 1396, Application US/10033145
is publication No. U52002015155A1
is equence 1396, Application US/10033145
is publication No. U52002015155A1
is experied to the comparation:
is applicant: General Corporation
is applicant: SHANKARA, SRINIVAS
intle OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
intle REPERBANCE: GAO201C
CURRENT APPLICATION NUMBER: US/10/033,145
ic CURRENT APPLICATION NUMBER: PT/US99/13800
is PRIOR PILING DATE: 1999-06-18
is NUMBER OF SEQ ID NOS: 2137
is SOFTWARE: Patentin version 3.0
is SEQ ID NO 1396
il LENGTH: 10
il TYPE: DNA
il CRANISM: Homo sapiens
il US-10-033-145-1396
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US-10-033-145-1419
is dequence 1419, Application US/10033145
is gequence 1419, Application US/10033145
is publication No. US20020151515A1
is GENERAL INFORMATION:
APPLICANT: GENERATS, BRUCE
APPLICANT: SHANKARA, SRINUYAS
itTLE OF INVENTION: PREPRARTION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GAOZOLC
CURRENT APPLICATION NUMBER: US/10/033,145
icurrent PLING DATE: 1001-11-05
icurrent APPLICATION NUMBER: PCT/US99/13800
iprior Filing DATE: 1999-06-18
independence of SEC ID NOS: 2137
is SOFTWARE: PatentIn version 3.0
ibrogram:
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US-10-033-145-1496
US-10-033-145-1496
Sequence 1496, Application US/10033145
Publication No. US20020151515A1
GENERAL INFORMATION:
APPLICANT: GENEYING CORPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SRINIYAS
ITILE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REPERENCE: 6A0201C
CURRENT APPLICATION NUMBER: US/10/033,145
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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88.9%;
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Best Local Similarity 88.9'
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Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-10-033-145-1419
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| GS-10-033-145-1342/c
| GS-Quence 1342, Application US/10033145
| Publication No. US2020151515A1
| Publication No. US2020151515A1
| Publication No. US2020151515A1
| Publication No. US2020151515A1
| APPLICANT: GNERTS, BRUCE
| APPLICANT: SHANKARA, SRINIVAS
| TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
| FILE REFERENCE: GA0201C
| CURRENT APPLICATION NUMBER: US/10/033,145
| CURRENT PLING DATE: 1999-06-18
| NUMBER OF SEQ ID NOS: 2137
| SEQ ID NO 1342
| LENGTH 1042
| LENGTH 1042
                                                                                                                                                                                                                                                                              RESULT 252
US-10-033-145-835
Squence 835, Application US/10033145
Squence 835, Application US/10033145
Squence 835, Application US/200201515A1
GGNERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SCHANKARA, SRINIVAS
ITILE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GAOGUC
CURRENT PELING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ.ID NOS: 2137
SOFTWARE: PAGENTIN VERSION 3:0
SEQ.ID NOS: 2137
SEG.ID NOS: 2137
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                                                       Query Match 33.6%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 1.3e+02; Matches 8; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-10-033-145-1342
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ORGANISM: Homo sapiens
US-10-033-145-835
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               US-10-033-145-813
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APPLICANT: Duca, Amy APPLICANT: Duca, Amy APPLICANT: Duca, Amy APPLICANT: Nandabalan, Krishnan APPLICANT: Stephens, J. Claiborne APPLICANT: Stephens, J. Claiborne APPLICANT: Windemuth, Andreas TITLE OF INVENTION: Drug Target Isogenes: Polymorphisms in the Interleukin FILE REFERENCE: MWH-0002US2 IL4R alpha GURENT APPLICATION NUMBER: US/10/010,802 CURRENT APPLICATION NUMBER: US/10/010,802 PRIOR FILING DATE: 2000-01-11.09 PRIOR FILING DATE: 2000-01-11.09 RIVER PRIOR FILING DATE: 2000-07-13 NUMBER OF: SEQ ID NOS: 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.6%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
                                        Length 10;
                                                                                                  1; Indels
                                     Score 7.4; DB 1;
Pred. No. 1.3e+02;
                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 261, Application US/10010802
Publication No. US20030078220A1
GENERAL INFORMATION:
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Publication No. US20030078220A1
GENERAL INFORMATION:
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Denton, R. Rex
Duda, Amy
Nandabalan, Krishnan
                                 Query Match 33.6%;
Best Local Similarity 88.9%;
Matches 8; Conservative
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Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-10-010-802-261
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CAGANISM: Homo sapiens
US-10-010-802-287
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Sequence 1773, Application US/10033145

Sequence 1773, Application US/10033145

Publication No. US2002015155A1

GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
APPLICANT: STRUYAR, SRINIVAS

TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GA0201C
CURRENT FILING DATE: 2001-11-05
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137

SOFTWARR: PATENTIN VERSION NUMBER: PCT/US99/13800
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137

SOFTWARE: PATENTIN VERSION 3.0

SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               % Sequence 1999, Application US/10033145
; Sequence 1999, Application US/10033145
; Publication NO. USC020151518A1
; GENERAL INFORMATION:
; APPLICANT: GENZIME CORPORATION
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REPERENCE: GA0201C
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                 33.6%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.3e+02; ative 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: Patentin version 3.0
SEQ ID NO 1496
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Best Local Similarity 88.9
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-10-033-145-1496
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; ORGANISM: Homo sapiens
US-10-033-145-1999
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Best Local Similarity
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LENGTH: 10
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Pred. No. 1.3e+02;
0; Mismatches 1;
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Publication No. US2030175771A1

GENERAL INFORMATION:
APPLICANT: Velculescu, Victor E.
APPLICANT: Velculescu, Victor E.
TITLE OF INVENTION: Human Transcriptomes
FILE REPERENCE: 001107,00319
CURRENT FILING DATE: 2002-12-30
FRIOR PLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 399
                                               SQUENCE 238, Application US/10330627

Publication No. US20030175771A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Valculescu, Victor E.

APPLICANT: Volculescu, Victor E.

APPLICANT: Vogelstein, Bert

TILLE OF INVENTION: Human Transcriptomes

TILLE OF INVENTION: Human Transcriptomes

FILE REPERENCE: 001107.00319

CURRENT FILING DATE: 2002-12-30

FRIOR APPLICATION NUMBER: US 09/448,480

FRIOR FILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 1564

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 238

LENGTH: 10
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APPLICANT: Kazemi, Amir
APPLICANT: Lachowicz, Michael F.
APPLICANT: Pabon, Vicente
APPLICANT: Shah, Nisha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.6%;
88.9%;
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Best Local Similarity 88.9.
The Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-330-627-238
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US-10-330-627-399/c
                      RESULT 263
US-10-330-627-238/c
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Sequence 95, Application US/10329465

Sequence 95, Application No. US20030165949A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENES ABNORWALLY EXPRESSED IN MYELOID LEUXEMIA CELLS WITH AN MLITILE OF INVENTION: FUS.103

TITLE OF INVENTION: GENES ABNORWALLY EXPRESSED IN MYELOID LEUXEMIA CELLS WITH AN MLITILE OF INVENTION: UNMERR: US/10/329,465

CURRENT FILING DATE: 2002-12-23

PRIOR PELLOR UNMERR: US 60/343,826

PRIOR PELLOR OF SEQ ID NOS: 315

SOFTWARE PATENTING DATE: 2001-12-27

NUMBER OF SEQ ID NOS: 315

SEQ ID NO 95

LENGTH: 10
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Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                  RESULT 261
US-10-176-464A-59
; Sequence 59, Application US/10176464A
; Publication No. US203030165902A1
; GENERAL INFORMATION:
; APPLICANT: Bieglecki, Karyn
; APPLICANT: Lee, Helen
; APPLICANT: Monroe, Glen
; TILE OF INVENTION: HAPLOTYPES OF THE F2R GENE
; TILE REFERENCE: F2R_WMH-1457US
; CURRENT APPLICATION NUMBER: US/10/176,464A
; CURRENT FILING DATE: 2002-06-20
; PRIOR FILING DATE: 2001-10-01
; PRIOR FILING DATE: 2001-09-29
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NOS: 66
; SEQ ID NO 59
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                 739 CAGAACACC 747
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CORGANISM: Homo sapiens
US-10-176-464A-59
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US-09-918-715-66/C

Sequence 66, Application US/09918715

Publication Wo. US20030017157A1

GENERAL INFORMATION:
APPLICANT: Bert VOGELStein
TITLE DF INVENTION: BNOOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134

CURRENT APPLICATION NUMBER: US/09/918,715

CURRENT FILING DATE: 2000-08-01

PRIOR PILING DATE: 2000-08-02

PRIOR FILING DATE: 2000-08-02

PRIOR FILING DATE: 2000-08-11

PRIOR PILING DATE: 2000-08-11

PRIOR FILING DATE: 2000-08-11

PRIOR FILING DATE: 2000-04-11

PRIOR FILING DATE: 2000-04-11

SPRIOR FILING DATE: 2000-04-11
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APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
FILE REPERBNCE: 00486.78633
CURRENT APPLICATION NUMBER: US/09/249,155
CURRENT FILING DATE: 1999-02-12
FARLIER APPLICATION NUMBER: 60/074,737
EARLIER APPLICATION NUMBER: 60/074,737
EARLIER APPLICATION NUMBER: 60/097,937
FARLIER APPLICATION NUMBER: 60/102,051
EARLIER APPLICATION NUMBER: 60/102,051
EARLIER APPLICATION NUMBER: 60/102,051
EARLIER FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FastSEQ for Windows Version 3.0
           EARLIER FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 124, Application US/09249155
; Publication No. US20030037345A1
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-86
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                                                                                           SEQ ID NO 86
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US-09-735-363A-82/C
; Sequence 82, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
APPLICANT: Filion, Mario
APPLICANT: Phillip, Nigel
TILLE REFERENCE: 02811-011
; TILLE REFERENCE: 02811-011
; FILLE REFERENCE: 02811-011
; PRIOR PPLICATION NUMBER: 60/170,325
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR PILING DATE: 1999-12-33
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3:0
; SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.6%; Score 7.4; DB 1; Length 11;
88.9%; Pred. No. 1.46+02;
tive 0; Mismatches 1; Indels
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Sequence 86, Application US/09249155

Publication No. US2030037345A1

GENERAL INFORMATION: US20300037345A1

APPLICANT: Heber-Katz, Ellen

TITLE OF INVENTION: Compositions and Methods for Wound

TITLE OF INVENTION: Compositions and Methods for Wound

TITLE OF INVENTION: Compositions and Methods for Wound

TITLE OF INVENTION: Healing

FILE REFERENCE: 00486.78503

CURRENT PRILICE DATE: 1999-02-12

EARLIER PILING DATE: 1999-02-12

EARLIER PILING DATE: 1999-02-13

EARLIER PILING DATE: 1998-02-13

EARLIER FILING DATE: 1998-02-13

EARLIER FILING DATE: 1998-08-26

EARLIER PILING DATE: 1998-08-26

EARLIER PILING DATE: 1998-08-26

EARLIER PILING DATE: 1998-08-26
TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE CURRENT APPLICATION NUMBER: US/10/193,507 CURRENT FILING DATE: 2002-07-12 PRIOR APPLICATION NUMBER: 60/304,573 PRIOR FILING DATE: 2001-07-11 NUMBER OF SEQ ID NOS: 86 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                  TYPE: DNA
GRGANISM: Homo sapiens
US-10-193-507-79
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Best Local Similarity
Matches 8; Conserv
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LENGTH: 10
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
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US-10-314-322-124

| Sequence 124, Application US/10314322 |
| Sequence 124, Application US/10314322 |
| Publication No. US20030229911A1 |
| GENERAL INPORMATION: GENERAL INPORMATION: GENERAL INPORMATION: Compositions and Methods for WOUNTION: PROPERCE: 000486.0016 |
| TITLE OF INVENTION: DATE: 2002-12-09 |
| CURRENT FILING DATE: 2002-12-09 |
| PRIOR PILING DATE: 1998-02-13 |
| PRIOR FILING DATE: 1998-02-13 |
| PRIOR FILING DATE: 1998-02-13 |
| PRIOR FILING DATE: 1998-02-13 |
| PRIOR PILING DATE: 1998-02-26 |
| PRIOR APPLICATION NUMBER: US 60/102,051 |
| PRIOR APPLICATION NUMBER: US 09/249,155 |
| PRIOR PILING DATE: 1999-02-12 |
| NUMBER OF SEQ ID NOS: 346 |
| SEQ ID NO 124 |
| LENGTH: 11 |
| LENGTH: 11 |
| LENGTH: 11 |
                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: Healing
FILE REPRENCE: 000486.00016
CURRENT APPLICATION WUMBER: US 60/074,737
FRIOR PEDITOR DATE: 2002-12-09
FRIOR PEDITOR DATE: 1998-02-13
FRIOR FILING DATE: 1998-02-13
FRIOR APPLICATION NUMBER: US 60/097,937
FRIOR FILING DATE: 1998-02-13
FRIOR APPLICATION NUMBER: US 60/102,051
FRIOR APPLICATION NUMBER: US 60/102,051
FRIOR FILING DATE: 1998-09-28
FRIOR FILING DATE: 1998-09-28
FRIOR FILING DATE: 1998-09-12
SUGTAMER: FASESEQ for Windows Version 4.0
SEQ ID NO 86
LENGTH: 11
FYPE: DNA
ORGANISM: MUMS musculus
US-10-314-322-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.9%;
Matches 8; Conservative
US20030229911A1
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US-10-314-322-124
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US-10-191-302-8

Sequence 8, Application US/10191302

Publication No. US2003009265A1

GENERAL INPOWATION:

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING TITLE OF INVENTION: METHODS AND COMPOSITIONS SOUTH STREET:

TITLE OF INVENTION: METHODS: 8

CORRESPONDENCE ADDRESS: 8

CORRESPONDENCE ADDRESS: 9

CONTRY: HORKING ADDRESS: 1000 HSTREET

STATE: MA

CONPUTER: END FOR COMPATIBLE

CONPUTER: END FOR COMPATIBLE

CONPUTER: ISM PC-DOS/MS-DOS

SOUTHAND APPLICATION DATA:

APPLICATION NUMBER: US/10/191,302

CLASSIFICATION NUMBER: US/10/191,302

FILING DATE: PROPRATION:

REFERENCE APPLICATION DATA: 39,061

RECEINGE APPLICATION NUMBER: US/10/191,302

FILING DATE: REPORMATION:

REFERENCE PROPRATION:

REFERENCE PROPRATION NUMBER: US/10/191,302

TELEPHONE: (617)-248-7100

TELEPHONE: (617)-248-7100

TELEPHONE: (617)-248-7100

TELEPHONE: (617)-248-7100

TELEPHONES: (617)-248-7100

TELEPHONES: SINGLE

FRANTER:

FRANTER:
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33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.46+02;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.46+02;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1.11
OTHER INFORMATION: /product= "MEF-2 MUTANT CONSENSUS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    736 AAACAGAAC 744
                                                                                                                                                                                                                                                                                                      734 AGAAACAGA 742
                                               TYPE: DNA
CORGANISM: Homo sapiens
US-09-918-715-66
                                                                                                                                                                                                                                                                                                                                                                       9 AGAAGCAGA 1
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                    LENGIH: 11
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Gaps

; Sequence 78, Application US/10612224 ; Publication No. US20040137011A1 3 ACCGAACAC 11

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Gaps

RESULT 271 US-10-314-322-86 ; Sequence 86, Application US/10314322

3 AAACATAAC 11

schultz1-727.rnpb

Page 80

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APPLICANT: Peterson, Dirk
APPLICANT: Corract, Marcus
APPLICANT: Corract, Marcus
APPLICANT: Corract, Marcus
APPLICANT: Hofmann, Kay
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
CURRENT APPLICATION NUMBER: US/10/450,797
CURRENT FILING DATE: 2001-12-0
PRIOR PELING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: DE 101 00 121.5
PRIOR APPLICATION NUMBER: DE 101 00 121.5
NUMBER OF SEQ ID NOS: 1435
SOFTWARE: PatentIn version 3.2
SEQ ID NO 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 285, Application US/10450797

Bublication No. US20040142335A1

GENERAL INFORMATION.

APPLICANT: Petersohn, Dirk

APPLICANT: Conradt, Marcus

APPLICANT: Conradt, Marcus

APPLICANT: Moffmann, Kay

TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

UNRENT APPLICATION NUMBER: US/10/450, 797

CURRENT FILING DATE: 2003-12-04

PRIOR PILING DATE: 2001-12-20

PRIOR PELING DATE: 2001-12-20

PRIOR FILING DATE: 2001-01-03
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.6%; Score 7.4; DB 1; Best Local Similarity 88.9%; Pred. No. 1.4e+02; Matches 8; Conservative 0; Mismatches 1
FILE REFERENCE: HENK-0041
CURRENT APPLICATION NUMBER: US/10/450,797
CURRENT FILING DATE: 2003-12-04
FRIOR APPLICATION NUMBER: PCT/EP01/15178
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-01-03
NUMBER OF SEQ ID NOS: 1435
SOFTWARE: PatentIn version 3.2
LENGTH: 11.
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Publication No. US20040142335Al
GENERAL INFORMATION:
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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US-10-450-797-284
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Publication No. US20040142335A1

GENERAL INFORMATION:

APPLICANT: Petersohn, Dirk

APPLICANT: Conradt, Marcus

APPLICANT: Hoffmann, Kay

TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

FILE REPERENCE: HERK-0041

CURRENT FILING DATE: 2003-12-04

PRIOR PILING DATE: 2001-12-20

PRIOR PILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-01-03

PRIOR FILING DATE: 2001-01-03

SOFTWARE: Patentin Version 3.2

SEQ ID NOS: 1435

LENGTH. 11
           APPLICANT: CURNINGHAM, Philip R.
TITLE OF INVENTION: IDENTIFICATION OF ANTIBIOTICS THAT ARE NOT SUSCEPTIBLE TO TITLE OF INVENTION: IDENTIFICATION OF ANTIBIOTICS THAT ARE NOT SUSCEPTIBLE TO TITLE OF INVENTION: ANTIBIOTIC RESISTANCE TITLE OF INVENTION: ANTIBIOTIC RESISTANCE CURRENT APPLICATION NUMBER: US/10/612,224 CURRENT FILING DATE: 2003-07-01
PRIOR PAPLICATION NUMBER: 60/39327
PRIOR PLILING DATE: 2002-07-01
PRIOR PLILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 245
SOFTWARE: FASCESQ for Windows Version 4.0
SEQ ID NO 78
LENGTH: 11
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Publication No. US20040142335A1

GENERAL INFORMATION:
APPLICANT: Petersohn, Dirk
APPLICANT: Conradt, Marcus
APPLICANT: Hofmann, Kay
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.6
Best Local Similarity 88.9
Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-10-450-797-51
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| Sequence 538, Application US/10450797
| Publication No. US20040142335A1
| GENERAL INFORMATION
| APPLICANT: Petersohn, Dirk
| APPLICANT: Hofmann, Kay
| TILLE OF INVENTION: METHOF FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
| FILE REFERENCE: HENK-0041
| CURRENT FILING DATE: 2003-12-04
| CURRENT FILING DATE: 2001-12-20
| PRIOR FILING DATE: 2001-01-03
| PRIOR FILING DATE: 2001-01-03
| NUMBER OF SEQ ID NOS: 1435
| SEQ ID NO 538
| LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                           gequence 335, Application US/10450797

publication No. US20040142335A1

GENERAL INCORMATION:
APPLICANT: Petersohn, Dirk
APPLICANT: Petersohn, Dirk
APPLICANT: Petersohn, May
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
FILE REFERENCE: HENK-0041
CURRENT APPLICATION NUMBER: US/10/450,797
CURRENT FILING DATE: 2003-12-04
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: PCT/EP01/15178
PRIOR PLING DATE: 2001-03
NUMBER OF SEQ ID NOS: 1435
SOFTWARE: Patentin version 3.2
LENGTH: 11
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                           33.6%;
88.9%;
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NUMBER OF SEQ ID NOS: 1435
SOFTWARE: PatentIn version 3.2
SEQ ID NO 285
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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US-10-450-797-538
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CONGANISM: Homo sapiens
US-10-450-797-335
                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-285
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US-10-450-797-335/c
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Sequence 662, Application US/10450797

Sequence 662, Application US/10450797

Publication No. US20040142335A1

GENERAL INFORMATION:
APPLICANT: Petersonh, Dirk
APPLICANT: Conradt, Marcus
APPLICANT: Hofmann, Kay
TITLE OF INVANTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
TITLE OF INVANTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
CURRENT APPLICATION NUMBER: US/10/450,797

CURRENT PILING DATE: 2001-12-20

PRIOR PILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-01-03

NUMBER OF SEQ ID NOS: 1435

SOFTWARRE, Patentin version 3.2
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Sequence 626, Application US/10450797

Publication No. US20040142335A1

GENERAL INFORMATION

APPLICANT: Petersohn, Dirk

APPLICANT: HORMATION

TILLE OF INVENTION: MATCH

CURRENT APPLICATION NUMBER: US/10/450,797

CURRENT APPLICATION NUMBER: PCT/EP01/15178

PRIOR PILOR DATE: 2003-12-04

CURRENT APPLICATION NUMBER: PCT/EP01/15178

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-01-03

NUMBER OF SEQ ID NOS: 1435

SOFTWARE: Patentin version 3.2

LENGTH: 11
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Score 7.4; DB 1; Length 11; Pred. No. 1.4e+02; 0; Mismatches 1; Indels
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88.9%; Pred. No. 1.4e+02;
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       33.6%;
88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
       Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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CRGANISM: Homo sapiens
US-10-450-797-626
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US-10-450-797-662/c
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Sequence 1286, Application US/10450797

Sublication No. US20040142335A1

GENERAL INCORMATION:

APPLICANT: Petersohn, Dirk

APPLICANT: Conract, Marcus

APPLICANT: Conract, Marcus

TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

FILE REFRENCE: HENK-0041

CURRENT APPLICATION NUMBER: US/10/450,797

CURRENT FILING DATE: 2003-12-04

PRIOR PILING DATE: 2001-12-20

PRIOR PILING DATE: 2001-01-03

NUMBER OF SEQ ID NOS: 1435

SOFTWARE: Patentin version 3.2

SEQ ID NO 1286
GENERAL INFORMATION:
APPLICANT: Petersohn, Dirk
APPLICANT: Conradt, Marcus
APPLICANT: Conradt, Marcus
APPLICANT: Conradt, Marcus
APPLICANT: Hofmann, Kay
TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
FILE REPRENCE: HENK-0041
CURRENT APPLICATION NUMBER: US/10/450,797
CURRENT APPLICATION NUMBER: PCT/FF01/15178
FRIOR APPLICATION NUMBER: DC 2001-12-20
PRIOR PELING DATE: 2001-01-03
NUMBER OF SEQ ID NOS: 1435
SOFTWARE: Patentin version 3.2
SEQ ID NO 1280
LENGTH: ...
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"Sequence 1320, Application US/10450797

"Sequence 1320, Application No. US20040142335A1

"Bublication No. US20040142335A1

"APPLICANT: Peterschin, Dirk

"APPLICANT: Corradt, Marcus

APPLICANT: Hofmann, Kay

"TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

"FILE REFERENCE: HENK-0041

"CURRENT APPLICATION NUMBER: US/10/450,797
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Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1
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; ORGANISM: Homo sapiens
US-10-450-797-1280
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US-10-450-797-1286
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Publication No. US20040142335A1

GENERAL INFORMATION:

APPLICANT: Petersohn, birk

APPLICANT: Conradt, Marcus

APPLICANT: Hofmann, KAY

TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

FILE REFERENCE: HENK-0041

CURRENT APPLICATION NUMBER: US/10/450,797

CURRENT PILING DATE: 2003-12-04

FRIOR FILING DATE: 2001-11-220

FRIOR FILING DATE: 2001-01-03

NUMBER OF SEQ ID NOS: 1435

SOFTWARE: PATENTIN UNDS: 1435

SEQ ID NO 1118

LENGTH: 11
                                                                                                                                                                                                 APPLICANT: Peterson, Dirk
APPLICANT: Peterson, Dirk
APPLICANT: Conradt, Marcus
APPLICANT: Hofmann, Kay
TITLE OF INVENTION: WITHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
FILE REFERENCE: HENK-0041
CURRENT APPLICATION NUMBER: US/10/450,797
CURRENT PILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: PCT/EP01/15178
PRIOR APPLICATION NUMBER: DC1/2-20
PRIOR APPLICATION NUMBER: D01 10 0 121.5
PRIOR APPLICATION NUMBER: D01-01-03
NUMBER OF SEQ ID NOS: 1435
SOFTWARE: PatentIn version 3.2
SEQ ID NO 681
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                                                                                                                                 ; Sequence 681, Application US/10450797; Publication No. US20040142335A1; GENERAL INFORMATION:
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Best Local Similarity 88.9
Matches 8; Conservative
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GORGANISM: Homo sapiens
US-10-450-797-681
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; ORGANISM: Homo sapiens
US-10-450-797-1118
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US-10-450-797-681/c
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## CURRENT FILING DATE: 2003-12-04
| FRIOR APPLICATION NUMBER: PCT/SP01/15178 |
| PRIOR PILING DATE: 2001-12-20 |
| PRIOR PILING DATE: 2001-12-20 |
| PRIOR PILING DATE: 2001-01-03 |
| PRIOR PILING DATE: 2001-01-03 |
| PRIOR FILING DATE: 2001-01-03 |
| SEC ID NO 1320 |
| FAMILY 11 |
| TYPE: DNA |
| ORGANISM: Homo sapiens |
| ORGANISM: Homo sap
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Search completed: October 18, 2004, 14:11:19
Job time : 1 secs

ACCESSION: A67108 ACCESSION: A67111 ACCESSION: AR065607 ACCESSION: 106264	ACCESSION: AR292914 ACCESSION: BD241241	ACCESSION: AX729374 ACCESSION: AX729839 ACCESSION: AX728877	ACCESSION: A67102 ACCESSION: A67104 ACCESSION: AR190011	ACCESSION: AR324988 ACCESSION: AX499951	ACCESSION: AX674143 ACCESSION: AX732557	ACCESSION: EDS. COSCI. ACCESSION: EDS. COSCI.	ACCESSION: AR325471 ACCESSION: AX325471	ACCESSION: AX692031 ACCESSION: AX692032	ACCESSION: B11101 ACCESSION: A11101 ACCESSION: AR362726 ACCESSION: 161456	ACCESSION: AX635865 ACCESSION: BD208396	ACCESSION:A09424 ACCESSION:A10627 ACCESSION:A11575 ACCESSION:A35095	ACCESSION: AX076025 ACCESSION: 128559	ACCESSION: 158721 ACCESSION: A40588 ACCESSION: A89112	ACCESSION:A89603 ACCESSION:AR061873	ACCESSION: AR232868 ACCESSION: AR407925	ACCESSION: AX316484 ACCESSION: BD066625	ACCESSION: BD067116 ACCESSION: 161457	ACCESSION: AR180064	ACCESSION: AX635867 ACCESSION: A22593	ACCESSION: AR096276 ACCESSION: AX076029	ACCESSION: AX255620	ACCESSION: AX452095	ACCESSION: BD208458 ACCESSION: BD208459	ACCESSION:AR123024 ACCESSION:AX626398	ACCESSION: AR180388	ACCESSION: AZS806	ACCESSION: A40589 ACCESSION: A87922	ACCESSION: A89889	ACCESSION: AR029997 ACCESSION: AR030009	ACCESSION:126228 ACCESSION:152188 ACCESSION:152193
34 12.4 56.4 18 1 35 12.4 56.4 18 1 36 12.2 56.4 18 1 37 12.2 55.4 18 1	38 12.2 55.5 18 1 AR29291 39 12 54.5 17 1 BD24124	11.8 53.6 17 1 AX7529 11.8 53.6 17 1 AX7529 11.8 53.6 17 1 AX762	44 11.8 53.6 18 1 A67102 45 11.8 53.6 18 1 A67104 46 11.4 51.8 17 1 AR19001	47 11.4 51.8 17 1 AR32498 48 11.4 51.8 17 1 AX49995	11.4 51.8 17 1 AX674 11.4 51.8 17 1 AX674	52 11.2 50.9 17 1 E54495 17.1 17.1 17.1 17.1 17.1 17.1 17.1 17.	54 11.2 50.9 17 1 AR35547 54 11.2 50.9 17 1 AR35547 55 17 1 AR35547	11.2 50.9 17 1 AX692 11.2 50.9 17 1 AX692	58 11.2 50.9 1/ 1 BD10509 59 11 50.0 15 1 All101 60 11 50.0 15 1 AR36272 61 10.8 49.1 15 1 IG1456	62 10.8 49.1 15 1 AX63 63 10.8 49.1 15 1 BD20	c 64 10.8 49.1 16 1 A09424 c 65 10.8 49.1 16 1 A10627 c 66 10.8 49.1 16 1 A11575 c 67 10.8 49.1 16 1 A35095	68 10.8 49.1 16 1 AXO7 69 10.4 47.3 12 1 1285	70 10.4 47.3 12 1 1587 71 10.4 47.3 14 1 A405 72 10.4 47.3 14 1 A891	10.4 47.3 14 1 A896	10.4 47.3 14 1 AR20 10.4 47.3 14 1 AR40	10.4 47.3 14 1 AX33 10.4 47.3 14 1 AX31 10.4 47.3 14 1 BD06	10.4 47.3 14 1 BD06 10.4 47.3 15 1 1614	82 10.4 47.3 15 1 ARIB	10.4 47.3 15 1 AX63	10.4 47.3 16 1 AR09	88 10.4 47.3 16 1 AX25	90 10.4 47.3 16 1 AX45	10.2 46.4 15 1 BD20 10.2 46.4 15 1 BD20	10 45.5 11 1 AR12 10 45.5 11 1 AX62	95 10 45.5 15 1 ARIB	9.8 44.5 1.4 1. 25.55	98 9.8 44.5 14 1 A803 99 9.8 44.5 14 1 A879	100 9.8 44.5 14 1 A891 101 9.8 44.5 14 1 A898	102 9.8 44.5 14 1 AR029 103 9.8 44.5 14 1 AR030	9.8 44.5 14 1 9.8 44.5 14 1 9.8 44.5 14 1
o.1.6 Compugen Ltd.		arch time 0.001 Seconds hout alignments)					rs: 1268				cted by chance to have a of the result being printed, score distribution.		Description	BD17419	ACCESSION: BD185146 ACCESSION: AR096376	AX59845	AR19522	AR24142	AX13204	AX28627	ACCESSION: AX286288	AX13230	AX44052 A67109	ACCESSION: A67103 ACCESSION: A67105	ACCESSION: A67106	AX13204	AX13230 AX13231	ACCESSION:AX499947 ACCESSION:AX499948	AX02398 AX25571	AX07602 AX49994 AX49995
GenCore version 5.1 Copyright (c) 1993 - 2004 Con	OM nucleic - nucleic search, using sw model	Run on: . October 18, 2004, 14:05:37 ; Search (without 333.432 M	Title: US-09-695-451-1 Perfect score: 22	equence:	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 0.5	Searched: 634 segs, 7578 residues	Total number of hits satisfying chosen parameters	Minimum DB seq length: 8 Maximum DB seq length: 30	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 634 summaries	Database : rgel-727.seq:*	Pred. No. is the number of results predicted I score greater than or equal to the score of tl and is derived by analysis of the total score	KINS	Result Query No. Score Match Length DB ID	1 12 85.55	21 95.5 21 1	5 16.4 74.5 22 1 6 15 4 70.0 18 1	7 15.4 70.0 18 1 8 15.4 70.0 18 1	9 15.4 70.0 18 1	1 15.4 70.0 19 1 2 15 68.2 18 1	13 14.6 66.4 22 1 14 14.6 66.4 22 1	15 14.6 66.4 22 1	17 14.2 64.5 19 1	18 14.2 64.5 21 1 19 14 63.6 18 1	20 13.4 60.9 18 1 21 13.4 60.9 18 1	22 13.4 60.9 18 1	24 H3.2 60.0 199 H	25 13.2 60.0 19 1 26 13.2 60.0 19 1	7 12.8 58.2 17 1 8 12.8 58.2 17 1	29 12.8 58.2 19 1 30 12.4 56.4 16 1	56.4 17 56.4 17 56.4 17

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DNA linear PAT 18-FEB-2003

Periplastic converting agent.

NO 8D174191

BD174191

BD17 PAT 17-JUN-2003 PAT 18-FEB-2003 ACCESSION: BD083230
ACCESSION: BD161207
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i. .21

location/Qualifiers

Location/Qualifiers

1. .21

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Gaps

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Baker, B.F. and Cowsert, L.M.
Antisense modulation of TWFR1 expression
Patterns modulation of TWFR1 expression
ISIS PHARMACEUTICALS INC
OS Unidentified
PN J0202519015-A47
D0 2-JUL-2002
PF 77-JUN-1999 UP 2000557265
PR 77-JUN-1999 UP 2000557265
PR 26-JUN-1999 US 09/106638
PI BRENDA F BAKER, LEX M COWSERT
PC C1201/68,
PC C1201/68,
PC C12N15/09
CC Strandedness: Single,
CC Strandedness: Single,
CC Antisense modulation of TWFR1 expression
FH Key
Location/Qualifiers
FT source

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Systems and method for detection assay production and sale Patent: WO 0244994-A 726 06-JUN-2002;
THIRD WANG TECHNOLOGIES, INC. (US)
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94.4%; Pred. No. 14;
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Sequence 726 from Patent WO0244994.
AX598452.1 GI:28398628
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Matches 17; Conservative
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Matches 17; Conserv
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                                    TITLE
JOURNAL
      REFERENCE
                       AUTHORS
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AUTHORS
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synthetic construct
synthetic construct
artificial sequences.

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S (all differentiating agent
L Patent: JP 2002356438-A 37 13-DEC-2002;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 200235438-A/37
PD 13-DEC-200
PF 21-FEB-2002 JP 2002044741
PI YUKIKO HIXICHI, YASUSHI SHINTANI, HIDEKI MATSUI PC
A611X88/00, A61X11/7088, A61P15/00, A61P21/04, A61P35/00, CIZNIS/09// PC
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Location/Qualifiers
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BD217424
JP 2002519015-A/47.
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1 (bases 1 to 18)

1 Saker, B.F. and Cowsert, L.M.

Antisense inhibition of TNFR expression

Patent: US 6007995-A 47 28-DEC-1999;

Location/Qualifiers
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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95.5%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 2;
Matches 21; Conservative 0; Mismatches
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Sequence 47 from patent US 6007995.
AR096376
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/organism="unknown"
/wol_type="unassigned DNA"
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Best Local Similarity
Matches 17; Conserv
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AR096376/c
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BD217424/c
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18 CAGGAGAAACACACAC 2
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Homo sapiens
Best Local Similarity 94.19
Matches 16; Conservative
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AR241422/c
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BD014788/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unclassified.

1 (Dasses 1 to 18)

Priedman,J.M., Zhang,Y. and Proenca,R.
OB polypeptides and modified forms as modulators of body weight Patent: US 6350730-A 45 26-FEB-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                        Gaps
                                                Unknown.
Unclassified.
Unclassified.
Unclassified.
I (bases I to 18)
Friedman, J. M. Shang, Y. and Proenca, R.
Modulators of body weight, corresponding nucleic acids and proteins, and diagnostic and therapeutic uses thereof Patent: US 6309553-A 45 30-OCT-2001;
Location/Qualifiers
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Friedman,J.W., Zhang,Y. and Proenca,R.
Polypeptides, modified forms and derivatives
Patent: US 6429290-A 45 06-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45 from patent US 6350730. AR195221. GI:20244658
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Sequence 45 from patent US 6429290.
AR222303
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AR175645
AR175645.1 GI:17916944
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AR195221/c
                                                          ORGANISM
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AR222303/c
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Bases I to 18)

E Friedman, J.M., Zhang, Y., Proenca, R., Maffei, M., Halaas, J.L.,
Kajiwara, K. and Burley, S. K.
Modulator of weight, Corresponding nucleic acid and protein, and diagnosis and remedy utilization thereof

E PACKEFELLER UNIVERSITY

OS Homo sapiens (human)

PD 2001157591-A, 29

THE ROCKEFELLER UNIVERSITY

OS HOMO Sapiens (human)

PD 12-UNN-2001

PP 29-SEP-2000 JP 2000301496

PR 29-SEP-2000 JP 2000301496

PR 30-NOV-1994 US 08/483211

PI JEFRRY M FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA PI
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PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68//(C12N1/19,C12R1:72), PC (C12N1/19,C12R1:07), PC (C12N1/19,C12R1:07), PC (C12N1/12,C12R1:05), C(12N1/12,C12R1:07), PC (C12N1/21,C12R1:045), (C12N1/21,C12R1:07), PC (C12P21/02,C12R1:07), C12N1/21,C12R1:07), PC (C12N5/00,C12R1:07)
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CIZNIS,09,A61K31/711,A61K38/00,A61K39/395,A61K45/00,A61K48/00, PC
A61P3/04,
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified.
Unclassified.
1 (bases 1 to 18)
Priedman, J. M., Zhang, Y. and Proenca, R.
Ob polypeptides, modified forms and compositions thereto Patent: US 6471956-A 45 29-0CT-2002;
Location/Qualifiers
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Sequence 45 from patent US 6471956.
94.1%; Pred. No. 17; tive 0; Mismatches
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                                                                                         730 CAGGAGAAACAGAACAC 746
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AR241422.1 GI:27287112
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PAT 21-NOV-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                      Lin, H.H., Gordon, D.S., Mcknight, A.J. and Stacey, M.S.
Human emz2, a g-protein coupled receptor from the egf-tm7 family
Patent: WO 0179296-A 7 25-OCT-2001;
Isis Innovation Limited (GB)
Location/Qualifiers
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Human emr2, a g-protein coupled receptor from the egf-tm7 family
Patent: WO 0179296-A1 25-OCT-2001;
Isis Innovation Limited (GB)
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                                      Query Match 68.2%; Score 15; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 21; Matches 15; Conservative 0; Mismatches 0; Indels
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81.0%; Pred. No. 29;
iive 0; Mismatches 4;
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Best Local Similarity 81.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 11 from Patent W00179296.
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/organism="Homo sapiens"
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Sequence 7 from Patent WO0179296.
AX286278 GI:17048526
         /db_xref="taxon:32644"
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AX286282.1 GI:17048530
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Best Local Similarity 81.08
Matches 17; Conservative
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AX286278/c
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AX286282/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                      Key
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                Topology: Linear, PCR primer sWSS2359 specific in sequence tag site FH Location/Qualifiers
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/db_xref="taxon:9606"
/note="Cyclin B1 ribozyme binding site"
                                                                  ce 1. .18
/organism='Homo sapiens
Location/Qualifiers
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1 (bases 1 to 18)
Stuyver,L., Rossau,R. and Maertens,G.
MeTHOD FOR TYPING AND DETECTING HBV
Patent: WO 9740193-A 274 30-OCT-1997;
INNOGENETICS NV (BE)
                                                                                                                                                                                                                                                                                                                                                                                                      DNA
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/organism="unidentified"
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/organism="Homo sapiens"
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Strandedness: Single;
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A67107.1 GI:4538478
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PAT 28-JUN-2002
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                       Robbins, J.M. and Tritz, R. Ribozyme therapy for the treatment of proliferative skin and eye diseases
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                                                                                                                                                                                                                                                                                 Query Match 64.5%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 30; Matches 16; Conservative 0; Mismatches 3; Indels
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="PCR primer 5F1"
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unclassified.
1 (bases 1 to 18)
Stuyver, L., Rossau, R. and Maertens, G.
Stuyver, L., Wossau, R. and Maertens, G.
METHOD FOR TYPING AND DETECTING HBV
Patent: WO 9740193-A. 276 30-OCT-1997;
INNOGENETICS NV (BE)
Location/Qualifiers
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IMMUSOL, INC. (US)
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Seguence 276 from Patent WO9740193.
A67109
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AX440525 AX440525.1 GI:21665328
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/organism="unidentified"
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/organism="Homo sapiens"
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Location/Qualifiers
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artificial sequences.
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A67109/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                       Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                             Lin, H.H., Gordon, D.S., Mcknight, A.J. and Stacey, M.S.
Human emr2, a g-protein coupled receptor from the egf-tm7 family
Patent: WO 0179296-A 17 25-0CT-2001;
Isis Innovation Limited (GB)
Location/Qualifiers
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|mol_type="unassigned DNA"
|dox zref=traxon:9606"
|note="Cyclin Bl ribozyme binding site"
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IMMUSOL, INC. (US)
Location/Qualifiers
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AX132045.1 GI:14138350
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Seguence 3527 from Patent WO0130362.
AX132309
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    .22
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/db_xref="taxon:9606"

                                   22 bp
Sequence 17 from Patent WO0179296.
AX286288
AX286288.1 GI:17048536
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Homo sapiens
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E26485/c
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unclassified.
1 (bases 1 to 18)
Stuyver, L., Rossau, R. and Maertens, G.
METHOD FOR TYPING AND DETECTING HBV
Patent: WO 9740193-A 272 30-OCT-1997;
INNOGENETICS NV (BE)
                                      ch 63.6%; Score 14; DB 1; Similarity 100.0%; Pred. No. 31; 14; Conservative 0; Mismatches
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Stuyver, L., Rossau, R. and Maertens, G.
METHOD FOR TYPING AND DETECTING HBV
PATENT: WO 9740193-A 270 30-OCT-1997;
INNOGENETICS NV (BE)
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60.9%; Score 13.4; Di
Best Local Similarity 93.3%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches
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    .18
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/db_xref="taxon:32644"

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RESULT 22

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unidentified
unclassified.
1 (bases i to 20)

K Azuaki,S. and Hiromitsu,K.
Highly sensitive method for detecting lamivudine-tolerant hepatitis
B virus
B virus
F AZUAKI SAYAMA
OS Unidentified
BN 1999127860-A/1
BD 18-MAY-1999;
RAZUAKI SAYAMA,HIROMITSU KUMADA
PR 28-OCT-1997 JP 1997296042
PR 720-OCT-1997 JP 1997296042
PR 720-OCT-1997296042
PR 720-OCT-1997296042
PR 720-OCT-1997296042
PR 720-OCT-199
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Highly sensitive method for detecting lamivudine-tolerant hepatitis
B virus.
             PAT 29-MAR-1999
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/organism='Unidentified'.
Location/Qualifiers
                                                                                                                                                                                                                                                     unclassified
unclassified.
1 (bases 1 to 18)
Stuyver, L., Rossau, R. and Maertens, G.
Stuyver, L., Wossau, R. and Maertens, G.
METHOD FOR TYPING AND DETECTING HBV
Patent: WO 9740193-A 273 30-OCT-1997;
INNOGENETICS NV (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
60.9%; Score 13.4; Di
Best Local Similarity 93.3%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches
18 bp | 1873 from Patent WO9740193. A67106 | GI:4538477
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/organism="unidentified"
/mol_type="unassigned DNA"
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/organism="unidentified"
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JP 1999127860-A/1.
unidentified
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PAT 27-SEP-2002

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                Robbins, J.M. and Tritz, R.
Ribozyme therapy for the treatment of proliferative skin and diseases
Datent: WO 0130362-A 3528 03-MAY-2001;
IMMUSOL, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.2%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 48; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                         Query Match 60.0%; Score 13.2; DB 1; Length 19; Best Local Similarity 83.3%; Pred. No. 45; Matches 15; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                        1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="teaxon:9606"
/note="Cdc25 hs ribozyme binding site"
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Human testis expressed patched like protein
Patent: EP 1229046-A 1255 07-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human testis expressed patched like protein Patent: BP 1229046-A 1254 07-AUG-2002; Aeomica, Inc. (US) Location/Qualifiers
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Sequence 1255 from Patent EP1229046.
AX499948.
AX499948.1 GI:23382241
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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              Homo sapiens (human)
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AX499948/c
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AX499947/C
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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60.0%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 3; Indels
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/noTe="Cyclin B1 ribozyme binding site"
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/organism="Homo sapiens"
/or_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdc25 hs ribozyme binding site"
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                                                       DNA
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Patent: WO 0130362-A 3526 03-MAY-2001;
IMMUSOL, INC. (US)
                                                                                                                                                                                                                                                                               Patent: WO 0130362-A 3265 03-MAY-2001;
IMMUSOL, INC. (US)
Location/Qualifiers
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Sequence 3528 from Patent W00130362.
AX132310
AX132310.1 GI:14138615
                                                    19 bp D:
WO0130362.
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Sequence 3526 from Patent W00130362.
AX132308.1 GI:14138613
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Location/Qualifiers
                                                           Sequence 3265 from Patent
AX132047
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                                                                                                      AX132047.1 GI:14138352
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Homo sapiens
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AX132310/c
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AX132308/c
LOCUS
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                RESULT 24
AX132047/C
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PAT 27-SEP-2002

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PAT 06-FEB-2001

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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Patent: WO 0104358-A 2 18-JAM-2001;
INNOGENETICS N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human testis expressed patched like protein
Patent: BP 129046-A 1256 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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    .17.
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|db_xref="taxon:10407"

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Sequence 1257 from Patent EP1229046.
AX499950
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                                                                                          Sequence 2 from Patent W00104358.
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Matches 13; Conservative
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15 AGAACAGACCACC
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Best Local Similarity
Matches 13; Conserv
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AX499950/c
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AX076026/c
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ACCESSION
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Agents for the immunotherapy of tumoral diseases
Patent: WO 0004918-A 3 03-FEB-2000;
XERKMANN TUCEK ALDA (DE)
Location/Qualifiers
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Brca-1 regulators and methods of use
Patent: WO 0170982-A 131 27-SEP-2001;
Immusol Incorporated (US); Beger, Carmela
Location/Qualifiers
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/organism="synthetic construct"
/orlarism="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

    .19
        /organism="synthetic construct"
        /mol type="unassigned DNA"
        /db_xref="taxon:32630"

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                                                                                                            Query Match 58.2%; Score 12.8; I
Best Local Similarity 87.5%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches
                                                              /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX255710
                                 1. .17
/organism="Homo sapiens"
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             Location/Qualifiers
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synthetic construct
artificial sequences.
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artificial sequences.
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Best Local Similarity
Matches 13; Conserv
 Aeomica,
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AX255710/c
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AX023982
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Unclassified.
Unclassified.
I (bases 1 to 18)
Grotendorst,G.R. and Iida,N.
DNA encoding leukcoyte derived growth factor-2 (LDGF-2)
Patent: US 5849534-A 6 15-DEC-1998;
Location/Qualifiers
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AR292914.1 GI:31680198
                        Query Match 56.4%; Score 12.4; D
Best Local Similarity 92.9%; Pred. No. 59;
Matches 13; Conservative 0; Mismatches
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56.4%; Score 12.4; D
Best Local Similarity 92.9%; Pred. No. 59;
Matches 13; Conservative 0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                       Sequence 6 from patent US 5849534.
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AR292914/c
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ORGANISM
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AR065607/c
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I06264/c
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human testis expressed patched like protein
Patent: EP 1229046-A 1257 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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unclassified.
1 (bases 1 to 18)
Stuyver,L., Rossau,R. and Maertens,G.
METHOD FOR TYPING AND DETECTING HBY
Patent: WO 9740193-A 275 30-OCT-1997;
INNOGENETICS NV (BE)
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Stuyver, L., Rossau, R. and Maertens, G.
METHOD FOR TYPING AND DETECTING HBV
PATCHT: WO 974019-A 278 30-OCT-1997,
INNOGENETICS NV (BE)
Location/Qualifiers

    .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 275 from Patent W09740193.
A67108

    .18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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Sequence 278 from Patent W09740193.
A67111
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Best Local Similarity 92.9
Matches 13; Conservative
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A67111/c
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A67108/c
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
Patent: WO 03004526-A 3017 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
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                                                                                         Zhan,J.

Human testis expressed patched like protein
Patent: EP 1229046-A 1253 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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AX729839.1 GI:30509182
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Sequence 3017 from Patent W003004526.
AX674572 GI:29332920
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86.7%; Pred. No. 71;
ive 0; Mismatches
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Homo sapiens
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Matches 13; Conservative
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Best Local Similarity
Matches 13; Conservat
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AX674572/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(CE 1 (bases 1 to 17);
RS Landers, J.E., Jordan, B., Housman, D.E. and Charest, A.

Methods and products related to genotyping and DNA analysis

AL Methods and products related to genotyping and DNA analysis

AL Patent: JP 200255127-A 188 13-AUG-2002;
AMCS REPLISTITE OF TECHNOLOGY

OS Homo sapiens (human)

PN JP 200255127-A/188

PD 13-AUG-2002

PF 24-SEP-1999 US 2000572407

PR 25-SEP-1999 US 60/10177

PR 25-SEP-1999 US 60/101737

PR 25-SEP-1999 US 60/101737

PR 25-SEP-1999 US 60/101737

PR 25-SEP-1999 US 60/101737

PR 25-SEP-1999 US 60/101737
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Methods and products related to genotyping and DNA analysis.
BD241241
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                                                       1 (bases 1 to 18)
Cohen.D., Chumakov,I. and Blumenfeld,M.
Biallellic markers for use in constructing a high density
disequalibrium map of the human genome
Patent: US 6537751-A 4649 25-MAR-2003;
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100.0%; Pred. No. 66;
atrive 0; Mismatches (
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EP1229046.
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/organism="Homo sapiens"
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Sequence 1253 from Patent
AX499946
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JP 2002525127-A/188.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 12; Conservative
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AX499946/c
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BD241241/c
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(bases 1 to 17)

Asvo.P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 5499 12-FRB-2002;
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US 6566127.
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Stuyver, L., Rossau, R. and Maertens, G.
METHOD FOR TYPING AND DETECTING HBV
Patent: WO 9740193-A 271 30-OCT-1997,
INNOGENETICS NV (BE)
Location/Qualifiers
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                                                                                                                                                  18 bp 18 Sequence 271 from Patent W09740193. A67104
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92.3%; Pred. No. 83;
Live 0; Mismatches
     Mismatches
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/organism="unknown"
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Sequence 2390 from patent
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Best Local Similarity 92.3
Matches 12, Conservative
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A67104/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as
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Patent: WO 03025175-A 1473 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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medicines
Patent: WO 03040369-A 6198 15-MAX-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Stuyver,L., Rossau,R. and Maertens,G.
METHOD FOR TYPING AND DETECTING HBV
PATENT: WO 9740193.A 269 30-OCT-1997;
INNOGENETICS NV (BE)

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Seguence 269 from Patent WO9740193.
A67102
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Pred. No. 75;
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RESULT 44 A67102/c

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AUTHORS TITLE

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FATURES

REFERENCE

schultz1-727.rge

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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JP 2002539849-A/301.
synthetic construct
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92.3%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                             Tasss 1 to 17)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 2390 20-MAY-2003;
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Seguence 1258 from Patent EP1229046.
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92.3%; Pred. No. 83;
ive 0; Mismatches
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

                                                                                                                                                /organism="unknown"
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PC C12Q1/68, C12M1/00, C12N15/09, C12N15/09, C12N15/09, G01N33/53, PC
G01N33/566,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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E 1 (bases 1 to 17)
S Fan, J.B., Hirschhorn, J.N., Huang, X., Kaplan, P., Lander, E.S., Lockhart, D.J., Ryder, T. and Sklar, P.
Universal arrays
L Patent: JP 2002539849-A 301 26-NOV-2002;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC OS Artificial Sequence
PN JP 200239849-A/301
PD 26-NOV-2002
PF 27-NAR-2000 P 2000608794
PR 26-NAR-2000 US 60/126473,23-JUN-1999 US 60/140359 PI
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JIAN BING FAN, JOEL N HIRSCHHORN, XIAOHUA
HUANG, PAUL KAPLAN, ERIC
STANDER,
  DB 1;
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Pred. No. 83;
0; Mismatches
51.8%; Score 11.4; Ilarity 92.3%; Pred. No. 83; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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728 GCCAGGAGAACAGAA 743
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Best Local Similarity 91.29
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S 201120270-A/19.
Synthetic construct
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Is synthetic construct
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It shads I to 17)

S Itaya, M., Kimura, E., Kawara, Y. and Sugimoto, S.
Heat-resistant lysine biosynthesis enzyme gene of thermophilic
coryneform bacterium
ALINOMOTO CO INC
AJINOMOTO CO INC
OS Artificial Sequence
PN JP 2001120270-A/19
PD 08-MAY-2001
PF 01-NOV-1999 JP 199311148
PF 01-NOV-1999 JP 199311148
PT 01-NOV-1999 JP 199311149
PT 01-NOV-1999 JP 19931
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Unclassified.
1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
                                                                             ce 1..17 /organism='Artificial Sequence'
Location/Qualifiers
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G01N37/00,C12N15/00,C12N15/00,C12N15/00
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/db_xref="taxon:32630"
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Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 17)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 656127-A 2873 20-MAY-2003;
Location/Qualifiers
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 6036 12-FEB-2002;
Location/Qualifiers
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Patent: WO 0157206-A 983 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                          17 bp RNA
Sequence 2873 from patent US 6566127.
AR325471.
AR325471.1 GI:33711279
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81.2%; Pred. No. 90;
tive 0; Mismatches
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Sequence 983 from Patent WO0157206.
AX227611.1 GI:15556752
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Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches
                                                                                                1. .17
/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned RNA"
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TAEKO

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WO 0192572- #11165.
WO 0192572- #11165.
Synthetic construct
artificial sequences.
1 (bases 1 to 17)
Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and
Nishida, M.
Kit and method for determining HLA type
Patent: WO 0192572- #1196 06-DEC-2001;
NISSHINBO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDETOSHI INOKO, TA
KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
                                                                                                                                                                                                                                                                                                                                      Artificial Sequence
W0 0192572-A/1196
06-DEC-2001
01-JUN-2001 W0 2001JP004662
01-JUN-2000 JP 00P 164798
HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism='Artificial Sequence'
Location/Qualifiers
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C1201/68, C12M1/00, C12N15/09, G01N33/53
Description of Artificial Sequence: capture
Key

    1.7
    ^17
    ^2organism="synthetic construct"
    ^mol_type="genomic DNA"
    ^db_xref="taxon:32630"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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synthetic construct
artificial sequences.

I (bases 1 to 15)
Ikehara,M. and Kida,M.
Synthetic gene for human lysozyme
Patent: EP 0181634-A 45 21-MAY-1986;
Takeda Chemical Industries, Ltd
Location/Qualifiers
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Oligonucleotide U23.
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AR362726
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: EP 1281758-A 4764 05-FEB-2003;
Acomica, Inc. (US)
Location/Qualifiers
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Sequence 4764 from Patent EP1281758.
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Best Local Similarity 81.2%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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Location/Qualifiers
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AX692032.1 GI:29414976
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                                                                                                                                                                                  DEFINITION
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BD105092
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PAT 03-DEC-1993

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Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
to hepatitis C virus infection
RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/1986
PD 08-MAY-2002
PF 26-ARP-1999 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
                                                                                                                                                                                                                                                                                                            BD208396 15-JUL-2003 Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
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C1230/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
A61X9/06,
C12N15/00
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85.7%; Pred. No. 94;
iive 0; Mismatches 2;
                                                                                                                               Query Match
49.1%; Score 10.8; DB 1;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 2;
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Patent: EP 1260586-A 3004 27-NOV-2002; RIBOZYME PHARMACEUTICALS, INC. (US) Location/Qualifiers

    .15
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1. 15
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BD208396.1 GI:33018166
JP 2002512791-A/1986.
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Oligonucleotide (a6).
A09424
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A09424/c
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   PAT 03-SEP-2003
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                                                                                                                                     1 (bases 1 to 15)
Nakahama, K., Kaisho, Y. and Yoshimura, K.
Method for increasing gene expression using protease deficient
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(bases 1 to 15)
Stinchomb, D.T., Draper, K.G. and McSwiggen, J.
Stinchomb, D.T., Draper, K.G. and McSwiggen, J.
Paten a targeted ribozymes
Patent: US 5658780-A 10 19-AUG-1997;
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Location/Qualifiers
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Patent: US 5182195-A 60 26-JAN-1993,
Location/Qualifiers
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49.1%; Score 10.8; Dest Local Similarity 85.7%; Pred. No. 94; Matches 12; Conservative 0; Mismatches
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Sequence 10 from patent US 5658780.
161456.
161456.1 GI:2479404
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/organism="unknown"
/mol_type="unassigned DNA"
 AR362726 15 bp
Sequence 60 from patent US 5182195.
AR362726 1 GI:34423106
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/organism="unknown"
/mol_type="genomic DNA"
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PAT 06-DEC-1996

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Jeda,I., Niwa,M., Satoh,S., Saitoh,Y. and Kusunoki,C.
Process for production of isulin-like growth factor I and plasmid
for production thereof
Patent: EP 0219814-A 45 29-APR-1987;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
                                                                ch 49.1%; Score 10.8; DB 1; Length 16; 1. Similarity 85.7%; Pred. No. 1e+02; 12; Conservative 0; Mismatches 2; Indels
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Detection of anti-hepatitis b drug resistance
Metent: WO 0104358-A 1 18-JAN-2001;
INNOGENETICS N.V. (BE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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    16
    /organism="Hepatitis B virus"

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/db_xref="taxon:10407"
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A35095
A35095.1 GI:1926754
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1 (bases 1 to 16)
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Matches 12; Conservative
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AX076025/c
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A35095/c
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synthetic construct
artificial sequences.
1 (bases 1 to 16)
Ueda, I., Niwa, M., Saito, Y., Sato, S., Ono, H. and Kitaguchi, T.
59 Valine insulin-like growth factor I and process for production
thereof
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artificial sequences.

I (bases 1 to 16)
Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.
Process for production of gamma-interferon
Parent: Bp 01/6916-A 12 09-APR-1986;
FUJISAWA PHARWACEUTICAL CO., LTD
Location/Qualifiers
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Pred. No. 1e+02;
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                               synthetic construct
synthetic construct
artificial sequences.

I (baces 1 to 16)
Ueda,I., Niwa,M., Saitoh,Y., Satoh,S. and Yamada,H.
Process for production of somatostatin
Patent: EP 019758-A 30 15-OCT-1986;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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A11575
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Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
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Pred. No. 1e+02;
0; Mismatches 1; Indels
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Brysch, W. and Schlingensiepen, K.
AN ANTIENSE OLICONUCLEDEDTIDE PREPARATION METHOD
Patent: WO 9833904-A 1260 06-AUG-1998,
BIOGNOSTIK GES (DE), BRYSCH WOLFGANG (DE)
Location/Qualifiers
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Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLECTIDE PREPARATION METHOD Patent: WO 9833904-A 1751 06-AUG-1998,
BIOGNOSTIK GES (DE), BRYSCH WOLFGANG (DE)
Location/Qualifiers
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Sequence 1751 from Patent WO9833904.
A89603
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Sequence 1260 from Patent W09833904.
A89112 GI:6737682
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/organism="unidentified"
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    .14
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Best Local Similarity 91.77,
Best Local Similarity - 742
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PALENT: WO 9425578-A 125 10-NOV-1994;
BIOGNOSTIK GES (DE)
                             PAT 06-FEB-19
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                                                                                                                                       Matanabe, K.A., Ren, W.-Y. and Weil, R. Complementary DNA and toxins Patent: US 5571937-A 12 05-NOV-1996; Location/Qualifiers
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Pred. No. 90;
0; Mismatches
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Watanabe,K.A., Ren,W.-Y. and Weil,R.
Complementary DNA and toxins
Patent: US 5552350-A 12 29-UL-1997;
Location/Qualifiers
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Sequence 125 from Patent W09425578.
A40588
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Sequence 12 from patent US 5571937.
128559
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Sequence 12 from patent US 5652350.
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Schlingensiepen, G.-F., Brysch, W., Schlingensiepen, K.-H., Schlingensiepen, G.-F., Brysch, W., Schlingensiepen, R. and Bogdahn, U.
Antisense-oligonucleotides for transforming growth factor..beta.
(TGF..beta.)
Patent: US 6455689-A 125 24-SEP-2002;
                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                     1 (bases 1 to 14)
Rothemund, P.W.K.
Method for construction universal DNA based molecular turing machine.
Patent: US 5843661-A 4 01-DEC-1998;
Location/Qualifiers
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Pred. No. 1e+02;
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Sequence 125 from patent US 6455689.
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Sequence 18 from patent US 6632057.
AR407925.
AR407925.1 GI:40157912
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Sequence 4 from patent US 5843661.
AR061873
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Fauchet,C.R.J.
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Antisense-oligonuclectides for the treatment of immunosuppressive effects of transforming growth factor-beta (tgf-beta)
Patent: EP 1160319-A 125 05-DEC-2001;
BIOGNOSTIK GESELISCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Fixing unit with an end imprint in a threaded terminal portion Patent: US 6632057-A 18 14-OCT-2003; Location/Qualifiers
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/mol type="unassigned DNA"
/mole="bescription of unknown"
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Sequence 125 from Patent EP1160319.
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Homo sapiens
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Vogelstein, B., Kinzler, K. W., Zhang, L. and Zhou, W. Gene expression profiles in normal and cancer cells Patent: US 633152-A 132 25-DEC-2001;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 15)
Stinchcomb.D.T., Draper.K.G. and McSwiggen,J.
Rel a targeted ribozymes
Rel a targeted ribozymes
Patent: US 5658780-A 11 19-AUG-1997;
Location/Qualifiers
                               /organism='Unknown'.
Location/Qualifiers
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AR180064
AR180064.1 GI:20222097
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Sequence 11 from patent US 5658780.
161457
161457.1 GI:2479405
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/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"

    .14
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/db_xref="taxon:32644"

   Location/Qualifiers
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Best Local Similarity 91.7
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                  unidentified
unclassified.
1 (bases 1 to 14)
Schlingensiepen, K.H. and Brysch, W.
An antisense oligonucleotide preparation method
Patent: JP 2001511000-A 1260 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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1 (bases 1 to 14)
Schlingensiepen,K.H. and Brysch,W.
An antisense oligonucleotide preparation method
Patent: JP 2001511000-A 1751 07-AUG-2001;
BICGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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10 2001511000-A/1751
07 2001511000-A/1751
30-JAN-1998 UP 1998532533
30-JAN-1997 EP 97101531.8
XARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11, COTH2L1/04, A61K31/70
An antisense oligonucleotide preparation method FH
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KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11, C07H21/04, A61K31/70
An antisense oligonucleotide preparation method FH
Location/Qualifiers
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Score 10.4; DB 1; Length 14;
Pred. No. 1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                   An antisense oligonucleotide preparation method. BD066625 BD06625, I GI:22612228 UP 200151100-A/1260.
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UP CO1511000-A/1751.
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2001511000-A/1260
07-AUG-2001
30-JAN-1998 JP 1998532533
31-JAN-1997 EP 97101531.
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   Query Match
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Matches 11; Conservative
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731 AGGAGAAACAGA 742
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Unclassified.
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Matches 11; Conserv
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AX076029/C
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AR096276
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                                                                                                                  Unclassified.

1 (bases 1 to 15)
Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
Gene expression profiles in normal and cancer cells
Patent: US 6333152-A 867 25-DEC-2001;
Location/Qualifiers
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47.3%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   15 bp RA Sequence 3006 from Patent EP1260586. AX635867
                          15 bp D
Sequence 867 from patent US 6333152.

    .15
/organism="unidentified"
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/db_xref="taxon:32644"

    .15
    /organism="unknown"
    /mol_type="unassigned DNA"

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                                                                    AR180799.1 GI:20222832
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A22593
A22593.1 GI:641563
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Petunia x hybrida
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Best Local Similarity
'-has 11; Conserve
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AX635867/c
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A22593
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RESULT 83
AR180799
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PAT 08-SEP-2000
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots,
asterids, lamide, Solanales, Solanaceae, Petunia.
1 (bases 1 to 16)
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Word Tunen, Johannes., Van Der Meer, I.Maria. and
Mol, G.Nicolaas, Maria.
Male-sterile plants, method for obtaining male-sterile plants and
recombinant DNA for use therein
Patent: US 600167-A 2 1.DEC-1999;
Location/Qualifiers
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Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels
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Detection of anti-hepatitis b drug resistance
betent: WO 0104358-A 5 18-JAN-2001;
INNOGENETICS N.V. (BE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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    16. Organism="Hepatitis B virus"
/mol_type="unassigned DNA"
/db_xref="taxon:10407"

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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                       Patent: WO 9218625-A 4 29-OCT-1992;
Location/Qualifiers
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Sequence 4 from patent US 6005167.
AR096276
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AX076029.1 GI:12710682
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Best Local Similarity 91.7%;
Matches 11; Conservative
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unidentified
unclassified.

1 (base 1 to 15)

8 Blatt.L., Meswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

8 Blatt.L., Meswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

8 Blatt.L., Meswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

8 Blatt.L., Meswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

8 Blatt.L., Meswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

8 Blatt.L., Meswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

8 Blatt.L., Meswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

8 Blatt.L., Meswiggen, J.A., Roberts, E., Pavco, P.A.

8 Blatt.L., Meswiggen, J.A., Roberts, Pawer, D.

8 Blatt.L., Meswiggen, B., Pavco, P.A.

8 Blatt.J., Jawes A. McSwiggen, E., Pavco, P.A.

8 Blatt.L., Meswiggen, B., Pavco, P.A.

8 Blatt.J., Jaker, P.A.

8 Blatt.J., Meswiggen, B., Pavco, P.A.

8 Blatt.J., Jaker, P.A.

8 Blatt.J., Jak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
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1. .15
/organism='Hepatitis virus (hepatitis C
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86.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 3; Indels
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    16. 16
    /organism="synthetic construct" | /mol_type="unassigned DNA" | /db xref="traxon;32630" | /noTe="Primer"

                                                                                                                                                                                   Blair, E.D., Snowden, B.W. and Ward, C.L. Diagnostic method Patent: EP 1211326-A 2 05-JUN-2002; GLAXO GROUP LIMITED (GB) Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
  Sequence 2 from Patent EP1211326.
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JP 2002512791-A/2048.
unidentified
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AX452095.1 GI:21712097
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BD208458/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Brca-1 regulators and methods of use
Patent: WO 0170982-A 84 27-SEP-2001;
Immusol Incorporated (US); Beger, Carmela (DE)
Location/Qualifiers
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Brca-1 regulators and methods of use
Patent: WO 0170982-A 41 27-SEP-2001;
Immusol Incorporated (US); Beger, Carmela (DE)
Location/Qualifiers
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/organism="synthetic construct"
/wol type="unassigned RNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
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    .16
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Sequence 84 from Patent WO0170982.
AX255663
                                                                                                                                                                                                                                        Sequence 41 from Patent WO0170982.
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synthetic construct
artificial sequences.
       Best Local Similarity 91.7%;
Matches 11; Conservative
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Homo sapiens
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AX255663
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Indels

PAT 21-FEB-2003

linear

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Homo sapiens (human)
Memo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 15)

Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
Vogelstein,B., Kinzler,K.W., zhang,L. and zhou,W.
Vogelstein,B., Kinzler, K.W., zhang,L. and zhou,W.
Vogelstein,B., Kinzler, K.W., zhang,L. and zhou,W.

Location/Qualifiers
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                                                             Length 11;
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                                                         Query Match 45.5%; Score 10; DB 1; Best Local Similarity 100.0%; Pred. No. 97; Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                            AX626398 11 bp DNA Sequence 3439 from Patent W002053774. AX626398
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/organism="unknown"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/wol_type="unassigned DNA"
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Matches 10, Conservative
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BD208460/c
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AX626398
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                                                                                                                                                                                                                                                                                    unclassified.

It (bases 1 to 15)

S Blatt.L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
to hepatitis C virus infection

ND Patent: JP 2002512791-A 2049

ND PATENTICALS INC.
S Hepatitis virus (hepatitis C virus)
NN JP 2002512791-A/2049

PN JP 2002512791-A/2049

PN 2 A-APR-1999 JP 200545991

PR 26-APR-1999 US 60/083217,18-SEP-1999 US 60/100842 PR 25-APR-1999 US 09/2576668,23-MAR-1999 US 09/257668,23-MAR-1999 US 09/257668,23-MAR-1999 US 09/257668,23-MAR-1999 US 09/25766 PA CI2NS/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC CL2NS/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC CL2NS/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC Enzymatic nucleic acid treatment of diseases or conditions CC
                                                                                                                                            BD208459 17-JUL-2003 Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
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Key
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Methods for making modified recombinant vesiculoviruses
Patent: US 6168943-A 15 02-JAN-2001;
Location/Qualifiers
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    .15
    /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

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JP 2002512791-A/2049.
unidentified
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                   729 CCAGGAGAACAGAA 743
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Best Local Similarity 80.09
Matches 12; Conservative
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unclassified.
1 (bases 1 to 14)
3 Hysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLECTIDE PREPARATION METHOD
L. Patent: WO 9833904-A. 70 06-AUG-1998,
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Sequence 1261 from Patent W09833904.
A89113.1 G1:6737683

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Sequence 126 from Patent WO9425578.
A40589
A40589.1 GI:2296624
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Sequence 70 from Patent WO9833904.
A87922
A87922.1 GI:6736492
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Best Local Similarity 84.6%;
Matches 11; Conservative
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(bases 1 to 14)
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 BD208460 17-JUL-2003 Enzymatic nucleic acid treatment of diseases or conditions related
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Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
Patent: JP 2002512791-A 2050 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2050
PP 2-APR-1999 JP 2000545991
PR 27-APR-1999 JP 2000545991
PR 27-APR-1999 US 60/083217,18-SEP-1999 US 09/274553 PI
LAWRENCE BLAIT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA P PI
                                                                                                                                                                                                                                                                                                                                                             DENNIS MACEJAK
C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
A61K37/66,
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1; Conservative 0; Mismatches 2; Indels
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/db_xref="taxon:32630"

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Location/Qualifiers

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/mol_type="genomic RNA"
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                                to hepatitis C virus infection.
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JP 2002512791-A/2050.
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1 (bases 1 to 14)
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A25806
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1 (bases 1 to 15)
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A25806
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Vergrands.
Vergrands.
Process for detection of new polymorphic loci in a DNA sequence,
nucleotide sequences forming hybridization probes and their
applications
Patent: US 5556955-A 13 17-SEP-1996;
Location/Qualifiers
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1 (Dases 1 to 14)

Wang,C. G. and Hepburn,A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 198 19-JAN-1999;
Location/Qualifiers
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84.6%; Pred. No. 1.3e+02;
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Sequence 13 from patent US 5556955.
126228
126228.1 GI:1606098
    Mismatches
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Sequence 11 from patent US 5646031.
152188 152188.1 GI:2473389
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Best Local Similarity 84.6
Matches 11; Conservative
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Matches 11; Conserv
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AR030009/c
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Unclassified.
1 (bases 1 to 14)
Nang.C.-G. and Hepburn,A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US S861244.A 186 19-7AN-1999;
Location/Qualifiers
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44.5%; Score 9.8; DB 1; Length 14;

Best Local Similarity 84.6%; Pred. No. 1.3e+02;

Matches 11; Conservative 0; Mismatches 2; Indels
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44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
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1 (Jean Control of Schlingensiepen, K.
Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLECTIDE PREPRATION METHOD Patent: WO 9833904-A 1261 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
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Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonucleotide preparation method
Patent: EP 0856579-A 70 05-AUG-1998;
BIOGNOSTIK GES (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 186 from patent US 5861244. AR029997.1 GI:5943211

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Sequence 70 from Patent EP0856579.
A89889
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PAT 16-SEP-2000
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Antisense-oligonuclectides for the treatment of immunosuppressive effects of transforming growth factor-beta (tgf-beta)
Patent: EP 1160119-A 126 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 126 from Patent EP1008649.
AX030164
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Best Local Similarity 84.6%;
Matches 11; Conservative
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84.6%;
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Schlingensiepen, G.-F., Brysch, W., Schlingensiepen, K.-H.,
Schlingensiepen, R. and Bogdahn, U.
Antisense-oligonucleotides for transforming growth factor-.beta,
(TGF-.beta.)
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M Unknown.
Unclassified.
1 (bases 1 to 14)
2 DeYoung M. Beth., Siwkowski, A.M. and Hampel, A.E.
S DeYoung M. Beth., Siwkowski, A.M. and Hampel, A.E.
SArMV and sCYMVI hairpin ribozymes
AL Patent: US 5646031-A 11 08-UUL-1997;
Location/Qualifiers
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1 Similarity 84.5%; Score 9.8; DB 1; Length 14
1 Similarity 84.6%; Pred. No. 1.3e+02;
11; Conservative 0; Mismatches 2; Indels
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Unclassified.
1 (bases 1 to 14)
S DeYoung M. Beth., Siwkowski, A.M. and Hampel, A.E.
SArMV and sCYMVI hairpin ribozymes
AL Patent: US 5646031-A 16 08-UUL-1997;
Location/Qualifiers
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84.6%; Pred. No. 1.3e+02;
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Location/Qualifiers
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AR232869.1 GI:27275207
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Sequence 16 from patent US 5646031.
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2B latt, L., Mewalgean, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

Blatt, L., Mewalgean, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

Braymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection

AL Patent: JP 200212791-A 2890

CS Hepatitis virus (hepatitis C virus)

BY 200221791-A/2890

BY 20022179-A/2890

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BD066626 14 bp DNA linear An antisense oligonuclectide preparation method.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                Blanche, F. and Cameron, B. Methods for purifying and detecting double stranded dna target sequences by triple helix interaction Patent: Wo Patent: Wo 13-0CT-2002; Aventis Pharma S.A. (FR) Location/Qualifiers
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Schlingensiepen, K.H. and Brysch, W.
An artisense oligonucleotide preparation method
Patent: JP 2011511000-A 70 07-AUG-2001,
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MEH
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31-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPER, WOLFGANG BRYSCH
C2N15/11,/C07H21/04,A61K31/70
An antisense oligonucleotide preparation method PH
Location/Qualifiers
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BD065435
BD065435.1 GI:22611038
JP 2001511000-A/70.
                linear
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Location/Qualifiers

    .14
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

            AX571850 14 bp
Sequence 9 from Patent WO02077274.

    .14
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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07-AUG-2001
                                                                                AX571850
AX571850.1 GI:26003984
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Best Local Similarity 84.6%;
Matches 11; Conservative (
                                                                                                                                                                   Homo sapiens (human)
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Nielsen, P.E. and Good, L.
Antibacterial and antibiotic methods using peptide nucleic acids
and pharmaceutical compositions therefor
Patent: US 6300318-A 11 09-OCT-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shchepinov, M.S. and Southern, E.M. Polymuclectide multimers and their use in hybridisation assays Polymuclectide multimers and their use 1995,662-42 02-DEC-1999; SHCHEPINOV MIXHAIL SERGEEVICH (GB); SOUTHERN EDWIN MELLOR (GB);
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84.6%; Pred. No. 1.4e+02;
iive 0; Mismatches 2;
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M Unknown.
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E 1 (bases 1 to 15)

KS Fresco, "R. and Johnson, M.D.
Triplex in-situ hybridization
Triplex in-situ hybridization

NAL Patent: US 6461810-A 60 08-OCT-2002;
Location/Qualifiers

15 "...known"
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                                             AR235561 15 bp L
Sequence 60 from patent US 6461810.
AR235561.1 GI:27278782
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Sequence 2 from Patent W09961662.
AX009449 GI:9996735
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artificial sequences.
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Best Local Similarity 84.6
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AX009449/c
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AR370348/c
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Nielsen, P. E. and Good, L.
Netheds of bacterial gene function determination using peptide nucleic acids
Patent: US 6190866-A 11 20-FEB-2001;
Location/Qualifiers
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 organism='Hepatitis virus (hepatitis C
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1 (bases 1 to 15)
Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W.
Gene expression profiles in normal and cancer cells
Patent: US 6333152-A 460 25-DEC-2001;
Location/Qualifiers
                                                                                                                         Query Match
44.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
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Sequence 11 from patent US 6190866.
AR130724

    15. 15
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    /mol_type="unassigned DNA"

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    mol_type="unassigned DNA"

                                                1. .14
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/wol_type="genomic RNA"
/db_xref="taxon:32644"
                            Location/Qualifiers
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                virus)'
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Best Local Similarity 84.67
Matches 11, Conservative
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Best Local Similarity
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AR180392/c
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U8-MAY-2002
PF 26-APR-1999 UP 2000545991
PR 27-APR-1999 US 60/100842 PR 25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI PAVCO, PI DENNIS MACEJAK
PC CIZUN/00, AGIK31/7105, AGIK38/21, AGIK40*/**
PC CIZUN/27/66, PC CLENIS/00
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Enzymatic nucleic acid treatment of diseases or conditions related
                                                                                                                                                                                                           C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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    15
/organism='Hepatitis virus (hepatitis C

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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1219 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
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                to hepatitis C virus infection
Patent: JP 2002512791-A 1987 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/1987
PD 08-MAY-2002
PP C-APR-1999 US 60/083217,18-SEP-19
PR 27-APR-1999 US 60/083217,18-SEP-19
                                                                                                                                                                                                                                                                                Enzymatic .....
related to
hepatitis C virus infection.
Location/Qualifiers
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LOCUS AX627643 11 bp DN
DEFINITION Sequence 4684 from Patent WO02053774.
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/db_xref="taxon:9606"
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/organism="unidentified"
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/organism="Homo sapiens"
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/db_xref="taxon:32644"
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Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
                                                                                                                                                                              Gaps
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PD 13-FEB-2018-27-6/-29
PD 13-FEB-2010-1
PF 03-OCT-1997 JP 1998517095
DS-NAY-1997 DK 0512/97
PI HENRIX STENDER, KAARE LUND, TINA ANDRESEN MOLLERUP PC C1201/68, CO7K14/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT scurce / organism='Unidentified'.
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                                                                                                                                         44.5%; Score 9.8; DB 1; Length 15; illarity 84.6%; Pred. No. 1.4e+02; Conservative 0; Mismatches 2; Indels
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Novel probes for the detection of Mycobacteria.
BD005884
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Stender,H., Lund,K. and Mollerup,T.A.
Novel probes for the detection of Mycobacteria
Patent: JP 2001501825-A 95 13-FEB-2001;
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/organism='Unidentified'
Location/Qualifiers
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JP 2001501825-A/95
13-FEB-2001
03-OCT-1997 DP 1998517095
04-OCT-1996 DK
                  Location/Qualifiers
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                   Query Match 42.7%; Score 9.4; DB 1; Length 12; Best Local Similarity 90.9%; Pred. No. 1.38+02; Matches 10; Conservative 0; Mismatches 1; Indels
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Brenner,S.
DNA extension and analysis with rolling primers
DA extension and analysis with rolling primers
Patent: US 5962228-A 15 05-0CT-1999;
Location/Qualifiers
1 . 12
/organism="unknown"
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Flanagan, W.M. and Crabtree, G.R.
Screening methods for immunosuppressive agents
Patent: US 5989810-A 14 23-NOV-1999;
Location/Qualifiers
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Sequence 162 from patent US 6287769.
AR167798.1 GI:17903601
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AR077199.
AR077199.1 GI:10003945
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Seguence 14 from patent US 5989810.
AR087821
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                                                                                                                                                                                                                                                                                      Unknown.
Unclassified.
1 (bases 1 to 12)
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Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 90.9
Matches 10; Conservative
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Unclassified.
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AR167798
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AR077199/c
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AR087821
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                                                               Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: US 5763175-A 9 09-JUN-1998;
Location/Qualifiers
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Patent: US 5780231-A 13 14-UUL-1998;
Location/Qualifiers
                                                                                                                         Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053794-A 4684 11-UUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
                                                                                                                                                                                                           1. .11
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Sequence 13 from patent US 5780231.
AR017794 1 GI:3973397

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 AX627643.
AX627643.1 GI:28455681
                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown.
Unclassified.
1 (bases 1 to 12)
Brenner,S.
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Best Local Similarity 90.9
Matches 10; Conservative
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1 (bases 1 to 12)
Brenner,S.
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AR011923/c
LOCUS
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             BD269489.1 GI:33079257
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E29682.1 GI:13021185
UP 1999276176-A/162.
unidentified
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BD26489/c
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BD269489
DEFINITION Stable recombinant influenza virus free from helper virus.
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                                                      Inoue,T.
Method of amplifying DNA fragment, apparatus for amplifying DNA fragment, method of analyzing microorganisms, method of analyzing microorganisms and method of assaying contaminant microorganisms and method of assaying contaminant betent: US 6287769-A 162 11-SEP-2001;
Location/Qualifiers
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PR 30-0CT-1998 US 60/106308,26-MAY-1999 US 60/136078 PI
RENNETH A GUILIANO,GARY BRIGHT,KEITH OLSON,SARAH BURROUGHS PI
TENCZA

PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/02,C12Q

PC 37,G3N33/56,C12N15/00,C12N5/00

CC Description of Artificial Sequence: Caspase-8 substrate CC
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G01N33/50,C12N15/00,C12N5/00
Description of Artificial Sequence: Caspase-8 substrate
recognition
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/organism='Artificial Sequence'.
Location/Qualifiers
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    .12
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                                                                                                                                                                                                                                 0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 90.9%;
Matches 10; Conservative (
                                             (bases 1 to 12)
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Best Local Similarity 90.9
Matches 10; Conservative
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ORGANISM
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                                                         AUTHORS
TITLE
                                                                                                                JOURNAL
FEATURES
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JOURNAL
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                                             REFERENCE
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BUDGS489.1 G4133079257

Synthetic construct

Synthetic construct

artificial sequences.

I (bases 1 to 12)

Stable recombinant influenza virus free from helper virus

Stable recombinant influenza virus free from helper virus

Stable recombinant influenza virus free from helper virus

ARTEMIS PHARMACENTICALS GMBH

ON TO 2002537844-A/13

PD 12-NOV-2002

PR 06-WRR-1999 EP 99104519.6

PI GERD HOBOM, RAMON FILCK, ANETTE MENKE, MAYSA AZZEH PC

C12N15/09, AG1X39/145, AG1X48/00, AG1P31/16, C12N7/00, C12P21/02// PC

AG1X5/12,

PC (C12N7/00, C12R1:93), C12N15/00

CC Description of Artificial Sequence: Modified influenza A 3'

CC Description of Artificial Sequence: Modifiers

F Source

C (PHL1104 and 1920)

FH Key

FT Source

1.0.12

CO OCCUPATIONAL ARTIFICIAL SEQUENCE'.
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Kolchi.

Kolchi.

Kolchi.

Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of waste patent: JP 1999276176-A 162 12-OCT-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES

OS Unidentified

PN JP 1999276176-A/162

PN JC 1999276176-A/162
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Method for amplifying DNA fragment, method for estimating state of
microorganism existing and method for estimating state of waste.
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PN JP 199276176-A/162

PN JP 199276176-A/162

PD 12-OCT-1999

PR 31-MAR-1998 JP 1998087652

PR KOICHI NOUB

PC C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC

Strandedness: Single;

Location/Qualifiers

FT source

/organism='Unidentified'.
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Location/Qualifiers
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Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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Location/Qualifiers
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/mol_type="genomic RNA"
/db_xref="taxon:32630"
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Topology: Linear;
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Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 90.9
Matches 10; Conservative
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E64214
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DEFINITION
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AR217456
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VERSION
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Method and device for amplifying DNA fragment
Patent: JP 200270867-A 162 03-OCT-2000;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
OS Unidentified
PD 03-000270867-A/162
PP 19-MAR-1999 JP 1999076844
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Bydney, B.

BNA elongation and analysis with the use of rolling primer Patent: UP 1999151092-A 15 08-JUN-1999;

LYNX THERAPEUTICS INC
OS Artificial Sequence
PD 08-JUN-1999
PP 24-AUG-1999 JP 1998237840
PP 24-AUG-1999 JP 1998237840
PR 22-AUG-1999 JP 1998237840
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/organism='Artificial Sequence'.
Location/Qualifiers
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                                       Query Match
42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
  /mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                               synthetic construct
synthetic construct
artificial sequences.
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E3878
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E38120/c
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E64214

Nethod for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, method for analyzing a group of microorganisms, method for analyzing a group of microorganisms, method contaminating substance.

ON E64214 I G1:13019618

S UP 199941989-A/162.

S Withhelt Construct

SYNTHHELT CONSTRUCT

REASON I (bases I to 12)

RS Koichi I (bases I to 12)

RS Koichi I (bases I to 12)

RS Koichi I (bases I to 12)

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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.7%; Score 9.4; DB 1; Length 12; 90.9%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                              ce 1. .12 /organism='Unidentified'.
Location/Qualifiers
KOICHI INOUE
C12N15/09,C12M1/00,C12Q1/68,C12N15/00
Strandedness: Single;
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C12N15/09,C12M1/00,C12Q1/68,C12N15/00
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                                                                                                                                                                                 location/Qualifiers
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'note="3'-terminale Nukleotidsequenz"
                                                                                                                                                                                                                          AX100750 12 bp
Sequence 7 from Patent WO0122083.
AX100750
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Sequence 8 from Patent WO0122083.
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AX100751.1 GI:13619697
                                                                         Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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ACCESSION
VERSION
KEYWORDS
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AX100750/c
LOCUS
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AX100751/c
LOCUS
DEFINITION
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AUTHORS
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        PAT 25-SEP-2002
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Hobom,G., Neumann,G. and Menke,A.
Attenuated vaccination and gene-transfer virus, a method to make the virus and a pharmaceutical composition comprising the virus Patent: US 6524588-A 9 25-FEB-2003;
                                                                                                                                                                                                                                                                   Gaps
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Stable recombinant influenta viruses free of helper viruses
Patent: EP 1035209-A 13 13-SEP-2000;
ARTEMIS PHARMACEUTICALS GMBH (DE)
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    .12
    /organism="synthetic construct"

        DNA
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Giuliano, K. and Kapur, R.
System for cell-based screening
Patent: US 6416959-A 73 09-JUL-2002;
AR217456 12 bp I
Sequence 73 from patent US 6416959.
AR217456
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AR282763
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Sequence 13 from Patent EP1035209.
AX035438

    .12
/organism="unknown"
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    .12
    /organism="unknown"
    /mol_type="genomic RNA"

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                                              AR217456.1 GI:23317149
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Influenza A virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A.
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Influenza A virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A.
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Method for identifying mhc-restricted antigens
Patent: Wo 0122083-A 7 29-MAR-2001;
GSF-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE) ; ARTEMIS
Pharmaceuticals GmbH (DE)
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Method for identifying mhc-restricted antigens
Patent: W0 0122083-A 8 29-MAR-2001;
GSF-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE) ; ARTEMIS
Pharmaceuticals GmbH (DE)
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza A 3' sequence (pHL1104 and 1920)"
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                                                                                                                             Length 12;
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/note="3'-terminale Nukleotidsequenz"

                                                                                                                          Score 9.4; DB 1;
Pred. No. 1.3e+02;
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/organism="Influenza A virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11320"
/ .12
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/db_xref="taxon:11320"
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Hobom, G., Menke, A. and Meyer-Rogge, S.
Recombinant influenza viruses with bicistronic vrnas coding for two genes in transpenent genes in transpenent arrangement woo 2008444-A. S. 31-GAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
                                                                                                                                                                                                    Hobom,G., Menke,A. and Meyer-Rogge,S.
Recombinant influenza viruses with bicistronic vrnas coding for two genes in tandem arrangement
Patent: WO 0208434-A 4 31-AAN-2002,
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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/db_xref="texon:32630"
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/organism="synthetic construct"
/organism="unassigned RNA"
/db xref="taxon:32630"
/noTe="Modified influenza A 3'-sequence (pHL1948)"
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42.7%; Score 9.4; DB 1; Length 12
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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AX362219 GI:18694557
                                          12 bp
Sequence 4 from Patent WO0208434.
AX362218
AX362218.1 GI:18694556
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Sequence 4 from Patent BP1201760.
AX428931
AX428931.1 GI:21540315
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Best Local Similarity 90.9
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Recombinant influenza viruses with bicistronic vrnas coding for two genes in tandem arrangement parangement in FP 117454-A 4 23-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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Recombinant influenza viruses with bicistronic vrnas coding for two genes in tandem arrangement.
Patent: EP 1174514-A 5 23-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="modified influenza A 5'-sequence (pHL1104 and pHL1920)"
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/db xref="taxon:32630"
/noTe="Modified influenza A 3'-sequence (pHL1948)"
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42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.38+02;
Matches 10; Conservative 0; Mismatches 1; Indels
Query Match 42.7%; Score 9.4; DB 1; Length 12; Best Local Similarity 90.9%; Pred. No. 1.3e+02; Matches 10; Conservative 0; Mismatches 1; Indels
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Sequence 5 from Patent EP1174514.
AX352661
AX352661.1 GI:18617791
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2 Equence 4 from Patent EP1174514.
AX352660
AX352660.1 GI:18617790
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AX352660/c
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AX352661/c
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Patent: EP 1233059-A 5 21-AUG-2002;
ARTENIS Pharmaceuticals GmbH (DE)
                                                                                                                                                                                                                                                                                     Gaps
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                                                        Schuler, G.D., Hobom, G., Steinkasserer, A.D., Strobel, I.D. and Grassmann, R.
Influenza victor for human dendritic cells
Patent: EP 1201760-A 4 02-MAY-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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/db_xref="taxon:32630"
/note="Modified influenza A 3'-sequence"
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Patent: EP 1201760-A 5 02-MAY-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
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AX428932 AX428932.1 GI:21540316
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Sequence 5 from Patent EP1233059.
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AX512614.1 GI:23503837
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AX428932/c
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AX512614/c
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Patent: Ep 1233059-A 6 21-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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                                                                                                                                   ch 42.7%; Score 9.4; DB 1; Length 12; 1 Similarity 90.9%; Pred. No. 1.38+02; 10; Conservative 0; Mismatches 1; Indels
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//organism="synthetic construct"
//ol type="unassigned RNA"
//db xrtef="texton:32630"
//note="Modified influenza A 3'-sequence"
                                                    /mol_type="unassigned RNA"
/db_xref="taxon:32630"
/noTe="Modified influenza A 3'-sequence"
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Modified influenza A 3'-sequence"
                       1. .12
/organism="synthetic construct"
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ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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Sequence 6 from Patent BP1233059.
AX512615
AX512615.1 GI:23503838
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Sequence 5 from Patent W002064757.
AX522265
cocation/Qualifiers
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synthetic construct
artificial sequences.
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artificial sequences.
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AX512615/c
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DEFINITION
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Note: acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof.
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DD237463.1 GI:33047233
DP 20053444-A/1.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 14)
Dale, R.M.K., Gatton, S.L. and Arrow, A.
Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof Parent: UP 2002534434-A 1 15-OCT-2002;
OLIGOS ETC INC.
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                                                                                      Unclassified.

1 (bases 1 to 13)

4 Hobom, G., Neumann, G. and Menke, A.

Attenuated vaccination and gene-transfer virus, a method to make the virus and a pharmaceutical composition comprising the virus patent: US 6524588-A 4 25-FEB-2003;

Location/Qualifiers
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Fauchet, C.R.J.
Fixing unit with an end imprint in a threaded terminal portion Patent: 105 632057-A 59 14-0CT-2003;
Location/Qualifiers
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Sequence 59 from patent US 6632057.
AR407966.1 GI:40157953
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/mol_type="unassigned RNA"
Sequence 4 from patent US 6524588
                                                                                                                                                                                                   1. .13
/organism="unknown"
/mol_type="genomic RNA"
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JP 2002534434-A/1
                   AR282758.1 GI:29719537
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Best Local Similarity 90.9*
....hes 10; Conservative
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Best Local Similarity 90.9
Matches 10; Conservative
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BD237463
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AR407966/c
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Influenza viruses with enhanced transcriptional and replicational
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/db xref="trace;"12630"
/db xref="trace;"12630"
/noFe="Caspase-8 substrate recognition sequence"
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Best Local Similarity 90.9%; Pred. No. 1.38+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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/organism="synthetic construct"
/mol type="unassigned RNA"
/db xref="taxon:32630"
/noTe="Modified influenza A 3'-sequence"
        1; Indels
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                                                                                                                                             RNA
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A system for cell-based screening
Patent: EP 1314960-A 73 28-MAY-2003,
Cellomics, Inc. (US)
                                                                                                                                                                                                                                                                                                            Capacities
Patent: WO 02064757-A 6 22-AUG-2002;
Patents Pharmaceuticals GmbH (DE)
ARTEMIS Pharmaceuticals GmbH (DE)
         Mismatches
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Sequence 73 from Patent EP1314980.
AX766784
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Sequence 6 from Patent W002064757.
AX522266
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         Conservative
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KEYWORDS
SOURCE
ORGANISM
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AR282758/c
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SOURCE
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AX522266/c
LOCUS
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Matches
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AUTHORS
TITLE
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TITLE
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Synthetic construct

Synthetic construct

Synthetic construct

artificial sequences.

I (bases 1 to 14)

R Hobom, G., Flick, R., Menke, A. and Azzeh, M.

Stable recombinant influenza virus free from helper virus

Rather: JP 2002537844-A 26

ARTERIANS PHARACEUTICALS GMBH

OS Artificial Sequence

PN JP 2002537844-A/26

PN JP 200253784-A/26

PN JP 200253784-A/26

PN GEND HOBOM, RAMON FLICK, ANETTE MENKE, MAYSA AZZEH PC

CL2N15/09, A61K39/145, A61K48/00, A61P31/16, C12N7/00, C12P21/02// PC

A61K35/12, A61K39/145, A61K48/00, A61P31/16, C12N7/00, C12P21/02// PC

CC Description of Artificial Sequence: Modified influenza C 3'

CC Description of Artificial Sequence: Location/Qualifiers

FH Key

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FT source

'Organism='Artificial Sequence'.
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Stable recombinant influenza virus free from helper virus.
BD269502
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/db_xref="taxon:32630"
/note="Modified influenza C 3' sequence"

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/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

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Sequence 26 from Patent BP1035209.
AX035451
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                                                                                                                                                                                                                                                                                  BD269502.1 GI:33079270 JP 2002537844-A/26.
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artificial sequences.
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               3 TGTCAGGAGAA 13
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                 RESULT 154
BD269502/C
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PF 16-DEC-1999 JP 2000592300
PR 30-DEC-1998 US 09/223498,19-JUL-1999 US 09/356069 PI
RODERIC M K DALE, STEVEN L GATTON, AMY ARROW
PC C07H21/00, A61K9/127, A61K9/50, A61K31/7088, A61K47/44, A61K48/00,
PC C07H21/00, A61E29/00, A61E31/10, A61E31/12, A61E35/00,
PC C12N5/10,
PC C12N5/10,
PC C12N5/10,
PC C12N5/10,
PC C12N15/09, C12N5/00
CC Nucleic acid having blocked terminals modified with an acid-stable corrected and therapeutic method thereof
FH Key Location/Qualifiers
FT source 1...14
//crganism='Artificial Sequence'.
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Synthesized Oligonucleotide
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AG1P17/06,
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AG1P29/00,
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/organism='Artificial Sequence'
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synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 14)
Dale,R.M.K., Arrow,A. and Thompson,T.
Phosphodiesterase inhibitors for therapeutic use
Patent: JP 2002534086-A 32 15-OCT-2002;
OLIGOS ETC INC

    .14
        /organism="synthetic construct"
/mol type="genomic DNA"
        /db_xref="taxon:32630"

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/organism="synthetic construct"
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42.7%; Score 9.4; DB 1; Length 14;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1; Indels

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PAT 24-OCT-2002
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Influenza viruses with enhanced transcriptional and replicational
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Influenza virus vector for human dendritic cells
Patent: EP 1201760-A 17 02-MAY-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/noTe="Modified influenza C 3'-sequence"
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//organism="synthetic construct"
//mol type="unassigned RNA"
/db xref="taxon:32630"
/note="Modified influenza C 3'-sequence"
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42.7%; Score 9.4; DB 1;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 1;
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ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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AX512628
AX512628.1 GI:23503851
 Sequence 17 from Patent EP1201760.
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Recombinant influenza viruses with bicistronic vrnas coding for two genes in tandem arrangement
Patent: WO 0208434-A 17 31-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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Recombinant influenza viruses with bicistronic vrnas coding for two genes in tandem arrangement andem arrangement.
Patent: EP 1174514-A 17 23-JAN-2002,
ARTEMIS Pharmaceuticals GmbH (DE)
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Pred. No. 1.5e+02;
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/organism="synthetic construct"
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/coganism="synthetic construct"
/mol type="unassigned RNA"
/db_xref="taxon:32630"
/noTe="Modified influenza C 3'-sequence"
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Sequence 17 from Patent EP1174514.
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Query Match DEFINITION ACCESSION VERSION KEYWORDS RESULT 163 AR232778 RESULT 165 BD066538 ORGANISM DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 164 AX316394 REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS JOURNAL TITLE TITLE LOCUS g ठे ò ö ö PAT 22-JAN-2000 PAT 05-MAR-1997 ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE PEFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b)) Patent: WO 9425578-A 35 10-NOV-1994; BIOGNOSTIK GES (DE) Influenza viruses with enhanced transcriptional and replicational Gaps Gaps .. 0 ö Query Match 42.7%; Score 9.4; DB 1; Length 14; Best Local Similarity 90.9%; Pred. No. 1.5e+02; Matches 10; Conservative 0; Mismatches 1; Indels 41.8%; Score 9.2; DB 1; Length 14; 78.6%; Pred. No. 1.6e+02; ative 0; Mismatches 3; Indels /organism="synthetic construct"
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Ab refe"tracon:32630"
/db refe"tracon:32630"
/noTe="Modified influenza C 3'-sequence" linear linear 1 (bases 1 to 14)
Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
PALENT: WO 9833904-A 1173 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers DNA capacities
Patent: WO 02064757-A 19 22-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers .14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644" 14 bp Sequence 35 from Patent WO9425578. A40498 Location/Qualifiers A40498.1 GI:2296533 730 CAGGAGAACAGAA 743 (bases 1 to 14) Conservative 731 AGGAGAAACAG 741 14 AGTAGAAACAG 4 unidentified unclassified. unidentified Query Match Best Local Similarity Matches 11; Conserv LOCUS DEFINITION ACCESSION LOCUS DEFINITION ACCESSION VERSION KEYWORDS source RESULT 161 A40498 ORGANISM SOURCE ORGANISM RESULT 162 A89025 JOURNAL REFERENCE AUTHORS TITLE JOURNAL VERSION KEYWORDS SOURCE REFERENCE AUTHORS JOURNAL FEATURES FEATURES TITLE FEATURES g 셤

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Antisense-oligoniclectides for the treatment of immunosuppressive effects of transforming growth factor-beta (tgf-beta)
Patent: EP 1160119-A 35 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 14)
Schlingensiepen, G.-F., Brysch, W., Schlingensiepen, K.-H.,
Schlingensiepen, R. and Bogdahn, U.
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
                                   Gaps
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                                   Indels
                                                                                                                                                                                                       linear
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Description of unknown"
             Pred. No. 1.6e+02;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.8%; Score 9.2; DB 1; L. 78.6%; Pred. No. 1.6e+02; tive 0; Mismatches 3;
                                                                                                                                                                                                       DNA
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Location/Qualifiers
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                                                                                                                                                                                               Sequence 35 from patent US 6455689.
AR232778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35 from Patent EP1160319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
/mol_type="genomic DNA"
78.6%; Prev
0;
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             Best Local Similarity 78.6
Matches 11; Conservative
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Best Local Similarity 78.6
Matches 11; Conservative
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unidentified
unclassified.
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Matches 11; Conserv
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14 bp mRNA linear ROD 11-OCT-2002 GM-CSF-granulocyte-macrophage colony-stimulating factor [mice, WEHI-274 cell line, mRNA Partial, 14 nt, segment 1 of 2]. S59977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leslie,K.B., Lee,F. and Schrader,J.W.
Intracisternal A-type particle-mediated activations of cytokine genes in a murine myelomonocytic leukemia: generation of functional cytokine mRNAs by retroviral splicing events
92017836
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Homo sapiens
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

(bases 1 to 10)
(bases 1 to 10)
Preparation and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1787 15-OCT-2002;
                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenBank staff at the National Library of Medicine created the entry (NCBI gibbsq 59977) from the original journal article. This sequence comes from fig6b.
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                      /organism='Homo sapiens (human)'.
Location/Qualifiers
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vaccines.
                                                                                                                                                               41.8%; Score 9.2; DB 1; 78.6%; Pred. No. 1.6e+02; iive 0; Mismatches 3;
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/organism="Mus musculus"
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/db xref="taxon:10090"
/cell_line="WEHI-274"
                                                                    1. .14
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db xref="taxon:9606"
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Preparation and use of superior BD240369
BD240369
JP 2002534056-A/1787.
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Best Local Similarity 78.0.
Fig. 11; Conservative
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Best Local Similarity 78.6:
Matches 11; Conservative
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KEYWORDS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
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TITLE
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                                                 FEATURES
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 14)
S Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
molecule participating in vasculogenic response
ID Patent: JP 2002509721-A 2381 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/2381
PN JP 20APR-2002
PR 24-MAR-1999 JP 2000541291
PR 27-MAR-1999 JP 2000541291
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            PAT 27-AUG-2002
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24-MR-1999 UP 2000541291
27-MAR-1999 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
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14 bp RNA linear PAT 17-JUL-200 molecule and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.

BD199355 GI:33009125

BD199355.1 GI:33009125

Homo sapiens (human)
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C A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00,
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C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06,
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                                                                                                                                          unclassified.

1 (bases 1 to 14)
Schlingensiepen,K.H. and Brysch,W.
An antisense oligomoclectide preparation method
Patent: JP 2001511000-A 1173 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
                                                                                                                                                                                                                                                                                                                    30-JAN-1998 JP 1998532533
31-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11, C07H21/04, A61K31/70
An antisense oligonucleotide preparation method FH
Location/Qualifiers
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An antisense oligonucleotide preparation method.
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participating in vasculogenic response
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism='Unknown'

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                                                                                                                                                                                                                                                              Unknown
JP 2001511000-A/1173
07-AUG-2001
                                                                BD066538.1 GI:22612141
JP 2001511000-A/1173.
unidentified
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Best Local Similarity
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ORGANISM
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BD199355/C
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19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR 19-JUN-1998 US 60/090044,19-JUN-1996 US 60/080844 PR 19-JUN-1998 US 60/080080,19-JUN-1998 US 60/080833 PR 19-JUN-1998 US 60/080994,19-JUN-1998 US 60/080077 PR 19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR 19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090078,19-JUN
                                                                                                                                                                                                                                                                                                    C12N1/19,
PC C12N1/21, C12NS/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566,
G01N37/00,
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1 (bases 1 to 10)

2 (bases 1 to 10)

3 Shimmarto.

4 Puruichi,Y., Shibata,Y., Funaki,H., Chara,E. and Matahiki,M.

Method for synthesizing cDNA from mRNA sample

Patent: US 6544736-A 21 08-APR-2003;

Location/Qualifiers
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Unclassified.
1 (bases 1 to 10)
Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Location/Qualifiers
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Preparation and use of superior vaccines
Key
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40.9%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 9; Conservative 0; Mismatches
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Sequence 21 from patent US 6544736.
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    .10
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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/organism="unknown"
/mol_type="genomic DNA"
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Sequence 30 from patent AR303305
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1 (bases 1 to 10)
1 (bases 1 to 10)
2 Preparation and Shankara, S.
Preparation and use of Superior vaccines
Patent: JP 2002534056-A 1921 15-OCT-2002;
GENZYME CORP
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60/089993 PR
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Preparation and use of superior vaccines
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Pred. No. 1.3e+02;
0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                        Homo sapiens (human)
JP 202534056-A/1787
15-OCT-200
18-JUN-1999 UP 2000554749
19-JUN-1998 US 60/090039
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JP 2002534056-A/1921
15-CCT-2002
18-JUN-1999 US 60/090039
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100.0%; Pred
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JP 2002534056-A/1921.
Homo sapiens (human)
Homo sapiens
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Homo sapiens
Eukaryota, Metazca; Chordata; Crániata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 167 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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40.9%; Score 9; DB'1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                        40.9%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
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40.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AX470590.1 GI:22205715
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AX623138.1 GI:28451079
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Matches 9; Conserv
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E 1 (bases 1 to 10)

E Nagai,S., Matsuahima,K. and Hashimoto,S.

Human activated Th1 and Th2 cell expression genes

L Patent: JP 2002186482-A 134 02-UUL-2002;

JAPAN SCIENCE AND TECRNOLOGY CORP

OS Homo sapiens (human)

PN JP 2002186482-A/134

PD 02-UUL-2002

PP 19-DEC-2000 JP 2000385816

PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC

C12NIS/09,C07K1447,C07K6/18,C12P21/08,C12NIS/09

C12NIS/09,C07K1447,C07K6/18,C12P21/08,C12NIS/09

FT source

//organism='Homo sapiens (human)'.

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Unclassified.
Unclassified.
1 (bases 1 to 10)
Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 64 08-APR-2003;
Location/Qualifiers
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Location/Qualifiers
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                                                                                                                                                                                    0; Indels
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                                                                                                                                             Query Match

40.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
Watahiki,M.
Method for synthesizing CDNA from mRNA sample
Patent: US 6544736-A 30 08-APR-2003;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                             AR303339 10 bp Sequence 64 from patent US 6544736.
AR303339
                                                                               1. .10
/organism="unknown"
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Best Local Similarity
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BD161312/c
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens
Eukaiyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammālia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                     Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Hethert WO 0205374-A 3448 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Nethod (2005) 714-A 5088 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 7600 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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AX628047.1 GI:28456085
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AX630559.1 GI:28458597
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Best Local Similarity 100.0
Matches 9, Conservative
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  Homo sapiens
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AX628047
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                     Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 2023774-A 1884 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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                                                                                            AX624843 11 bp DNA Sequence 1884 from Patent WO02053774.
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Homo sapiens
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AAACAGAAC 1
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AX626407/c
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synthetic construct
artificial sequences.

E (bases 1 to 12)
Guiliano, K.A., Bright, G., Olson, K. and Tencza, S.B.
A system for cell based screening
A system for cell based screening
CELLOMICS INC
OS Artificial Sequence
PD 03-SEP-2002;
PP 29-OCT-1999 JP 2000579780
PP 29-OCT-1999 UP 2000579780
PP 29-OCT-1998 US 60/106308,26-MAY-1999 US 60/136078 PI
KENNETH A GUILIANO, GARY BRIGHT, KEITH OLSON, SARAH BURROUGHS PI
TENCZA
C CLENAS (122N1/15, C12N1/19, C12N1/19, C12N5/10, C12O1/02, C12O1/
PC 37,GOIN33/15,
PC 037,GOIN33/15,
PC GOIN33/50,C12N1/15, C12N1/19 Sequence: proCaspase-8 substrate CC
                                                                                                                PAT 17-JUL-2003
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37,GDN3/20,C12N15/00,C12N5/00
Description of Artificial Sequence: proCaspase-8 substrate CC
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GGIN33/50,Cl2N15/00,Cl2N5/00
Description of Artificial Sequence: proCaspase-3 substrate
recognition
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Location/Qualifiers
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/db_xref="taxon:32630"
                                            12 bp
A system for cell based screening.
BD24525
BD24525.1 GI:33052295
JP 2002528136-A/31.
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A system for cell based screening,
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JP 2002528136-A/38.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                    Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 0203774-4 9306 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 9594 from Patent W002053774.
AX632552
AX63252.1 GI:28468167
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX632264.1 GI:28467879
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// Organism="synthetic construct"
// mol_type="unassigned DNA"
// db_xref="taxon:32630"
// note="procaspase-3 substrate recognition
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Mol.type="unassigned DNA"
Ab ref="temton:32630"
/db cref="temtocaspase-8 substrate recognition"
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A system for cell-based screening
Patent: EP 1314980-A 61 28-MAY-2003;
Cellomics, Inc. (US)
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A system for cell-based screening
Patent: EP 1314980-A 75 28-MAY-2003;
Cellomics, Inc. (US)
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Sequence 75 from Patent EP1314980.
AX766786
AX766786.1 GI:32260537
                                                                         AX766772 12 bp
Sequence 61 from Patent EP1314980.
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AX766772.1 GI:32260530
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AR364664
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Matches 9; Conservative 0; Mismatches 0; Indels
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40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                    /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                              Location/Qualifiers
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Giuliano, K. and Kapur, R.
System for cell-based screening
Patent: US 6416599-A 61 09-JUL-2002;
Location/Qualifiers
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Giullano, K. and Kapur, R.
System for cell-based screening
Patent: US 6416959-A 75 09-JUL-2002;
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AR217450
AR217450.1 GI:23317143
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Sequence 75 from patent US 6416959.
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/mol_type="genomic DNA"
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/wol_type="genomic DNA"
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AR217457.1 GI:23317150
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AR217450
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1 (bases 1 to 12)

1 (bases 1 to 12)

Crouzet, J. Scherman, D., Wils, P., Blanche, F. and Cameron, B. Purification of a triple helix formation with an immobilized oligonucleoride
Patent: US 6319672-A 28 20-NOV-2001;
Location/Qualifiers
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Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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40.0%; Score 8.8; DB 1;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2;
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Korneluk, R. G., Holcik, W. and Liston, P.
XIAP IRES and uses thereof
Patent: US 6171821-A 10 09-JAN-2001;
Location/Qualifiers
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                                                                12 bp 1
Sequence 10 from patent US 6171821.
AR123877
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Sequence 28 from patent US 6319672.
AR178311.1 GI:20219449
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Sequence 28 from Patent W00192511.
AX323393
AX323393.1 GI:18094155
                                                                                                                                                                                                                                                                                     /organism="unknown"
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/organism="unknown"
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AR123877/c
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                              1 (bases 1 to 13)
Bock, A., Binder, F.
Bock, A., Binder, F.
DNA-fragment having the cyclodextrin glycosyltranferase gene Patent: US 5395927-A 3 07-MAR-1995;
Location/Qualifiers
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Pred. No. 1.7e+02;
0; Mismatches 2; Indels
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40.9%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
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Unknown.
Unclassified.
1 (bases 1 to 12)
S Korneluk.R.G. Holcik,M. and Liston,P.
S XIAP IRES and uses thereof
AL Patent: US 6171821-A S 09-GAN-2001;
Location/Qualifiers
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Unknown.
Unclassified.
3 1 (bases 1 to 12)
S Korneluk,R.G., Holcik,M. and Liston,P.
XIAP IRES and uses thereof
AL Patent: US 6171821-A 6 09-JMN-2001;
Location/Qualifiers
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AR2040ence 6 from patent US 6171821.
AR123873.1 GI:14109234
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ARQUENCE 5 from patent US 6171821.
AR123872. GI:14109233

    13
/organism="unknown"
/mol_type="genomic DNA"

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734 AGAAACAGAACA 745
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1 (bases 1 to 13)
     13 AGAAGCAGCACA 2
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Woychik,R.P.
Isolation and characterization of Agouti: a diabetes/obesity
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40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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                                                                                                    1. .12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
oligonucleotide
Patent: WO 0192511-A 28 06-DEC-2001;
Aventis Pharma (FR)
Location/Qualifiers
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/organism="unknown"
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Patent: US 5789651-A B 04-AUG-1998;
Location/Qualifiers
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/organism="unknown"
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Squence 8 from patent US 5789651.
AR021478 GI:3976093
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AR061316
AR061316.1 GI:5989007
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Patent: US 5843652-A 8 01-DEC-1998;
Location/Qualifiers
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AR061316/c
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1 (bases 1 to 13)
Woychik,R.P.
Isolation and characterization of Agouti: a diabetes/obesity
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Woychik,R.P.
Isolation and characterization of Agouti: a diabetes/obesity
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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Patent: US 6080550-A 14 27-JUN-2000;
Location/Qualifiers
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                                                                                                                                                                                            related gene
Fatent: US 6080550-A 9 27-JUN-2000,
Location/Qualifiers
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Sequence 23 from patent US 6310034.
AR175971.
AR175971.1 GI:17917270
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AR100114 13 bp
Sequence 9 from patent US 6080550.
AR100114 GI:12810562
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Hobom, G., Menke, A. and Meyer-Rogge, S.
Recombinant influenza viruses with bicistronic vrnas coding for two genes in tandem arrangement part of the patent: EP 1174514-A 7 23-JAN-2002;
Patent: EP larangecuticals GmbH (DE)
Location/Qualifiers
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Method for identifying mhc-restricted antigens
Patent: WO 0122083-A 5 29-WAR-2001;
GSF-Forschungszentrum f. Umwelt und Gesundheit GmbH (DE); ARTEMIS
Pharmaceuticals GmbH (DE)
Location/Qualifiers
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/mol type="unassigned RNA"
/db xref="taxon:11520"
/note="5'-konservierte Region des Wildtyp-Influenzavirus"
/note="5'-konservierte Region des Wildtyp-Influenzavirus"
Azzey,M., Hobom,G., Menke,A. and Flick,R.
Stable recombinant influenza viruses free of helper viruses
Patent: EP 1035209-A 17 13-SEP-2000;
ARTEMIS PHARMACENICALS GMBH (DE)
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Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
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Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
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                                                                                                                                1. .13
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Sequence 7 from Patent EP1174514.
AX352663
AX352663.1 GI:18617793
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Best Local Similarity 72.7
Matches 8, Conservative
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Best Local Similarity
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
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            Woychik, R.P., Bultman, S.J. and Michaud, E.J. Agouti polypeptide compositions Patent: US 631034-A. 23 30-CT-2001; Location/Qualifiers
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Sequence 17 from Patent BP1035209.
AX035442
AX035442.1 GI:11191084
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Influenza viruses with enhanced transcriptional and replicational
apacities variates with a 22-AUG-2002;
Patent: WO 02064757-A 8 22-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
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Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 1;
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/mol_type="unassigned RNA"
/db_xref="taxon:11520"

    .13
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Patent: EP 1233059-A 8 21-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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AR026539
AR026539.1 GI:5937379
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Sequence 8 from Patent EP1233059.
AX512617
AX512617.1 GI:23503840
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Influenza B virus
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Recombinant influenza viruses with bicistronic vrnas coding for two genes in tandem arrangement genes in tandem arrangement batent: WO 0208434-A 7 31-JAM-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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Influenza B virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
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Pred. No. 1.9e+02;
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Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 1; Indels
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Patent: EP 12017560-A 702-MAY-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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/organism="Influenza B virus"
/mol_type="unassigned RNA"
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Sequence 7 from Patent WO0208434.
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                                              Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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ilarity 72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 10)
Proberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1175 15-OCT-2002;
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C12N1S/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15,
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Score 8.4; DB 1; Length 10;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
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18-JUN-1999 JP 2000554749

19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090035,19-JUN-1998 US 60/090035,19-JUN-1998 US 60/090035,19-JUN-1998 US 60/090035,19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090044,19-JUN-1998 US 60/090044,19-JUN-1998 US 60/090044,19-JUN-1998 US 60/090044,19-JUN-1998 US 60/090074,19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090078 US 
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Preparation and use of superior vaccines
Key
Location/Qualifiers
                                                                                                                                                                                                                                                                                                10 bp DNA Preparation and use of superior vaccines. BD239757
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Pred. No. 1.7e+02;
0; Mismatches 1;
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JP 2002534056-A/1175
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JP 2002534056-A/1175.
Homo sapiens (human)
Homo sapiens
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nilarity 90.0%;
Conservative 0
     38.2%;
Similarity 90.0%;
9; Conservative
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PD 15-OCT-2
PF 18-JUN-1
PR 19-JUN-1
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Matches 9; Conserv
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BD239797
LOCUS
DEFINITION
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BD239757
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AUTHORS
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1 (bases 1 to 10)
2 (boberts; B.L. and Shankara; S. Preparation and use of superior vaccines Patent: JP 2002534056-A 331 15-OCT-2002; GENZYME CORP
                                                                                         Unclassified.
Unclassified.
Gray.D.M.
Gray.D.M.
Method for selectively ranking sequences for antisense targeting
Patent: US 5856103-A 2 05-JAN-1999;
Location/Qualifiers
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38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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TOTANIS/00,C12NS/00,C12NIS/00
Preparation and use of superior vaccines
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/organism="unknown"
/mol_type="unassigned DNA"

    .10
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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JP 2002534056-A/331.
Homo sapiens (human)
Homo sapiens
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                                                                          Unknown.
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BD238913/c
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1. .10
/organism="unknown"
/mol__type="genomic DNA"
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 10)

Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1215 15-OCT-2002;
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1 (bases 1 to 10.)

Hashimoto, S., Mateushima, K. and Suzuki, T.

Genes with human dendritic cell expression

Patent: 19 200279181-A 193 10-0CT-2000;

SCIENCE & TECH AZBNCY

OS Homo sapiens (human)
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Location/Qualifiers
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Home sapiens (hum,
D 2002534056-A/1215
J 5-OCT-2002
PR 19-UN-1999 US 60/090041,19-UN-1999 US 60/089997,19-
19-UN-1998 US 60/089997,19-
19-UN-1998 US 60/089997,19-
19-UN-1998 US 60/089997,19-
19-UN-1998 US 60/089992,79-
19-UN-1998 US 60/089997,79-
19-UN-1998 US 60/08997,79-
19-UN-1998 US 60/0900
19-UN-1998 US 60/090
19-UN-1998 US 60/09
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C12N15/00,C12N5/00,C12N15/00
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  BD239797
BD239797.1 GI:330499
JP 2002534056-A/1215
                                                                 Homo sapiens (human)
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E39660/c
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Shimmanoto, A., Furuichi, Y., Shibata, Y., Funaki, H., Ohara, E. and Watahiki, M.
Watchiki, M.
Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 19 08-APR-2003;
Location/Qualifiers
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Shimmamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 41 08-APR-2003;
Location/Qualifiers
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PN JP 2000279181-A/193
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR SHINICHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI PC C12N15/09, C07K14/475, C07K16/18, C12N15/00
CC CT I LOCALION (Qualifiers I SOURCE I COGNIS (Homan) (Augman) (Augm
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Location/Qualifiers
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AR303294
AR303294.1 GI:31692070
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Sequence 41 from patent US 6544736.
AR303316.1 GI:31692092
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/mol_type="genomic DNA"
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PAT 22-JUN-2001

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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0138577-4 1363 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Patent: WO 0138577-A 1293 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Sequence 1363 from Patent W00138577.
AX153448
                                                                                                                 Human transcriptomes
Patent: WO 0138577-834 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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               Homo sapiens (human)
Homo sapiens
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AX153448/c
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Shimmoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 127 08-APR-2003;
Location/Qualifiers
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Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
Androgen-regulated gene expressed in prostate tissue
Patent: US 5566130-A 47 20-MAY-2003;
Location/Qualifiers
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                 38.2%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
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Sequence 127 from patent US 6544736.
AR303402
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Sequence 47 from patent US 6566130.
AR336872
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     Query Match
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AR303402/c
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/db_xref="taxon:32644"

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Best Local Similarity 90.v.
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PC C12N2

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BD166609
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BD166675
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DD083216.1 GI:22628826

JP 201327293-A/13.

Homo sapiens (human)

IGM Homo sapiens (human)

Homo matured/activated dendritic cell expression genes (human matured/activated dendritic cell expression genes (human matured/activated dendritic cell expression genes (human)

Homo sapiens (human)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Tumor markers in ovarian cancer
Patent: WO 017517-A 102 II-OCT-2001;
THE SECRETARY OF THE DEPRATMENT OF HEALTH AND HUMAN SERVICES (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Human liver disease-expressing genes
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Numan liver disease-expressing genes.
BD166675.1 GI:27872487

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BD166609
BD166609.1 GI:27872421
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                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                  Hofmann,K., Conradt,M. and Petersohn,D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 47 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: WO 0203773-A 532 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 537 11-JUL-2002;
HENKEL KGAA (DE)
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Best Local Similarity 90.0%; Pred. No. 1.8e+02;
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    .11
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   AX470470.1 GI:22205595
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unclassified.

I (bases I to 10)

S Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
Human liver disease-expressing genes
D Patent: JP 2002209591-A 419 30-JUL-2002;
JARAN SCIENDE AND TECHNOLOGY CORP
ON JP 2002209591-A/419
PD 30-JUL-2002
PP 19-JAN-2001 JP 201012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
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                                                     C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
 19-JAN-2001 JP 2001012328
KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
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/organism='Homo sapiens (human)'.
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Human liver disease-expressing genes
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Sequence 47 from Patent WO02053773.
AX470470

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JP 2002209591-A/419.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 0203374-4 673 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 1705 from Patent WO02053774.
AX624664 GI:28452605
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Seguence 673 from Patent WO02053774.
AX623632
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/mol_type="unassigned DNA"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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AX623587/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 741 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: Word (1987) 1 1 - JUL - 2002;
HENKEL KGAA (DE)
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Sequence 741 from Patent WO02053773.
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/organism="Homo sapiens"
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 4268 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                      Score 8.4; DB 1;
Pred. No. 1.8e+02;
0; Mismatches 1
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/db_xref="taxon:9606"
                   /mol_type="unassigned DNA"
/db_xref="taxon:9606"
/organism="Homo sapiens"
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Best Local Similarity 90.0%;
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Best Local Similarity 90.0
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 3163 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                       Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 1705 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Petent: WO 02053774-A 2012 11-UUL-2002,
Henkel Kommanditgesellschaft auf Aktien (DE)
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Sequence 3163 from Patent WO02053774..
AX626122.1 GI:28454160
                                                                                                                                                                                                    /organism="Homo sapiens"
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    /organism="Homo sapiens"
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    /db_xref="taxon:9606"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                       Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A. 5971 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Sequence 7081 from Patent WO02053774.
AX630040
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/wol_type="unassigned DNA"
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AX629191/c
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AX630040/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 4807 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 5971 from Patent WO02053774.
AX628930
AX628930.1 GI:28456968
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Sequence 4807 from Patent WO02053774.
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/mol_type="unassigned DNA"
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AX628930/c
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AX627766/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1.8e+02;
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Method for determining homeostasis of the skin
Petent: WO 0205374-A 8094 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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                                   AX631053 11 bp DNA Sequence 8094 from Patent WO02053774.
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/mol_type="unassigned DNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 0203774-A 8049 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 7340 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Sequence 7340 from Patent W002053774.
AX630299
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     /db_xref="taxon:9606"
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38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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            Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 2023774-8, 9434 11-UUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Korneluk,R.G., Holcik,M. and Liston,P.
XIAP IRES and uses thereof
Patent: US 6171821-A 18 09-JAN-2001,
                                                                                              /organism="Homo sapiens"
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Sequence 81 from Patent EP1164203.
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/organism="unknown"
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CC Strandedness: Single;
CC Topology: Unknown;
FH Kev
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JP 2002507883-A/81.
synthetic construct
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artificial sequences.
1 (bases 1 to 12)
Roster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Boom,D.V.D., Jutlinke,C. and Rupert,A.
DNA diagnosis method based on mass spectrometry
Patent: JP 2002507883-A 81 12-MAR-2002;
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PN JP 2002507883-A/81

PD 12-MAR-2002

PF 06-NOV-1997 JP 1998521832

PR 06-NOV-1996 US 08/744481,06-NOV-1996 US 08/7444590

06-NOV-1996 US 08/746055,06-NOV-1996 US 08/744590

23-JAN-1997 US 08/746058,06-NOV-1997 US 08/747839

19-SEP-1997 US 08/933792,08-OCT-1997 US 08/947801

KOSTER, DANIEL P LITTLE, ANDREAS BRAUN, DAVID M LOUGH, PI
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DNA diagnosis method based on mass spectrometry.
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       DNA
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12 bp
Sequence 86 from Patent EP1164203.
AX328589
AX328589.1 GI:18101788
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19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR 19-JUN-1998 US 60/080853 PR 60/080851 PR 60/080852 PR 60
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Homo sapiens (human)

Homo sapiens (human)

Homo sapiens

Homo sapiens

Homosial (human)

Homosial
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GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 73118] from the original journal article.
This sequence comes from 2.
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38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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Preparation and use of superior vaccines
Key
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16-0101-1999 JP 2000554749

19-0101-1998 US 60(090041,19-0101-1998 US 60(090041,19-0101-1998 US 60(09992,19-0101-1998 US 60(099076,19-0101-1998 US 60(099076,19-010101-1998 US 60(099076,19-010101-1998 US 60(099076,19-010101-1998 US
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                       Genet. 28 (12), 860-864 (1991)

    .10
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

    .12
    /organism="Homo sapiens"
/mol_type="genomic DNA"
    /db_xref="taxon:9606"

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JP 2002534056-A/537
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PP 18-JUN-1
PR 19-JUN-1998 U
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BD239119
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PUBMED
REMARK
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Synthetic construct
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artificial sequences.
artificial sequences.

I (bases 1 to 12)

Koster, H., Little, D.P., Braun, A., Lough, D.M., Xiang, G.,
Boom, D.V.D., Jurinke, C. and Rupert, A.

Boom, D.V.D., Jurinke, C. and Rupert, A.

Boom, D.V.D. Jurinke, C. and Rupert, A.

LD 2002507883-A 86 12-MAR-2002;

EN 2002507883-A/86

PN JP 2002507883-A/86

PN JP 2002507893-A/86

PN JP 2002507883-A/86

PN JP 2002507893-A/86

PN JP 2002507893-A/86

PN JP 2002507893-A/86

PN G-NOV-1996 US 08/74481, 06-NOV-1996 US 08/746036 PR 06-NOV-1997 US 08/744859 PR 06-NOV-1997 US 08/78599 PR 06-NOV-1996 US 08/78599 PR 06-NOV-1996 US 08/78599 PR 06-NOV-1997 US 08/78599 PR 06-NOV-1996 US 08/78599 PR 06-NOV-1997 US 08/78599 PR 06-NOV-1996 US 08/78599 PR 06-NOV-1997 US 08/78599 PR 06-NOV-1996 US 08/7859 PR 06-NOV-1996 US 08/78599 PR 06-NOV-1996 US 08/7859 PR 06-NOV-1996 US 
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 12)
Love, D.R., Flint, T.J., Genet, S.A., Middleton-Price, H.R. and
Davies, K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S73118S1 12 bp DNA linear PRI 07-MAY-dystrophin (intragenic deletion) [human, Genomic Mutant, 12 nt, segment 1 of 2].
S73118 G1:241100
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                                 Score 8.4; DB 1; Length 12;
Pred. No. 2e+02;
0; Mismatches 1; Indels
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DNA diagnosis method based on mass spectrometry.
BD132154.
BD132154.1 GI:23227099
JP 2002507883-A/86.
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    .12
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PI DIRK VAN DEN BOCM, CHRIST
C12Q1/68, C07H21/00, C07F9/24
CC Strandedness: Single;
CC Topology: Unknown;
FH Key
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                            38.2%;
728 GCCAGGAGAA 737
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BD132154
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Velculescu,V.E., Vogelstein,B. and Kinzler,K.W. Human transcriptomes
Patent: WO 0138977-A 85 31-MAY-2001,
The Johns Hopkins University (US)
Location/Qualifiers
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                                                                                                                Human transcriptomes
Patent: WO 01385774 77 31-MAX-2001,
The Johns Hopkins University (US)
Location/Qualifiers
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Patent: WO 0138577-A 79 31-MAY-2001,
The Johns Hopkins University (US)
Location/Qualifiers
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Sequence 79 from Patent W00138577.
AXIS2164
AXIS2164.1 GI:14533815
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Sequence 85 from Patent WO0138577.
AX152170
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                         Homo sapiens (human)
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Best Local Similarity luv..
Best Since 8; Conservative
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DEFINITION
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SOURCE
                               SOURCE
ORGANISM
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AX152170
                                                                                   REFERENCE
AUTHORS
                                                                                                                TITLE
JOURNAL
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                KEYWORDS
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                              1 (bases 1 to 10)
Tatake, R.J., Marlin, S.D. and Barton, R.W.
Self-regulated apoptosis of inflammatory cells by gene therapy
Patent: US 6537784-A 15 25-MAR-2003;
Location/Qualifiers
                               Gaps
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Pred, No. 2e+02;
                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Velculescu, V.E., Vogelstein, B. and Kinzler, K.W. Human transcriptomes
Patent: WO 0138577-A 26 31-MAY-2001,
The Johns Hopkins University (US)
Location/Qualifiers
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        100.0%; Preq. ....
                                                                                                                                                  Sequence 15 from patent US 6537784. AR300461
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Sequence 26 from Patent WO0138577.
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Sequence 77 from Patent W00138577.
AX152162 AX152162.1 GI:14533813
                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
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/organism="unknown"
                                                                                                                                                                                               AR300461.1 GI:31687903
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             Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
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                                                     741 GAACACCG 748
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Unclassified.
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AX152111
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Joses 1 to 10)

8 1 (Joses 1 to 10)

8 Human activated Thl and Th2 cell expression genes
Human activated Thl and Th2 cell expression genes
AL Patent JP 200216482-A 204 02-UUL-2002;
BN ADPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN PP 200216482-A/204
PP 19-DEC-2000 JP 2000365816
PP 19-DEC-2000 JP 200
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                                                                                                             BD083241 10 bp DNA linear PAT 27-AUG-2002 Human matured/activated dendritic cell expression genes.
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10)

Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
Human matured/activated dendritic cell expression genes
Patent: 19 2001227293-A 162 27-NOV-2001;
DAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)

PN JP 2001327293-A/162

PN JP 20001327293-A/162

PN JP 200013500 JP 2000150562

PT 22-MAY-2000 JP 2000150562

PT KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PY
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BD161382-1 GI:27867140
Homo sapiens (human)
Homo sapiens
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/organism="Homo sapiens"
/mol_type="genomic DNA"

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/mol_type="genomic DNA"
/db_xref="taxon:9606"

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JP 2001327293-A/162.
Homo sapiens (human)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0185941-A 96 15-NOV-2001;
Academisch Ziskenhuis bij de Universiteit van Amsterdam (NL)
Location/Qualifiers
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36.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Human transcriptomes
Patent: WO 0138577-A 1321 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Sequence 96 from Patent WO0185941.
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AX301382.1 GI:17382465
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AX153406/c
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Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 452 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers linear Sequence 452 from Patent W002053773.
AX470875
AX470875.1 GI:22206000 1. .11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 264 AX470875/c LOCUS AUTHORS TITLE JOURNAL REFERENCE FEATURES

Gaps ö Query Match 36.4%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels 736 AAACAGAA 743

11 AAACAGAA 4

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PAT 09-AUG-2002 ô Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Gaps Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 714 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers ô linear Query Match 36.4%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels DNA Sequence 714 from Patent WO02053773. AX471137 /mol_type="unassigned DNA" /db_xref="taxon:9606" /organism="Homo sapiens" AX471137.1 GI:22206262 Homo sapiens (human) 728 GCCAGGAG 735 Homo sapiens LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 265 AX471137 ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES ò

PAT 23-MAR-2002

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PAT 09-AUG-2002 Eukaryoča, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo. Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1387 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers linear DNA Sequence 1387 from Patent WO02053773. AX471810.1 GI:22206935 Homo sapiens (human) Homo sapiens DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 266 AX471810 AUTHORS TITLE REFERENCE JOURNAL LOCUS

Gaps ö 0; Indels Query Match 36.4%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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DNA 11 bp Sequence 27 from Patent EP1225233. AX482050 AX482050.1 GI:22316772 synthetic construct synthetic construct artificial sequences. DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 267 AX482050 LOCUS

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PAT 16-AUG-2002

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Query Match 36.4%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 92 11-UIL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Means and methods for treatment evaluation
Patent: WO 02059558-A 27 01-AUG-2002;
Amsterdam Support Diagnostics B.V. (NL)
Location/Qualifiers
      van der Kuyl,A.C. and Cornelissen,M.
Means and methods for treatment evaluation
Patent: EP 1225233-A 27 24-UUL-2002;
Amsterdam Support Diagnostics B.V. (NL)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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AX623196 11 bp DN Sequence 237 from Patent WO02053774. AX623196
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/db_xref="taxon:9606"

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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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AX624933 Sequence 197 AX624933.1 Homo sapiens Homo sapiens Eukaryotens Eukaryotens Mammalia; Eu Petersohn, D. Method for G Patent: WO Patent: WO Henkel Komma	Curce 11. Organism="Homo sapiens" Amol_type="unassigned DNA" Amol_type="unassigned DNA" Amol_type="unassigned DNA" Amol_type="unassigned DNA" Amolarity	AX624958/c LOCUS LOCUS DEFINITION Sequence 1999 from Patent W002053774. ACCESSION AX624958 VERSION AX624958 Homo sapiens (human) ORGANISM Homo sapiens Mammalia; Eucheria: Primates; Cararrhini: Hominidae: Homo.	REFERENCE 1 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K. TITLE Method for determining homeostasis of the skin JOURNAL Patent: WO 02053774-A 1999 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) FEATURES 1 110-(Qualifiers 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Query Match 36.4%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 736 AAACAGAA 743 Db 11 AAACAGAA 4	RESULT 274 XX624999/C LOCUS LOCUS DEFINITION Sequence 2040 from Patent W002053774. VERSION KEYWORDS HOMO sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                               Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 0203774-43 441 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 4031 from Patent WO02053774.
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AX626400.1 GI:28454438
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 2926 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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                                                                                                                                                              AX625885 11 bp DNA Sequence 2926 from Patent WO02053774. AX625885

    .11
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         Mismatches

    .11
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/mol_type="unassigned DNA"
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         8; Conservative
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AX625885/c
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Sequence 5288 from Patent W002053774. AX628247
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Homo sapiens
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     733 GAGAAACA 740
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AX628755/c
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AX628247/c
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AX628626/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 4764 from Patent WO02053774.
AX627723
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Homo sapiens
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AX627723
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PAT 21-FEB-2003
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Matches 8; Conservative 0; Mismatches 0; Indels
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ches 0; Indels
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Petersohn,D., Conradt,M. and Hofmann,K.
Pethod for determining homeostasis of the skin
Patent: WO 02053774-A 7658 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 2053774-4 7513 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 7658 from Patent WO02053774.
AX630617
AX630617.1 GI:28458655
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100.0%; Pred. No. 2.1
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Matches 8; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 6657 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Liocation/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 0203774-4 6391 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                      Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin patent: WO 0203774-4 5796 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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36.4%; Score 8; DB 1; Les
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX629616
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                       Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A, 9421 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Method for determining homeostasis of the skin
Petent: WO 02053714-A 9462 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 9715 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 9462 from Patent WO02053774.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Method for determining homeostasis of the skin
Petent: WO 02053/14-A 9396 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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                                                                                          AX630976
Sequence 8017 from Patent WO02053774.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX630976.1 GI:28459018
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Wang,C.-G. and Hepburn,A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 89 19-JAN-1999;
Location/Qualifiers
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Pred. No. 2.3e+02;
0; Mismatches 2; Indels
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Sequence 14 from patent US 5908972.
AR070933.1 GI:7221821
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/organism="unknown"
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Sequence 14 from patent US 6245541.
ARIS7632.1 GI:16218594
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/organism="unknown"
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AR029900.1 GI:5943114
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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1 (bases 1 to 11)
Houtz, R.L.
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Unclassified.
1 (bases 1 to 11)
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AR070933/c
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Urdea, M.S.
Ribozymes with product ejection by strand displacement
Patent: Us 5631148-A 5 20-MAY-1997;
Location/Qualifiers
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36.4%; Score 8; DB 1; Ler
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0;
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88.9%; Pred. No. 2.3e+02;
iive 0; Mismatches 1
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Unclassified.
1 (bases 1 to 12)
S. Wang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA triple
AL Patent: US 5861244-A 10 19-JAN-1999;
Location/Qualifiers
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Sequence 89 from patent US 5861244.
AR029900
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                                                Query Match 36.4%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.1
Matches 8; Conservative 0; Mismatches
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Sequence 10 from patent US 5861244.
AR029821.1 GI:5943035
    /mol_type="unassigned DNA"
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Sequence 5 from patent US 5631148.
143337
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Best Local Similarity 88.9
Matches 8; Conservative
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AR029821/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 297 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1044 11-JUL-2002;
HENKEL KGAA (DE)
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35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Sequence 1044 from Patent WO02053773.
AX471467 1 GI:22206592
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Sequence 297 from Patent WO02053773.
AX470720
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   AX393119.1 GI:19701169
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Beckner, M.B., Krutzsch, H.C. and Liotta, L.A.
Human cell adhesion protein AAMP-1 and uses thereof
Patent: US 6274134-A 8 14-AUG-2001;
Location/Qualifiers
                                               Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 2.3e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 81.8%; Pred. No. 2.38+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Heber-Katz, E.
Compositions and methods for wound healing Patent: US 6538173-A 73 25-MAR-2003;
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/organism≈"unknown"
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/mol_type="unassigned DNA"
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Sequence 49 from Patent WO0210217.
AX393119
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches 9; Conservative 0; Mismatches 2; Indels
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Sequence 856 from Patent WO02053774.
AX623815
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 2023774-A 430 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 251 11-JUD-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Sequence 430 from Patent W002053774.
AX623389
AX623389.1 GI:28451330
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Sequence 251 from Patent W002053774.
AX623210 GI:28451151
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 1282 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Petent: WO 2053774-A 1407 11-UUI-2002;
Henkel Kommanditgesellschaft auf Aktien (DB)
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 2284 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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81.8%; Pred. No. 2.38+02;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches 9; Conservative 0; Mismatches 2.
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Sequence 4522 from Patent WO02053774.
AX627481.1 GI:28455519
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Sequence 4310 from Patent WO02053774.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 2025374-4. 3355 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 3569 from Patent WO02053774.
AX626528
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Sequence 5686 from Patent WO02053774.
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Sequence 5888 from Patent W002053774.
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Sequence 5984 from Patent WO02053774.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.3e+02;
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Metersohn,D., Conradt,M. and Hofmann,K.

Method for determining homeostasis of the skin

Patent: WO 02053774-A 5395 11-JUL-2002;

Henkel Kommanditgesellschaft auf Aktien (DE)

Location/Qualifiers
                                                                                                                                                                                                                                           Sequence 5332 from Patent W002053774.
AX628291
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Sequence 5395 from Patent W002053774.
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/db_xref="taxon:9606"
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                                  Query Match
Best Local Similarity 81.8%;
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Best Local Similarity 81.8
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AX628354/c LOCUS DEFINITION

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Homo sapiens (human)
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Homo sapiens
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Best Local Similarity 81.0
Best Local Similarity 91.0
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AX629821/c
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AX630158/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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               Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5984 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Patent: WO 02053774 + 6736 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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AX629695.1 GI:28457733
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Sequence 6466 from Patent WO02053774.
AX629425
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Homo sapiens
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AX629695/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 2.3e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 6890 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 6862 from Patent WO02053774.
AX629821
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35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 2.3e+02;
        Method for determining homeostasis of the skin
Patent: WO 02053774-A 7672 11-JUL-2002;
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Best Local Similarity 81.8
Matches 9; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 81.8%; Pred. No. 2.38+02;
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AX630158 11 bp DNA Sequence 7199 from Patent W002053774. AX630158 GI:28458196
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Sequence 7672 from Patent WO02053774.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 81.8%; Pred. No. 2.38+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Method for determining homeostesis of the skin
Petent: WO 02053774-A 7831 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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AX630810.
AX630810.1 GI:28458850
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Sequence 8278 from Patent WO02053774.
AX631236
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 9796 11-JUL-2002;
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Sequence 9796 from Patent WO02053774.
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Sequence 9706 from Patent WO02053774.
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                  AX631787.1 GI:28459894
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 8704 from Patent WO02053774.
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AX631662.1 GI:28459769
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artificial sequences.

I (bases 1 to 11)

Mizubuchi,H., Fushimi,N. and Miyoshi,S.

Modified promote  

Mizubuchi,H., Fushimi,N. and Miyoshi,S.

Modified promote  

SHOWS SANGYO CO LTD DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCES INNUSTRAL SCIENCE AND  

SHOWS SANGYO CO LTD DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCES INSUSTRAL SCIENCE AND  

SHOWS SANGYO CO LTD DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCE INSUSTRAL SCIENCE AND  

PR 24-SEP-2002

PP 15-MAX-2001 JPD 2001074780

PP 15-MAX-2001 JPD 2001074780

PP 16-MAX-2001 JPD 2001074780

PP 17-MOVURI NIZUBUCHI,NAOYA PUSHIMI,SHINSUKE MIYOSHI PC CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI2NI/21,CI
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/organism='Mus musculus (mouse)'.
Location/Qualifiers
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35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                     Compositions and method for healing wound Key
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Pred. No. 2.3e+02;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Modified promoter.
BD174612.1 GI:29120302
JP 2002272466-A/1.
synthetic construct
synthetic construct
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JP 2002272466-A/6.
synthetic construct
synthetic construct
artificial sequences.
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Best Local Similarity 81.8%;
Matches 9; Conservative
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BD174612
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Compositions and method for healing wound
Patent: JP 2002503460-A 73 05-FEB-2002;
THE WISTAR INSTITUTE
OS Mus musculus (mouse)
PD 05-FEB-2002
PP 12-FEB-1999 UP 2000531545
PR 13-FEB-1999 US 60/074737, 26-AUG-1998 US 60/097937 PR 28-SEP-1999 US 60/102051
PR 13-FEB-1999 US 60/102051
PR 13-FEB-1999 US 60/102051
PR 13-FEB-1999 US FOILS/09, AUK67/027, CI2N5/10, CI2Q1/68, G01N33/50, CI2N15/00, PC
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 11)
                                                                                                                                                                                                                                         Gaps
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Drosophila melanogaster
Eukaryota, metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Moopeera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Method for identifying therapeutic targets by use of genetic screens in drosophila melanogaster
Patent: WO 03044407-A 19 22-MAY-2003,
BOEHRINGER INGELHEIM INTERNATIONAL GMBH; CD Patents (DE)
Location/Qualifiers
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35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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    .11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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JP 2002503460-A/73.
Mus musculus (house mouse)
Mus musculus
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1 (bases 1 to 12)
Mudeoulpar J., Haley, J.D., Niall, H.D. and Shine, J.
Molecular cloning and characterization of the gene sequence coding
for porcine relaxin
Patent: EP 0086649-A 11 24-AUG-1983;
HOWARD FLOREY INSTITUTE OF EXPERIMENTAL PHYSIOLOGY AND MEDICINE
Location/Qualifiers
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Pred. No. 2.5e+02;
0; Mismatches 2; Indels
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Nucleotide sequence 11 from patent number AU562012
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Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2:
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Location/Qualifiers
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Location/Qualifiers

    .12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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Best Local Similarity 81.8%;
Matches 9; Conservative (
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1 (bases 1 to 12)
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A16603.1 GI:641064
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A16604/c
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synthetic construct
artificial sequences.
1 (bases 1 to 12)
1 (bases 1 to 12)
Mudson,P.J., Hadey,J.D., Niall,H.D. and Shine,J.
Molecular cloning and characterization of the gene sequence coding
for porcine relaxin
Patent: EP 0086649-A 10 24-Aug-1983;
HOWARD FLOREY INSTITUTE OF EXPERIMENTAL PHYSIOLOGY AND MEDICINE
Location/Qualifiers
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Location/Qualifiers
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Pred. No. 2.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                             Score 7.8; DB 1; Length 11; Pred. No. 2.3e+02; 0; Mismatches 2; Indels
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Synthetic primer 579-590 (Reverse complement).
A06061.1 GI:411193
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Synthetic primer 579-590.
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81.8%;
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synthetic construct
artificial sequences.
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Best Local Similarity 81.8%;
Matches 9; Conservative
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A06060.1 GI:411192
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Best Local Similarity 81.6
Matches 9; Conservative
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Unknown.
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Unclassified.
Colote, S. and Pirotzky, E.
Colote, S. and Pirotzky, E.
Oligonucleotides to inhibit the expression of isoprenyl protein transferases
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Unclassified.

Unclassified.

I (bases 1 to 12)

Wang, C. -G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 21S 19-JAN-1999;

Location/Qualifiers
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Pred. No. 2.5e+02;
0; Mismatches 2; Indels
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         Pred. No. 2.5e+02;
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AR030026.
AR030026.1 GI:5943240
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Sequence 229 from patent US 5861244.
AR030040
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Sequence 3 from patent US 5856461.
AR027861
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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         81.8%;
    Best Local Similarity 81.8 Matches 9; Conservative
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Matches 9; Conservative
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AR030026
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AR027861
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CHIMAERIC OLIGONUCLEOTIDES AND USES THEREOF IN THE IDENTIFICATION
OF ANTISENSE BINDING SITES
Patent: WO 9710332-A 50 20-MAR-1997,
BRAX GENOMICS ITD (GB)
Location/Qualifiers
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Colore, S. and Pirotzky, E.
Oligonuclectides to inhibit the role of isoprenyl protein transferases
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 50 from Patent W09710332.
A61481
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Sequence 3 from Patent BP0692535.
A47643.
447643.1 GI:2301584
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Matches 9; Conservative
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11 GAAGCAGAAGA 1
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A47643
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BD248202 12 bp DNA linear PAT 17-JUL-2003
BD248202 1 G1:33057972
S BD248202.1 G1:33057972
S SYNTHETIC CONSTRUCT
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SYNTHETIC CONSTRUCT
ATLIFICIAL SEQUENCES.
SHORT-CHAIN Oligonuclectide for inhibiting VEGF expression
AL (bases 1 to 12)
S Short-chain oligonuclectide for inhibiting VEGF expression
AL PREADT. 17 2002554038-A 21 06-AUG-2002;
AVENTIS PHARMA DEUTSCHLAND GMBH
OS Artificial Sequence
PR 07-AUG-1999 BP 98114653.9
PR 07-AUG-1999 BP 98114653.9
PR 07-AUG-1999 BP 98114653.9
PR 07-AUG-1999 BP 98114653.9
PR 07-AUG-1999 CONSTRINAN PEYMAN, ALAN BITONTI, RICHARD WOESSNER
PC CL2MIS/09.A61K31/711, AGIK31/712, AGIK31/7125 PC
AGIK48/00, A61F831/711, AGIK31/7115, AGIK31/7125 PC
                                                                                                                                                                                           synthetic construct
synthetic construct
synthetic construct
artificial sequences.

I (bases 1 to 12)

Guiliano, K.A., Bright, G., Olson, K. and Tencza, S.B.

A system for cell based screening
B 20002528136-A33
B 30-3CELOMICS ING
B 31-3CELOMICS ING
B 32-3CE-1999 JP 2000579780
B 30-3CE-1999 US 60/106308,26-MAY-1999 US 60/136078 PI
RENNETH A GUILLANO, GARY BRIGHT, KEITH OLSON, SARAH BURROUGHS PI
TENCZA
C (12NIS/09,C12NI/15,C12NI/19,C12NI/21,C12NS/10,C12Q1/02,C12Q1/
BC 37,G01N33/15,C12NI/15,C12NI/19,C12NI/21,C12NS/10,C12Q1/02,C12Q1/
C Description of Artificial Sequence: Caspase-6 substrate CC
                                                                                                            PAT 17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/02, C12Q1/
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GOIN33/50,C12N15/00,C12N5/00
Description of Artificial Sequence: Caspase-6 substrate
recognition
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81.8%; Pred. No. 2.5e+02;
tive 0; Mismatches 2; Indels
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/organism='Artificial
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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A system for cell based screening.
BD242527
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Best Local Similarity 81.8
Matches 9; Conservative
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BD242527
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                                                                                                                                                                                                                                                  Gaps
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                       Unclassified.

1 (Dases 1 to 12)
Wang, C.-G. and Hepburn, A.G.
Generic sequence assay using DNA triple strand formation
Patent: US 5861244-A 229 19-JAN-1999;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 12)
Wang,C.-G. and Hepburn,A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US Sed1244-A 351 19-JAN-1999;
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Similarity 81.8%; Pred. No. 2.5e+02;
9; Conservative 0; Mismatches 2; Indels
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Sequence 271 from patent US 5837832.
AROS8694.1 GI:5984271
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/wol_type="unassigned DNA"

    .12
/organism="unknown"
/mol_type="unassigned DNA"

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/organism="unknown"
/mol_type="unassigned DNA"

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81.8%; Pred. No. 2.5e+02;
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JP 2002537844-A/14.
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Stable recombinant influenza virus free from helper virus.
BD269488
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GARY R PASTERNACK, JIMING BAI

AG1K48/00, AG1K31/7115, AG1K45/00, AG1P35/00, C12Q1/42, G01N33/15,

G01N33/50//

C12N15/09, C12N15/00
A61P13/12,A61P17/16,A61P27/02,A61P29/00,A61P35/00,A61P43/00,C12M15/00
C12M15/00
Description of Artificial Sequence: Antisense FH Key
Location/Qualifiers
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synthetic construct
artificial sequences.

E 1 (bases 1 to 12)
S Pasternack,G.R. and Bai,J.
Method of treating cancer by restoration of pp32 function
Datent: JP 2002536346-A 26 29-OCT-2002;
THE JOHNS HORKINS UNIVERSITY
ON JP 2002536346-A/26
PN JP 30-25-DCT-2002
PR 03-FEB-2000
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/organism='Artificial Sequence'
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/mol type="genemic DNA"
/db_xref="taxon:32630"
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JP 2002537844-A/12.
Influenza C virus
Influenza C virus
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BD269490
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Stable recombinant influenza virus free from helper virus FH
Location/Qualifiers
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PF 03-MAR-1090 JP 2000603407
PR 06-MAR-1999 EP 99104519.6
PI GERD HOBOW, RAMON FLICK, ANETTE MENKE, MAYSA AZZEH PC
C12N15/09, A61K39/145, A61K48/00, A61P31/16, C12N7/00, C12P21/02// PC
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Description of Artificial Sequence: Modified influenza A 3'
sequence
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Synthetic construct

artificial sequence.

I (bases 1 to 12)

S Hobom, G., Flick, R., Menke, A. and Azzeh, M.

Stable recombinant influenza virus free from helper virus

L Patent: UP 2002537844-A 14 12-NOV-2002;

ARTERIS PHARACEUTICALS GMBH

OS Artificial Sequence

PN UP 2002537844-A/14

PD UP-2002537844-A/14

PD UP-2002537844-B/14
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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Hsiung,H.M., Schoner,R.G. and Schoner,B.E.
Vectors for expressing bovine growth hormone derivatives
Vector: EP 0159123-A2 32 23-OCT-1985;
Location/Qualifiers
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/organism='Artificial Sequence'.
Location/Qualifiers
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Pred. No. 2.5e+02;
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Pred. No. 2.5e+02;
0; Mismatches 2; Indels
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35.5%; Score 7.8; DB 1; Length 12
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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NAESUBI MICHAEL
C12N15/09, C07K9/00, C12Q1/68, C12N15/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                  I (bases 1 to 12)

Kung.H.-F. and Yamazaki, S.

Rung.H.-F. tecombinant interleukin-2
Parent: EP 0147819-A2 6 10-JUL-1985;

Location/Qualifiers
                                         Location/Qualifiers
                                                                                                  1. .12
/organism="synthetic construct"
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/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                    DNA
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Sequence 32 from Patent EP 0159123.
107920.
107920.1 GI:589373
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/organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Sequence 6 from Patent EP 0147819.
104321.1 GI:591773
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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Best Local Similarity 81.8
Matches 9; Conservative
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Unclassified.
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 PE CC PE
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107920/c
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I04321
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JP 1993003789-A/1.
Cucumber mosaic virus (cucumber mosaic cucumcovirus)
Cucumber mosaic virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT 18-JUN-2001
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                                                                                                                                 PAT 29-SEP-1997
                                                                                                                                                                                                                                                                 1 (bases 1 to 12)
Kominato, M., Sato, S. and Sayama, H.
WEAK TOXIC VIRUS OF CUCUMBER MOSAIC VIRUS USING CLONED SATELLITE
                                                                                                                                                                                                                                                                                                                                                                                          PI XONINATO WASAYUKI, SATO SADAICHI, SAYAWA HARUKI PC C12N15/33 AO1N63/00,C12N1/21,C12N7/04,C12N15/10,(C12N1/21, PC C12R1:19); Carrandedness: Single; CC ctopology: Linear; EH Key Location/Qualifiers FT misc_RNA 1: .12
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    Gaps
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Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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// Organism="Cucumber mosaic virus"
//mol_type="genomic RNA"
//db_Xref="taxon:12305"
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Patent: JP 1999127876-A 1 18-MAY-1999;
BOBHININGER MANNHEIM GMBH
OS Artificial Sequence
PN JP 1999127876-A/1
PP 21-AUG-1999 JP 1998235065
PR 22-AUG-1997 DE 97 114 512:3
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NIPPON DERUNDATE KK
OS Cucumber mosaic virus
NP 1993003789-A/1
PD 14-JAN-1993
PF 30-SEP-1991 JP 1991252204
PR 11-OCT-1990 JP 90P 274465
    Mismatches
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JP 1999127876-A/1.
synthetic construct
synthetic construct
artificial sequence.
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       9; Conservative
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E04220/c
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PAT 20-DEC-2002
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Unclassified.
Unclassified.
1 (bases 1 to 12)
Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 329 29-OCT-2002;
Location/Qualifiers
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0
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35.5%; Score 7.8; DB 1;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2.
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unidentified
unclassified.
1 (bases 1 to 12)
Naesby,M.D.
Small Triplex Forming PNA Oligos
Patent: EP 0897991-A 1 24-FEB-1999;
BOEHRINGER MANNHEIM (ME)
   Polymorphic repeats in human genes
Patent: US 6472154-A 59 29-OCT-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                   AR242041 12 bp DN Sequence 329 from patent US 6472154. AR242041.1 GI:27287853
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Sequence 1 from Patent EP0897991.
AX000276
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .12
/organism="unknown"
/mol_type="genomic DNA"
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12 GGAGAGAGAGA 2
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AR242041/c
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AX000276
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                                                                                                                                                                                                                                   Chimeric oligonucleotides and uses thereof in the identification of antisense binding sites
Patent: US 6355418-A 31 12-MAR-2002;
Location/Qualifiers
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1 (bases 1 to 12)
Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Giuliano, K. and Kapur, R.
System for cell-based screening
Patent: US 6416559-A 65 09-UUL-2002;
Location/Qualifiers
                                                                                  12 bp 1
Sequence 33 from patent US 6355418.
AR199085
AR199085.1 GI:20249159
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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/wol_type="unassigned DNA"
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Sequence 65 from patent US 6416959.
AR217452
AR217452.1 GI:23317145
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AR241771
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Schmidt, G.
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AR199085/c
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AR217452
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AR241771
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Hobom,G., Menke,A. and Meyer-Rogge,S.
Recombinant influenza viruses with bicistronic vrnas coding for two genes in tandem arrangement
Patent: WO 0208434-A 3 31-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hobom, G., Menke, A. and Meyer-Rogge, S.
Recombinant influenza viruses with bicistronic vrnas coding for two genes in tandem arrangement
Patent: EP 1174514-A 3 23-JAN-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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                          Bornkamm,G.W., Hobom,G., Mautner,J. and Nimmerjahn,F.
Method for identifying mhc-restricted antigens
Patent: WO 0122083-A 3 29-MAR-2001,
GSF-Porschungszentrum f. Umwelt und Gesundheit GmbH (DE) , ARTEMIS
Pharmaceuticals GmbH (DE)
                                                                                                                                                                                                                   /note="3'-konservierte Region des Wildtyp-Influenzavirus"
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Influenza C virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
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Influenza C virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
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35.5%; Score 7.8; DB 1; Length 12;

Best Local Similarity 81.8%; Pred. No. 2.5e+02;

Matches 9; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2;
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Sequence 3 from Patent EP1174514.
AX352659
AX352659.1 GI:18617789
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Sequence 3 from Patent WO0208434.
AX362217
AX362217.1 GI:18694555
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Influenzavirus C.
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AX352659/c
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AX362217/c
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Stable recombinant influenza viruses free of helper viruses
Patent: BP 1035209-A 14 13-SEP-2000;
ARTEMIS PHARMACEUTICALS GMBH (DE)
Location/Qualifiers

    1.2
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    /note="Modified influenza A 3' sequence (pHL1948)"

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Stable recombinant influenza viruses free of helper viruses
Patent: BP 1035209-A 12 13-SEP-2000;
ARTEMIS PHARMACEUTICALS GMBH (DE)
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Influenza C virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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Influenza C virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
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                                              12 bp
Sequence 12 from Patent EP1035209.
AX035437
AX035437.1 GI:11191079
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Sequence 3 from Patent WC0122083.
AX100746.1 GI:13619692
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Sequence 14 from Patent BP1035209.
AX035439
AX035439.1 GI:11191081
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AX035439/c
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AX100746/c
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AX035437/c
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Influenza C virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
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/note="Modified influenza A 3'-sequence"
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Patent: EP 1233059-A 3 21-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
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Patent: EP 1233059-A 4 21-AUG-2002,
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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AX512612
AX512612.1 GI:23503835
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20 bp

AX512613

AX512613.1 GI:23503836
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AX512612/c
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AX512613/c
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AX522263/c
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Influenza virus vector for human dendritic cells
Patent: EP 1201760-A 26 02-MAY-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
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Influenza C virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grassmann,R.
Influenza virus vector for human dendritic cells
Patent: BP 1201760-A 3 02-MAX-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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Seguence 26 from Patent EP1201760.
AX428953
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Sequence 3 from Patent EP1201760.
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AX428930.1 GI:21540314
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Best Local Similarity 81.8
Matches 9; Conservative
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AX428930/c
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AX428953/c
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Wethod for analyzing nucleic acid sequences and gene expression
Patent: WO 03020968-A 6 13-MAR-2003;
Genovoxx Gmbh (DE)
Location/Qualifiers
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/note="Caspase-6 substrate recognition sequence"
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Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                         linear
                                                                      1. .12
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/noTe="ermittelte Sequenz (Beispiel 4)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 .12
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/note="Sequenz aus Beispiel 2"
Method for determining gene expression Patent: WO 2008831-A 1 07-NOV-2002; Genovoxx Gmbh (DE)
                                                                                                                                                                                                                                                                                                                                                         DNA
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A system for cell-based screening
Patent: BP 1314980-A 65 28-MAY-2003;
Cellomics, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                  12 bp
Sequence 6 from Patent W003020968.
AX742026
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Seguence 65 from Patent EP1314980.
AX766776
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                                                                                                                                                         Hobom, G. and Menke, A.
Influenza viruses with enhanced transcriptional and replicational
capacities
Patent: WO 02064757-A 3 22-AUG-2002;
ARTEMIS Pharmaceuticals GmbH (DE)
Location/Qualifiers
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Influenza C virus
Viruses; ssRMA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA
                                                                                                                                                                                                                                                                            /organism="Influenza C virus"
/mol_type="unassigned RNA"
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Sequence 1 from Patent W002088381.
AX711980 GI:29787762
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Sequence 4 from Patent W002064757.
AX522264 AX522264.1 GI:24411218
     Sequence 3 from Patent W002064757.
AX522263
AX522263.1 GI:24411217
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artificial sequences.
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8 g g

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Direct Submission

Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANG

Gaston Cremieux, 91057 Evry cedex, FRANG

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.info.gen.fr).
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Gullans, S.R., Kojima, R. and Randall, J.
Gullans, S.R., Kojima, R. and Randall, J.
Method for conducting sequential nucleic acid hybridization steps
Patent: US 5773213-A 5 30-UUN-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
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Pred. No. 2.5e+02;
0; Mismatches 2; Indels
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33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Sequence 5 from patent US 5773213.
AR013804.1 GI:3971258
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AR026540
AR026540.1 GI:5937380
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81.8%;
                                                2 (bases 1 to 12)
Balzergue, S.
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Best Local Similarity 81.8
Matches 9; Conservative
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AR013804/c
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12-DEC-1997 US 60/069677
GARY R PASTERNACK, GERALD J KOCHEAVAR, JONATHAN R BRODY, SHRIHARI
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
162009.
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Arbidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Buraryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; cosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)
                           Gaps
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synthetic construct
artificial sequences.

1 (bases 1 to 12)
Pasternack, G.R., Kocheavar, G.J., Brody, J.R. and Kadkol, S.S.
Gene family with transformation modulating activity
Patent: JP 2002508154-A 26 19-MAR-2002;
PHE JOHNS HOPKINS UNIVERSITY
OS Artificial Sequence
PN JP 2002508154-A/26
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Location/Qualifiers
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                           Indels
    Pred. No. 2.5e+02;
0; Mismatches 2;
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_Xref="taxon:32630"
                         0; Mismatches
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    81.8%;
Best Local Similarity 81.8
Matches 9; Conservative
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ATH528392
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1 (bases 1 to 10)
Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
Lopez-Nieto,C.Eduardo and compositions for characterizing nucleotide sequences based on K-tuple analysis
sequences based on K-tuple analysis
Patent: US 6110667-A 93 29-AUG-2000;
Patent: US 611067-A 93 29-AUG-2000;
                                                                                                                                                                                                                             Unclassified.

1 (bases 1 to 10)
1 (bases 1 to 10)
Lopez-Nieto, C. Eduardo. and Nigam, S. Kumar.
Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis
Patent: US 6110667-A 36 29-AUG-2000;
Location/Qualifiers
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Sequence 93 from patent US 6110667.
AR107847
AR107847.1 GI:12823334
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Sequence 41 from patent US 6326174.
AR170365
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 88.9
Matches 8; Conservative
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AR107790/c
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Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis
Petent: US 6110667-A 35 29-AUG-2000;
Location/Qualifiers
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1 (bases 1 to 10)

Lopez-Nieto, C.Eduardo. and Nigam, S.Kumar.
Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis
Patent: US 6110667-A 3 29-AUG-2000;

Location/Qualifiers
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                             Unknown.
Unknown.
Unclassified.
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I (bases 1 to 10)
Gray, D.M. and Clark, C.L.
Method for selectively ranking sequences for antisense targeting
Method for selectively anking sequences for antisense targeting
Patent: US 5856103-A 3 05-JAN-1939;
Location/Qualifiers
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Pred. No. 2.5e+02;
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Sequence 35 from patent US 6110667.
AR107789
AR107789.1 GI:12823276
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AR107757.1 GI:12823244
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60/089853 PR

60/08993 PR

50/08993 PR

70/08072 PR

70/08072 PR

70/08043 PR

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7777 PR

477 PR
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1. (bases 1 to 10)

Roberts, D.L. and Shankara, S.

Preparation and use of superior vaccines
Patent: JP 2002534056-A 196 15-OCT-2002;
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                      Gaps
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                      Indels
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Preparation and use of superior vaccines
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002534056-A/196
15-0CT-2002
18-JUN-1999 US 60/090039
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JP 2002534056-A/196.
Homo sapiens (human)
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C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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G01N37/00,
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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           Unknow...
Unclassified.
1 (bases 1 to 10)
Joyce G.F. and Breaker,R.R.
Enzymatic DNA molecules
Patent: US 6326774-A 41 04-DEC-2001;
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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18-JUN-1999 JP 2000554749
19-JUN-1998 US 60/09003
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JP 2002534056-A/75
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JP 2002534056-A/75.
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88.9%;
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.6
Best Local Similarity 88.9
Matches 8; Conservative
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PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090073 PR 19-JUN-1998 US 60/090073 PR 60/090073 PR 19-JUN-1998 US 60/090073 PR 60/080999 PR 19-JUN-1998 US 60/09000,19-JUN-1998 US 60/09004,19-JUN-1998 US 60/080991 PR 60/080991 US 60/09004,19-JUN-1998 US 60/09007 PR 19-JUN-1998 US 60/0
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 88.9
Matches 8; Conservative
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VERSION
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BD238955/c
LOCUS
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PN JP 202534056-A/236

PP 15-OCT-2009

PP 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

19-JUN-1998 US 60/090031,19-JUN-1998 US 60/08993 PR

19-JUN-1998 US 60/089978,19-JUN-1998 US 60/08993 PR

19-JUN-1998 US 60/089978,19-JUN-1998 US 60/08993 PR

19-JUN-1998 US 60/089000,19-JUN-1998 US 60/08993 PR

19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR

19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR

19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090048 PR

19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090047 PR

19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR

19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090045 PR

19-JUN-1998 US 60/090078,19-JUN-1998 US
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1 (bases 1 to 10)

Roberts, B.L. and Shankara, S.

Roberts, B.L. and Shankara, S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 339 15-OCT-2002;

GENZYME CORP
                                                                                                                                  Eukaryota, Metazoá, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.

[ Dases 1 to 10)

Roberts, B.L. and Shankara, S.

Roberts, B.L. and Shankara, S.

Perparation and use of superior vaccines

Patent: JP 2002534056-A 236 15-0CT-2002;
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Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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/organism="Homo sapiens"
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JP 2002534056-A/339
15-0CT-2002
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JP 2002534056-A/339.
Homo sapiens (human)
Homo sapiens
             JP 2002534056-A/236.
Homo sapiens (human)
Homo sapiens
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19-JUN-1998 US 60/090041,19-JUN-1998 US 60/08953 PR 19-JUN-1998 US 60/08997,19-JUN-1998 US 60/089953 PR 59-JUN-1998 US 60/08997,19-JUN-1998 US 60/08993 PR 60/089993 PR 60/089994 PR 60/089994 PR 60/089994 PR 60/090077 PR 60/090
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR 60/090098 US 60/090076,19-JUN-1998 US 60/090045 PR 08-DEC-1998 US 60/111715 PT BRUCE L ROBERTS, SRINIVAS SHANKARA PT CTAILS/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
                                                                                                                                          C12N1/19.
C12N1/19.
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC G01N37/00,
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(Obserts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 595 15-OCT-2002;
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/organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.6%; Score 7.4; DB 1; Length 10; 88.9%; Pred, No. 2.5e+02; ative 0; Mismatches 1; Indels
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Preparation and use of superior vaccines
Key
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002534056-A/595
15-0CT-2002
18-JUN-1999 US 60/090039
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Homo sapiens
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PN JP 20025
PD 15-OCT-2
PF 18-JUN-1
PR 19-JUN-1
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Best Local Similarity
Matches 8; Conserv
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BD239177/c
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19-JUN-1998 US 60/080927,19-JUN-1998 US 60/080553 PR 19-JUN-1998 US 60/080927,19-JUN-1998 US 60/080923 PR 60/080927,19-JUN-1998 US 60/080923 PR 60/080927 PR 60/0
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Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 780 15-OCT-2002;
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                                                                                                                                                                                    Score 7.4; DB 1; Length 10;
Pred, No. 2.5e+02;
0; Mismatches 1; Indels
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Preparation and use of superior vaccines
Key
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Preparation and use of superior vaccines.
BD239362
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33.6%; Score 7.4; DB 1;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1;

    .10
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002534056-A/780
15-OCT-2002
18-JUN-1999 UP 2000554749
19-JUN-1998 US 60/09003
   Location/Qualifiers
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JP 2002534056-A/780.
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88.9%;
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Homo sapiens
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Best Local Similarity 88.9,
                                                                                                                                                                                                                                                                                                                  730 CAGGAGAAA 738
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BD239362/c
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19-UTN-1998 US 60/090041,19-UTN-1998 US 60/080553 PR 19-UTN-1998 US 60/080079 PR 19-UTN-1998 US 60/080079 PR 19-UTN-1998 US 60/080079 PR 19-UTN-1998 US 60/080079 PR 60/080992,19-UTN-1998 US 60/080079 PR 60/080992,19-UTN-1998 US 60/08097 PR 60/0809992 US 60/08097 PR 60/0809991 PR 60/080991 PR 60/080904 PR 60/080991 PR 60/08091 
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1 (bases 1 to 10)
Roberts; B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 835 15-OCT-2002;
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60/089853 PR
60/090079 PR
60/089993 PR
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60/089853 PR
60/090079 PR
60/089993 PR
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Location/Qualifiers
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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PN JP 2002534056-A/835
PD 15-OCT-2002
PP 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089997,19-JUN-1998 US 19-JUN-1998 US 60/089997,19-JUN-1998 US 19-JUN-1998 US 60/090035,19-JUN-1998 US
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C C12N15/00,C12N5/00,C12N15/00
C Preparation and use of superior vaccines
Location/Qualifiers
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vaccines.
1 (bases 1 to 10)
Roberts, B.L. and Shankara, S.
Prepartation and use of superior vaccines
Patent: JP 2002534056-A 813 15-OCT-2002,
GENZYME CORP.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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superior
                                                                                                                         Homo sapiens (human)
JP 2002534056-A/813
15-0CT-2090
18-JUN-1999 UP 2000554749
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88.9%;
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity 88.9°
Local Similarity 88.9°
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BD239417
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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60/089853 PR
60/090079 PR
60/080993 PR
60/080991 PR
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Location/Qualifiers
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Preparation and use of superior vaccines
Key
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                                                                                                                   BD239376 10 bp DNA Preparation and use of superior vaccines.
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Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 794 15-0CT-2002;
GENZYME CORP
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/organism="Homo sapiens"
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19-JUN-1998 US 60/0900
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JP 2002534056-A/794
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JP 2002534056-A/813.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                             GI:33049146
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JP 2002534056-A/794.
Homo sapiens (human)
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Best Local Similarity
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BD239395/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Roberts, B.L. and Shankara, S.
Prepartation and use of superior vaccines
Patent: JP 2002534056-A 1396 15-OCT-2002;
GENZYME CORP
                                     PC C12N1/21,C12NS/10,G01N33/15,G01N33/50,G01N33/53,G01N33/56,
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key
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C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15,
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Location/Qualifiers
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vaccines.
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JP 2002534056-A/1396. Homo sapiens (human)
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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JP 2002534056-A/1396
15-OCT-2002
18-JUN-1999 JP 2000554749
19-JUN-1998 US 60/090039
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PN JP 2002534056-A/1342
PD 15-OCT-2002
PF 18-UN-1999 US 60/090039,19-UW-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-UW-1998 US 60/090079 PR
19-JUN-1998 US 60/090031,19-UW-1998 US 60/090079 PR
19-JUN-1998 US 60/090031,19-UW-1998 US 60/090079 PR
19-JUN-1998 US 60/09992,19-UW-1998 US 60/090079 PR
19-JUN-1998 US 60/099000,19-UW-1998 US 60/090048 PR
19-JUN-1998 US 60/090001,19-UW-1998 US 60/090048 PR
19-JUN-1998 US 60/090041,19-UW-1998 US 60/090048 PR
19-JUN-1998 US 60/090044,19-UW-1998 US 60/090047 PR
19-JUN-1998 US 60/090044,19-UW-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-UW-1998 US 60/090077 PR
P-JUN-1998 US 60/090077 PR
P-JUN-1998 US 60/090077 PR
P-JUN-1998 US 60/090077 PR
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19-JUN-1998 US 60/08992,19-JUN-1998 US 60/090072 PR 19-JUN-1998 US 60/08991 PR 19-JUN-1998 US 60/08991 PR 19-JUN-1998 US 60/08991 PR 19-JUN-1998 US 60/08904 PR 60/089991 J9-JUN-1998 US 60/090042,19-JUN-1998 US 60/09003 PR 19-JUN-1998 US 60/090042,19-JUN-1998 US 60/080934 PR 19-JUN-1998 US 60/080044,19-JUN-1998 US 60/08094 PR 60/080060,19-JUN-1998 US 60/089934 PR 19-JUN-1998 US 60/089934 PR 60/080078,19-JUN-1998 US 60/08097 PR 19-JUN-1998 US 60/08097 PR 60/080078,19-JUN-1998 US 60/080077 PR 19-JUN-1998 US 60/080077 PR 19-JUN-1998 US 60/080077 PR 19-JUN-1998 US 60/080078,19-JUN-1998 US 60/080077 PR 19-JUN-1998 US 60/080077 PR 19-JUN-1998 US 60/080077 PR 19-JUN-1998 US 60/080078,19-JUN-1998 US 60/080078,19-JUN-1998 US 60/0800747 PR 19-JUN-1998 US 60/080078,19-JUN-1998 US 60/0800747 PR 19-JUN-1998 US 60/080074 PR 19-JUN-1998 US
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(Dases 1 to 10)

Roberts, B.L. and Shankara, S.

Preparation and use of superior vaccines
Patent: JP 2002534056-A 1342 15-OCT-2002;
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Preparation and use of superior vaccines
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88.9%; Pred. No. 2.5e+02;
ative 0; Mismatches 1;
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/organism="Homo sapiens"
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JP 2002534056-A/1342.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 88.9
Matches 8, Conservative
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TITLE
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Homo sapiens
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1 (bases 1 to 10)

Roberts, B.L. and Shankara, S.

Preparation and use of superior vaccines
Patent: JP 2002534056-A 1496 15-OCT-2002;

GENZYME CORP
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G01N37/00,
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C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15,
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60/080079 PR
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Location/Qualifiers
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CI2NIS/00,CI2NS/00,CI2NIS/00
Preparation and use of superior vaccines
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Preparation and use of superior vaccines.
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BD240078.1 GI:33049848
JP 2002534056-A/1496.
Homo sapiens (human)
Homo sapiens
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BRUCE L ROBERTS, SRINIVAS SHANKARA

C CL2N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
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(bases 1 to 10)

Roberts; B.L. and Shankara; S.

Preparation and use of superior vaccines
Patent: JP 2002534056-A 1419 15-OCT-2002;
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G01N37/00,
CC 212N15/00,C12NS/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key
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66/089079 PR
66/089991 PR
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Location/Qualifiers
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                                   Score 7.4; DB 1; Length 10;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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llarity 88.9%; Pred. No. 2.5e+02;
Conservative 0; Mismatches 1;
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    organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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JP 2002534056-A/1419
18-OCT-2002
18-UJN-1999 JP 2000554749
19-JUN-1998 US 60/09003
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                                      33.6%;
88.9%;
                 PR 19-001-1998 US 19-
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

RESULT 403 BD240001 LOCUS

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Gaps

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Best Loc Matches

RESULT 404 BD240078 LOCUS

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10 bp DNA linear PAT 28-JUL-1999 for efficient protein transcription in
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: C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,
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JP 1998229881-A/34
02-25E-1999
19-FEB-1997 JP 1997035338
KOBAYASHI MIKI, MAN TOMOKO, YUGAWA HIDEAKI
C12N15/09, C07H21/04, C12N1/21//C12N9/38, C12Q1/68, (C12N15/09,
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Location/Qualifiers
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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C C12N15/00,C12N5/00,C12N15/00
C Preparation and use of superior vaccines
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/organism="Corynebacterium glutamicum"
/mol_type="genomic DNA"
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C12R1:19),
C (C12N1/21,C12R1:13),(C12N9/38,C12R1:19);
C strandedness: Double;
C topology: Linear;
C hypothetical: No;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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88.9%;
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Brevibacterium flavum.
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1 (bases 1 to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1999 15-OCT-2002;
GENZYME CORP
                                                                                                                                                                                                                                                                                                                     PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/56, G01N37/00,
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60/089853
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Key Location/Qualifiers
                                                           60/090039,19-JUN-1998
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Homo sapiens (human)
JP 2002534056-A/1773
15-OCT-2002
18-JUN-1999 JP 2000554749
19-JUN-1998 US 60/090039
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18-JUN-1999 JP 2000554749
19-JUN-1998 US 60/09003
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JP 2002534056-A/1999
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Homo sapiens
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Best Local Similarity 88.9
Matches 8; Conservative
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PN 15-02025
PF 18-07N-1
PR 19-07N-1
PF 19-07N-1998 U
19-07N-1998 U
19-07N-1998 U
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19-07N-1998 U
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E Tashimoto, S., Matsushima, X. and Suzuki, T.
Genes with human dendritic cell expression
L Patent: UP 2000279181-A 245 10-OCT-2000;
SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 2000279181-A/245
PD 10-OCT-2000
PP 01-APR-1999 UP 1999095481
PR 01-APR-1999 UP 1999095481
PR SHINICHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI PC
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SHINCHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI PC
C12N1S/09,C07K14/475,C07K16/18,C12N1S/00
CC
FF Key
Location/Qualifiers
1. 10
/organism='Homo sapiens (human)'.
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    /organism='Homo sapiens (human)'.
Location/Qualifiers
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33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Sequence 135 from patent US 6472154.
AR241847.1 GI:27287659
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/organism="Homo sapiens"
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E39712
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NONE

OC Artificial sequences.
PN 19 199334380-4/6
PD 08-SEP-1998
PF 28-FEB-1997 JP 1997062104
PI SHEBATA YOSHIKAZU, TAKASHINA TOMONORI, SHINDO YOSHIO, PI
TAKAHASHI ISAMU
PC CLIZNIS/09,C07H21/04,C12Q1/68//C12N1/14,(C12N1S/09,C12R1:77),
PC CLIZNIS/09, C07H21/14,C12R1:77);
PC CLIZNIS/09, Linear;
PC CLIZNIS/09, Linear;
PC CLIZNIS/09, Linear;
PC FT SOURCE
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E39629 1 GI:18621720
E39629.1 GI:18621720
TP 2000279181-A/162.
Homo sapiens (human)
SM Homo sapiens (human)
SM Homo sapiens (human)
SM Homo sapiens (human)
L Chases 1 to 10)
Hashimoto, S., Matsushima, K. and Suzuki, T.
Genes with human dendritic cell expression
Patent JP 2000279181-A 162 10-OCT-2000;
SCIENCE & TECH AGENCY
OS HOMO sapiens (human)
PN JP 2000279181-A/162
PD 10-OCT-2000
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                                                                                                                                                                                                                                                                                       unidentified
unclassified.
1 (bases 1 to 10)
Shibata,Y., Takashina,T., Shindo,Y. and Takahashi,I.
NUCLEIC ACID SEQUENCE FOR DETECTING FUNGUS OF GENUS FUSARIUM
PATCHI: JP 199824380-A 6 08-SEP-1998;
SHINKINRUI KINOU KAIHATSU KENKYUSHO:KK
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                                                                                                                                                                         10 bp DNA linear
Fusarium sp. - specific sequence in 18S rRNA gene.
E17077
       Pred. No. 2.5e+02;
0; Mismatches 1; Indels

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       Best Local Similarity 88.9%;
Matches 8; Conservative (
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JP 1998234380-A/6.
unidentified
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Best Local Similarity 88.9°
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E17077/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                Todd,J.A., Twells,R.C., Hess,J.W., Hey,P., Hey,P., Caskey,C.T., Hammond,H. and Metzker,M.L.
Human sit4 associated proteins like (sapl) proteins and encoding genes; uses thereof
Patent: WO 0129213-4 61 26-APR-2001;
The Wellcome Trust Limited as Trustee to the Wellcome Trust (GB)
Merck & Co., Inc. (US)
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Patent: WO 0188577-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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        0; Mismatches
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/db_xref="taxon:9606"

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Sequence 61 from Patent WO0129213.
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AX119668.1 GI:14036562
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Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8; Conservative
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AX119668/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 (Dases 1 to 10)
Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
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Unknown.
Unclassified.
Unclassified.
I (bases Lto 10)
Garner, H.s. Wren, J.D., Minna, J.D. and Fondon, J.W. III.
Garner, H.s. Wren, J.B., Minna genes
Polymorphic repeats in human genes
Patent: US 6472154-A 135 29-OCT-2002;
Location/Qualifiers
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Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 36 08-APR-2003;
Location/Qualifiers
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The il-111 gene and polypeptide products
Patent: WO 0105974-A 34 25-JAN-2001;
Interleukin Genetics, Inc. (US)
Location/Qualifiers
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88.9%; Pred. No. 2.5e+02;
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Sequence 36 from patent US 6544736.
AR303311
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Sequence 34 from Patent WO0105974.
AX080422
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AR303311/c
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Schweitzer, M., Anderson, R., Fiechtner, M., Mueller-Ibeler, J., Raddatz, S., Bruecher, C., Windhab, N., Orwick, J., Schneider, E., Pignor, M. and Kienle, S. Sorting and immobilization system for nucleic acids using synthetic binding systems of 30008633. As 30-JAN-2003; Batent: WO 03008633. Nanogen Recognomics CmbH (DE) Location/Qualifiers
   Raddatz,S., Bruecher,C., windiago,..., Piggot,M. and Kienle,S.
Sorting and immobilization system for nucleic acids using synthetic binding systems
Dinding systems
Patent: WO 03008638-A SS 30-JAN-2003;
Nanogen Recognomics GmbH (DE)
Location/Qualifiers
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JP 2001069993-A/185.
Homo sapiens (human)
Homo sapiens (buratoa; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 10)
Matsushima, K., Hashimoto, S. and Suzuki, T.
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Bruecher, C., Windhab, N., Orwick, J., Schneider, E.,
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Similarity 88.9%; Pred. No. 2.5e+02;
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LPS activated human monocyte expressing genes.
BD007909
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1. .10
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/mol_type="unassigned DNA"
/db_xref="taxon:3260"
/noTe="Synthetic binding system"
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88.9%; Pred. No. 2.5e+02;
tive 0; Mismatches 1;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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Sequence 56 from Patent WO03008638.
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/note="pyranosyl RNA"
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synthetic construct
artificial sequences.
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Best Local Similarity 88.5%,
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                          PAT 22-JUN-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0185941-A 212 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
Location/Qualifiers
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33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Patent: WO 0138577-4 399 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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    .10
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    /mol_type="unassigned DNA"
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                            AX152484 10 bp 10 bx1152484 ax152484 1 GI:14534135

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Versteeg, R. and Caron, H.N.
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synthetic construct
artificial sequences.
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schultz1-727.rge

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OS Artificial Sequence

OS Artificial Sequence

PN JP 200131344-A/5

PD 14-AUG-2001

PF 27-JUL-1998 JP 2000504246

PR 25-JUL-1997 GB 9715823.2,10-DEC-1997 US 08/988476 PI

SMITH MARFIN DAMIEN, LATCHWAN DAVID SEYMAR

PC C12N15/00, A61K37/12

PC C12N15/00, A61K37/12

CC Description of Artificial Sequence: primer

FH Key

Location/Qualifiers

FT source

/organism='Artificial Sequence'.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces creatisiae (baker's yeast)
Saccharomyces creatisiae
Saccharomyces creatisiae
Bukaryota; Fungi; Ascomycotae, Saccharomycotina; Saccharomycetaes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
Charen to 10)
Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
Charencerization of the yeast transcriptome
Characterization of the yeast transcriptome
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Saccharomyces cerevisiae (yeast)
PD 10-UUL-2001
PP 22-JAN-1999 JP 1998532117
PR 23-JAN-1999 US 60/035317
PR 33-JAN-1999 US 60/035317
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/mol_type="genomic DNA"
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artificial sequences.

I (bases 1 to 10)
Damien, S.M. and Seymar, L.D.
Utilization of transcription factor Brn-3a Patent: JP 2001511344-A 5 14-AUG-2001;
NBUROVEX LTD
OS Artificial Sequence
PN JP 2001511344-A/5
PD 14-AUG-2001
                                                                                                                                                                                                                                                                                                                                    Characterization of the yeast transcriptome. BD065354
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    /organism="synthetic construct"

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JP 2001509017-A/290
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BD065085.1 GI:22610688
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces

Characterization of the yeast transcriptome
Datent: JP 2001509017-A 21 10-UL-2001;
THE ADMNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Saccharomyces cerevisiae (yeast)
DP 10-UL-2001
DP 0-UL-2001
DP 0-UL-2001
DP 0-UL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
5/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
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    .10
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J 2004

JeS activated human monocyte expressing genes Patent: JP 2001069993-A 185 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORPOSE Home sapiens (human)
OS Home sapiens (human)
PN JP 200106993-A/185
PD 21-MAR-2001
PP 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA, SHINT
C12N15/09, C07K14/47, Cn7
AG1P21/00.C
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FT FT
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33.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity
Matches 8; Conserv
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ACCESSION
VERSION
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BD065085
LOCUS
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TITLE
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SOURCE
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Eukaropta, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Eukaropta, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

1 (Jeases I to 10)

RS
1 (Jeases I to 10)

RS
Human activated Th1 and Th2 cell expression genes
AL Patent: JP 2002166482-A 240 02-UUL-2002,
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PP 2002166482-A 240
PP 19-DEC-2000
PP 20040186482-A/340
PP 19-DEC-2000 JP 2000385816
PI SHIGENORI NACALI, XOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
CI2NIS/09, COTK14/47, COTK16/18, CI2P21/08, CI2NIS/09, COTK14/47, COTK16/18, CIANIS/09, COTK14/47, COTK16/18, CIANIS/09, COTK14/47, COTK16/18, CIANIS/09, COTK14/47, COTK16/18, CIANIS/09, COTK16/47, COTK16/18, CIANIS/09, COTK16/18, CIANIS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
          Human
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                                                                                        /organism='Homo sapiens (human)'
Cl2N15/09,CO7K14/47,CO7K16/18,Cl2P21/08,Cl2N15/00 CC activated Thl and Th2 cell expression genes FH Key Location/Qualifiers 1..10 /organism='Homo sapiens (human)'
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Pred. No. 2.5e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                 Score 7.4; DB 1;
Pred. No. 2.5e+02;
0; Mismatches 1
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD161433.1 GI:27867191
JP 2002186482-A/255.
Homo sapiens (human)
Homo sapiens
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JP 2002186482-A/240.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 88.9%;
Matches 8, Conservative (
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Best Local Similarity 88.9%;
Matches 8; Conservative
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SOURCE
ORGANISM
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VERSION
KEYWORDS
SOURCE
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BD161433/c
LOCUS
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ACCESSION
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BD161418/c
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AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases I to 10)
Matsushima, K., Hashimoto, S., Suzuki, T. and Nagai, S.
Human matured/activated dendritic cell expression genes
Patent: JP 2001327293-A 241 27-NOV-2001;
DAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PD 27-NOV-2001
PD 27-NOV-2001
PP 22-NAY-2000 JP 2000150562
PP 22-NAY-2000 JP 2000150562
PP 22-NAY-2001 MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
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I (bases I to 10)
Nagai, S., Matsushima. K. and Hashimoto, S.
Human activated Th1 and Th2 cell expression genes
Patent: JP 2002186482-A 162 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS THOMO Sapiens (human)
PN JP 2002186482-A/162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
                                                                                                                                      Gaps
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19-DEC-2000 JP 2000385816
SHIGENORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
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                                                                                33.6%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 2.5e+02; Live 0; Mismatches 1; Indels
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BD161340.
BD161340.1 GI:27867098
UP 2002186482-A/162.
Homo sapiens (human)
File appleas (human)
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Pred. No. 2.5e+02;
0; Mismatches 1;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
        /mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 88.9%;
Matches 8; Conservative (
                                                        Query Match
Best Local Similarity 88.5.
Pest Local 8 Conservative
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DEFINITION
ACCESSION
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BD161340
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TITLE
JOURNAL
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AUTHORS
TITLE
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PAT 17-JAN-2003
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                                                                                                                                            unidentified
unidentified
unidentified
unclassified.

1 (bases it co. 10)
Matsushima.K., Hashimoto,S., Kaneko,S. and Yamashita,T.
Human liver disease-expressing genes
Human liver disease-expressing genes
A Homo sapiens (human)
PAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A312 30-JUL-2002;
DD 30-JUL-2002
PP 19-JAN-2001 JP 2001012328
PP 19-JAN-2001 JP 2001012328
PP 19-JAN-2001 JP 2001012328
PP GILSTIA PC CILETION COTKIA/47, COTKI6/18, GOIN33/50//CI2P21/08,
PC CI2P21/08,
PC CI2P21/08,
PC CI2P1/08,
PC CI2P1
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unclassified.
In (Dasses 1 to 10)

El (Dasses 1 to 10)

Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T. Human liver disease-expressing genes
Human liver disease-expressing genes
LD Patent: UP 2002209591-A389 30-JUL-2002,
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Home sapiens (human)
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PF 19-JAN-2001 JP 2001012328
PF 19-JAN-2001 JP 2001012328
PF 19-JAN-2001 JP 2001012328
PF C12N15/09, CO7K14/47, CO7K16/18, G01N33/15, G01N33/50//C12P21/0;
PC C12N15/09
CC Human liver disease-expressing genes
FF Source Lordanism='Home sapiens (human)'.
FT
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Location/Qualifiers
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                                   linear
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                             BD166767

Human liver disease-expressing genes.
BD166767

JBD166767

JP 2002209591-A/312
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

    .10
    /organism="unidentified"

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JP 2002209591-A/389.
unidentified
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Best Local Similarity 88.9°
Matches 8; Conservative
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BD166844/C
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Nagai,S., Matsushima,K. and Hashimoto,S.

Human activated Th1 and Th2 cell expression genes

Datent: JP 2002186482-A 255 02-JUL-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)

PD 02-JUL-2002

PF 19-DEC-2000 JP 2000385816

PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12NN5/09,CO7X14/47,CO7X16/418,C12P21/08,C12N15/00 CC
T12NN5/09,CO7X14/447,CO7X16/418,C12P21/08,C12N15/00 CC
T12NN5/09,CO7X14/4187,CO7X16/418,C12P21/08,C12N15/00 CC
T12NN5/09,CO7X14/4187,CO7X16/418,C12P21/08,C12N15/09

FT source 1...0

/organism='Homo sapiens (human)'.
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unclassified.
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E 1 (bassified.
S micushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
Human liver disease-expressing genes
L Patent: JP 2002209591-A 153 30-JUL-2002,
JARAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/153
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012228
PI 19-JAN-2001 JP 2001012228
PI SOLI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
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Key Location/Qualifiers
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Human liver disease-expressing genes.
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/db_xref="taxon:9606"

    .10
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/db_xref="taxon:32644"

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JP 2002209591-A/153.
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Best Local Similarity 88.5.
Local 8; Conservative
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PF 19-JA
PI 50-JA
PC C12N1
PC C12N1
PC C12N1
CC Human
FH Key
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BD166608
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PAT 05-DEC-1998
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Gullans, S.R., Kojima, R. and Randall, J.
Method for conducting sequential nucleic acid hybridization steps
Patent: US 5773213-A 6 30-UN-1998,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.6%; Score 7.4; DB 1; Length 11; Best Local Similarity 88.9%; Pred. No. 2.7e+02; Matches 8; Conservative 0; Mismatches 1; Indels
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    .11
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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Sequence 6 from patent US 5773213.
AR013805.1 GI:3971259
                            1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Sequence 4 from Patent WO9528500.
A46920
Location/Qualifiers
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/organism="unknown"
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Best Local Similarity 88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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ORGANISM
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AR013805/c
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TITLE
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FEATURES
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TITLE
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1 (Dases 1 to 10)

Murakami,Y., Hayashi,K., Hirohashi,S. and Sekiya,T.

Aberrations of the tumor suppressor p53 and retinoblastoma genes in human hepatocellular carcinomas

Cancer Res. 51 (20), 5520-5525 (1991)
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GenBank staff at the National Library of Medicine created this entry (NCBI glubbay 62713) from the original journal article.
This sequence comes from Fig. 3b.
Arg to Cys change at codon 110 exon 4.
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                                                                         Score 7.4; DB 1; Length 10;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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Joyce, G.F. and Breaker, R.R.
Braymatic DNA molecules
Enzymatic DNA molecules
FALTH SCRIPPS RESEARCH INSTITUTE
FALTH SCRIPPS RESEARCH INSTITUTE
FALTH JOYCE, A1 14 - MAY-2002;
FR J9-APR-1999 UP 1998547359
FR 29-APR-1999 US 60/04528
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p53 (human, hepatocellular carcinoma,
862713
862713.1 GI:236756

    .10
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/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                         10 bp
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BD191628.1 GI:33001367
JP 2002514080-A/41.
unidentified
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic DNA molecules
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Key
                                                                            Query Match 33.6%;
Best Local Similarity 88.9%;
Matches 8; Conservative
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PAT 20-JUN-2002
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Pouchier,R.Adrianus. and Schuitemaker,J.
Fouchier,R.Adrianus. and Schuitemaker,J.
Nucleic acids and methods for the discrimination between syncytium inducing and non syncytium inducing variants of the human immunodeficiency virus
Patent: US 6379881-A 4 30-APR-2002;
Location/Qualifiers
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88.9%; Pred. No. 2.7e+02;
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Unclassified.
1 (bases 1 to 11)
Heber-Katz,E.
Compositions and methods for wound healing
Patent: US 6538173-A 86 25-MAR-2003;
Location/Qualifiers
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Thompson, J.D. and Draper, K.G.
ErbB2/neu targeted ribozymes
Patent: US 5599704-A 92 04-FEB-1997;
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 86 from patent US 6538173.
AR301505 AR301505.1 GI:31689307
                                                                       /organism="unknown"
/wol_type="unassigned DNA"
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Sequence 4 from patent US 6379881.
AR207570
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/organism="unknown"
/mol_type="genomic DNA"
                                           Location/Qualifiers
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Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8, Conservative
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AR301505
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1 (bases 1 to 11)

1 (bases 1 to ten)

Non-nucleoside linkers for convenient attachment of labels to oligomucleotides using standard synthetic methods

Patent: US 541407-A 3 09-MAY-1995;

Location/Qualifiers
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Unclassified.
1 (bases 1 to 11)
Sampath,K.T.
Methods and compositions for identifying morphogen analogs
Patent: US 6103491-A 8 15-AUG-2000;
Location/Qualifiers
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Sequence 92 from patent US 5599704.
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/wol_type="unassigned DNA"
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Sequence 8 from patent US 6103491.
AR106012
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1 (bases 1 to 11)
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    734 AGAAACAGA 742
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Wojnowski,L. and Eiselt,R.
Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in diagnostic and therapeutic applications
Patent: WO 0120025-A 71 22-MAR-2001;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in diagnostic and therapeutic applications
Patent: WO 0120025-A 76 22-MAR-2001;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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33.6%; Score 7.4; DB 1;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1;
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="artificial"
                                 1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="artificial"
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1.
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/noTe="artificial"
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Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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Heber-Katz, B.
Compositions and methods for wound healing
Patent: US 65381/3-A 124 25-MAR-2003;
Location/Qualifiers
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Anthraquinone-derivatives oligonucleotides
Patent: US 5214136-A 10 25-MAY-1993;
Location/Qualifiers
                                                          Sequence 124 from patent US 6538173. AR301543. GI:31689345
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Sequence 70 from Patent WO0120025.
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/organism="unknown"
/wol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                         /organism="unknown"
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synthetic construct
artificial sequences.
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Best Local Similarity 88.5.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 51 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Sequence 110 from Patent WO02053773.
AX470533
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Sequence 51 from Patent WO02053773.
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 Sequence 66 from Patent WO0210217.
                                AX393136.1 GI:19701186
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88.9%;
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Polymorphisms in the human cyp3a4 and cyp3a7 genes and their use in diagnostic and therapeutic applications
Patent: WO 120025-A 77 22-MAR-2001;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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Pred. No. 2.7e+02;
0; Mismatches 1; Indels
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Therapeutically useful synthetic oligonucleotides
Patent: Wo 0144465-A 82 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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/db xref="taxon:32630"
/noTe="artificial"

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/organism="synthetic construct"

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AX175318/c
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AX098770
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02033773-A 538 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 0205773-A 335 11-JUL-2002;
HENKEL KGAA (DE)
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1;
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Sequence 626 from Patent WO02053773.
AX471049
                                                                                                                                Sequence 335 from Patent WO02053773. AX470758

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                730 CAGGAGAAA 738
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining skin strees or skin ageing in vitro
Patent: WO 0203773-A 284 11-JUL-2002;
HENKEL KGAA (DE)
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 285 11-JUL-2002;
HENKEL KGAA (DE)
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Patent: WO 02053773-A 110 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                              Sequence 284 from Patent W002053773. AX470707

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Homo sapiens
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Homo sapiens
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1280 11-UUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Bethod for determining skin stress or skin ageing in vitro
Patent: WO (18) 1118 11-JUL-2002;
HENKEL KGAA (18)
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                                                                                                               Query Match 33.6%; Score 7.4; DB 1; Length 11; Best Local Similarity 88.9%; Pred. No. 2.76+02; Matches 8; Conservative 0; Mismatches 1; Indels
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/mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02033773-A 681 11-JUL-2002;
HENKEL KGAA (DE)
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Sequence 662 from Patent WO02053773.
AX471085
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                Hustert, E., Haberl, M. and Wojnowski, L.
Identification of the genetic determinants of the polymorphic cypals expression
Patent: WO 20283775-A 77 11-JUL-2002;
BPIDAUROS BIOTECHNOLOGIE AG (DE)
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88.9%; Pred. No. 2.7e+02;
tive 0; Mismatches 1; Indels
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Cloning vectors and method for molecular cloning
Patent: WO 02070720-A 37 12-SEP-2002;
Riken (JP)
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Method for determining homeostasis of the skin
Patent: WO 0205374.4A 90 11-UTL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Sequence 90 from Patent WO02053774.
AX623049.1 GI:28450990
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Sequence 37 from Patent WO02070720.
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artificial sequences.
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Homo sapiens (human)
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Best Local Similarity 88.9
Matches 8; Conservative
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                    Homo sapiens
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AX555201
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1286 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1320 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Sequence 1320 from Patent W002053773.
AX471743
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Sequence 1286 from Patent W002053773.
AX471709
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Sequence 77 from Patent WO02053775.
AX472086.1 GI:22207127

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Homo sapiens
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Matches 8; Conservative
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CAGGACACC 11
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AX471709/c
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Perant: WO 02053774-A 421 11-UUL-2002,
Henkel Kommanditgeseljschaft auf Aktien (DE)
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Sequence 592 from Patent WO02053774.
AX623551.1 GI:28451492
                                                                                      11 bp DN Sequence 421 from Patent W002053774.
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Sequence 559 from Patent WO02053774.
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AX623518.1 GI:28451459
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Best Local Similarity 88.9
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AX623551/c
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AX623518/c
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AX623380/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                    Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 372 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 147 from Patent WO02053774.
AX623106
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Sequence 372 from Patent WO02053774.
AX623331
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Petersohn,D., Conradt,M. and Hofmann,K.
Pethod for determining homeostasis of the skin
Patent: WO 02053774-A 887 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1;
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/db_xref="taxon:9606"
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AX623862.1 GI:28451803
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
        Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 2023774-4 680 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                             Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 592 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 680 from Patent WO02053774.
AX623639
AX623639.1 GI:28451580
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                            11 bp DN Sequence 1850 from Patent WO02053774.
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Sequence 1880 from Patent WO02053774.
AX624839
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                                                                        AX624809.1 GI:28452750
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
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AX625167
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RESULT 473
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 2208 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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                    linear PAT 21-FEB-2003
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Memo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 2937 from Patent WO02053774.
AX625896
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            Sequence 2712 from Patent W002053774. AX625671

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Homo sapiens
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AX625851/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 2546 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 2537 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 2537 from Patent W002053774.
AX625496
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Sequence 2546 from Patent W002053774.
AX625505
AX625505.1 GI:28453446
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88.9%;
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Homo sapiens
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Matches 8; Conservative
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Matches 8, Conservative
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AX625496
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Petent: WO 0205374-A 3494 11-JUL-2002;
Henkel Kommanditgeseljschaft auf Aktien (DE)
Pred. No. 2.7e+02;
0; Mismatches 1
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    .11
    /organism="Homo sapiens"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Petersohn,D., Conradt,M. and Hofmann,K. Method for determining homeostasis of the skin Patent: WO 2023/174. A 2937 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Sequence 2987 from Patent W002053774.
AX625946
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    11. (or sapiens")
    /organism="Homo sapiens"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    Patent: WO 02053774-A 3784 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1;
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33.6%; Score 7.4; DB 1;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1;
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Sequence 3822 from Patent W002053774.
AX626781
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Sequence 3843 from Patent W002053774.
AX626802
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Method for determining homeostasis of the skin
Patent: WO 0203774-A 3560 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
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  Seguence 3560 from Patent W002053774, AX626519
AX626519.1 GI:28454557

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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88.9%; Pred. No. 2.7e+02;
ative 0; Mismatches 1.
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Sequence 4242 from Patent W002053774.
AX627201
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 AX626901.1 GI:28454939
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 3942 from Patent WO02053774.
AX626901
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11 bp DNA
Sequence 5043 from Patent W002053774.
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AX627881/c
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AX628002/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 4625 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 4554 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 4554 from Patent W002053774.
AX627513 GI:28455551
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Sequence 4625 from Patent WO02053774.
AX627584
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Homo sapiens
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REFERENCE AUTHORS TITLE JOURNAL

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RESULT 497

AX627513

AX627584/c LOCUS RESULT 498

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linear PAT 21-FEB-2003 PAT 21-FEB-2003 linear PAT 21-FEB-2003 Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. . 0 . Query Match
33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.76+02;
Matches 8; Conservative 0; Mismatches 1; Indels Length 11; linear Query Match 33.6%; Score 7.4; DB 1; Length 11 Best Local Similarity 88.9%; Pred. No. 2.7e+02; Matches 8; Conservative 0; Mismatches 1; Indels Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 0203774-A 4922 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5043 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                       33.6%; Score 7.4; DB 1; ilarity 88.9%; Pred. No. 2.7e+02; Conservative 0; Mismatches 1
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Sequence 5324 from Patent WO02053774.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                            Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5086 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Sequence 5313 from Patent WO02053774.
AX628272
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   Homo sapiens (human)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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33.6%; Score 7.4; DB 1; Length 11
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                  Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 5423 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 5437 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 5458 from Patent WO02053774.
AX628417
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Sequence 5437 from Patent WO02053774.
AX628396
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 0203774-A 5398 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 5402 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
                                                                      AX628357 11 bp DNA Sequence 5398 from Patent WO02053774.
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Sequence 5402 from Patent WO02053774.
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AX628382
AX628382.1 GI:28456420

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                              Sequence 5868 from Patent W002053774.
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Sequence 5901 from Patent WO02053774.
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Sequence 5882 from Patent WO02053774.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Method for determining homeostasis of the skin
Patent: WO 0203774-A 5580 11-JUL-2002;
Henkel Kommanditgesellschaft auf Äktien (DE)
Location/Qualifiers
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Sequence 5580 from Patent WO02053774.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ax629180 GI:28457218

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AX629180
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AX629375
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Matches 8; Conservative 0; Mismatches 1; Indels
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Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 5901 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 6111 11-UUL-2002;
Henkel Kommanditgesellschäft auf Aktien (DE)
Location/Qualifiers
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Sequence 6111 from Patent WO02053774.
AX629070
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/db_xref="taxon:9606"

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    forganism="Homo sapiens"
|mol_type="unassigned DNA"
|db_xref="taxon:9606"

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Sequence 7237 from Patent W0020533774.
AX630196
AX629412
Seguence 6453 from Patent WO02053774.
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AX630470/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-4 7511 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Petent: WO 0205374-A 7568 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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AX630752.1 GI:28458790
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AX630527.1 GI:28458565
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                     Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 8013 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 8237 from Patent W002053774.
AX631195.1 GI:28459239
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/db_xref="taxon:9606"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                GI:28459014
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Homo sapiens
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AX631060/c
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                      Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 7842 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 7980 from Patent WO02053774.
AX630939
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/organism="Homo sapiens"
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GAG 735 GAG 1	AX632230 Sequence 9272 from Patent W002053774. AX632230 AX63230.1 GI:28467845 Homo sapiens (human) Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel	Primates; It, M. and F. Ing homeost A 9272 11- allschaft allfiers Homo sapie 'unassignec	33.6%; Score 7.4; DB 1; Length 11; Conservative 0; Mismatches 1; Indels 0; ACAGAA 743 GCAGAA 10	AX632260 Sequence 9302 from Patent W002053774. Sequence 9302 from Patent W002053774. AX632260. AX632260.1 GI:28467875 Homo sapiens (human) Homo sapiens Ebuaryota; Metazoa; Chordata; Craniata; Verrebrata; Eurel	tt,M. and H. and	33.6%; Score 7.4; DB 1; Length 11; Conservative 0; Mismatches 1; Indels 0; AAACAG 741	11 bp DNA linear PAT 2 9630 from Patent WO02053774. .1 GI:28468203
Oy 727 TGCCAGAG Db 9 TTCCAGGAG RESULT 532	AX632230 LOCUS LOCUS DEFINITION Sequence 9273 ACCESSION AX632230 VERSION AX632230.1 KEYWORDS SOURCE Homo sapiens ORGANISM Homo sapiens ORGANISM Homo sapiens	REFERENCE Mammai: AUTHORS Peters TITLE Method JOURNAL Patent FEATURES SOURCE	Query Match Best Local Similarity Matches Qy 735 GAACAGAA Db 2 GAAGCAGAA	RESULT 533 AX632260 LOCUS DEFINITION SEQUENCE 9300 ACCESSION AX632260 VERSION AX632260 VERSION AX632260.1 KEYWORDS SOURCE Homo sapiens ORGANISM FORMS AND SAPIENS	REFERENCE I AUTHORS Petersc TITLE Method JOURNAL Patent FEATURES Henkell	fatch ccal Simi s 8; 733 GAG 1 GGG	AX632588 LOCUS AX632588 DETINITION Sequence 96 ACCESSION AX632588 VERSION AX632586.1
Henkel Kommanditgesellschaft auf Aktien (DE) FEATURES Location/Qualifiers 1. :1 source /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 33.6%; Score 7.4; DB 1; Length 11; Best Local Similarity 88.9%; Pred. No. 2.7e+02; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 739 CAGAACACC 747 Db 11 CAGCACACC 3	AX631267 AX631267 AX631267 LOCUS AX631267 ACCESSION AX631267 VERSION AX631267 ACCESSION AX631267 VERSION AX631267 A	kin)	/db_xref="taxon:9506" Query Match	RESULT 531 AX631283/c LOCUS AX631283	REPERENCE 1 AUTHORS Petersohn, D., Conradt, M., and Hofmann, K. AUTHORS Petersohn, D., Conradt, M., and Hofmann, K. TITLE Method for determining homeostasis of the skin JOURNAL Patent: WO 02053774-A 32.5 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) FEATURES Location/Qualifiers Location/Qualifiers //organism="Homo sapiens" //db xref="Ftaxon:9606"	Query Match 33.6%; Score 7.4; DB 1; Length 11; Best Local Similarity 88.9%; Pred. No. 2.7e+02; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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schultz1-727.rge

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BD095115
A polynucleotide encoding mouse histidine decarboxylase.
BD095115
BD095115.1 GI:22640703
WO 812892-A/8.
Mus sp.
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DP 2002503460-A/86.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 11)
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Occu, H.

A polynucleotide encoding mouse histidine decarboxylase
Patent: WO 012892-A 8 10-MAY-2001,
JAPAN SCIENCE AND TECHNOLOGY CORP, HIROSHI OTSU
OS Mus sp. (mouse)
PN WO 012892-A/8
PD 10-MAY-2001
PF 01-NOY-2000 WO 2000JP007689
PF 02-NOY-1999 JP 99P 312559,23-MAR-2000 JP 00P 08
HIROSHI OTSU
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Patent: JP 2002503460-A 86 05-FEB-2002;
THE MSTAR INSTITUTE
OS MUS musculus (mouse)
                                                                                                                            Query Match 33.6%; Score 7.4; DB 1; Best Local Similarity 88.9%; Pred. No. 2.7e+02; Matches 8; Conservative 0; Mismatches 1.

    .11
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/db_xref="taxon:9606"

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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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33.6%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Method for determining homeostasis of the skin
Patent: WO 2023/774-4, 9819 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                      Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 9630 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Sequence 9687 from Patent WO02053774.
AX632645
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

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                      Homo sapiens (human)
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PN JP 2002503460-A/86
PD 05-FEB-2002
PP 12-FEB-1999 JP 2000531545
PR 13-FEB-1999 US 60/074737,26-AUG-1999 US 60/097937 PR 28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC CI2NIS/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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/organism='Mus musculus (mouse)'.
Location/Qualifiers
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Location/Qualifiers
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Datent JP 2002503460-A 124 05-FEB-2002;
THE WISTAR INSTITUTE
OS Mus musculus (mouse)
PD 5202503460-A/124
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US
28-SEP-1998 US 60/102051
PR ELLEN HEBER KATZ
PC C12N15/09,A01K67/027.C12N5/10 C1201/co C12017.
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RESULT 540 AJ601274

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Dates 1 to 11)

Educated Submission

Loudited (13-007-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Submitted (23-007-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evy cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
AJ601274 11 bp DNA linear PLN 23-OCT-2003
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
524112 AJ601274
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                                                                                                                                                                                                                                                                                                                                  Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chavin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Cabocche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)
22363335
                                                                                                              AJ601274.1 GI:37950902
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryora, Viridiplantaes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, eudicotyledons, core eudicots, resids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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artificial sequences.

1 (bases 1 to 8)
Schwarz, and Reeve M.A.
Sequencing by hybridisation
Schwarz Tener (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN
(GB)
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/cultivar="Wassillewskija"

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    /note="T-DNA flanking sequence"

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Sequence 11 from Patent W09947706.
AX017048
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Nielsen, P.E. and Good, L.
Antibiotic-free bacterial strain selection with antisense molecules
Patent: WO 02079467-A 3 10-0CT-2002;
Koebenhavns Univesitet (DK)
Location/Qualifiers
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                                                                                                                                                                                                                     synthetic construct
synthetic construct
synthetic activate
synthetic construct
1 (bases 1 to 8)
Schwarz,T. and Reeve,M.A.
Sequencing by hybridisation
Patent: WO 9947706-A 50 23-SEP-1999;
SCHWARZ TEREK (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN (GB)
                                                                                                                                                                                                                                                                                                                                                                                    1. .8
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/note="Fluorescently labelled capture oligonucleotide"
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                                                                                                                                          linear
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/organism="synthetic construct"
/mol_type="genomic DNA"
/mol_type="taxon:32630"
/note="Peptide nucleic acid no. 1832"
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Sequence 32 from Patent WO02079467.
AX573622
AX573622.1 GI:27551292
 0; Mismatches
                                                                                                                                     8 bp
Sequence 50 from Patent WO9947706.
AX017087
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synthetic construct
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 7; Conservative
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synthetic construct
artificial sequences.
1 thases 1 to 8)
5 chwarz, T. and Reeve, M.A.
Sequencing by hybridisation
Schwarz, Terek (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN (GB)
                                                                                                                                                                                                                                                                                                                                                  synthetic construct
artificial sequences.
I (bases 1 to 8)
Schwarz, T. and Reeve, M.A.
Sequencing by hybridisation
Batent: WO 9947706-A 12 23-SEP-1999;
SCHWARZ TEREK (GB); NYCOMED AMERSHAM PLC (GB); REEVE MICHAEL ALAN (GB)
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/organism="synthetic construct"
/organism="synthetic construct"
/mol_type="genomic DNA"
/mol_taxon:31630"
/note="Fluorescently labelled capture oligonucleotide"
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/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="HbA specific oligonucleotides"
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Sequence 12 from Patent W09947706.
AX017049
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8 bp

Sequence 49 from Patent W09947706.

AX017086.1 GI:10042052
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Location/Qualifiers
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JP 2002509701-A/49
02-APR-2009
02-APR-2009
19-MAR-1999 JP 2000536888
19-MAR-1998 GB 9805918.1
MICHAEL ALAN REEVE TRERK SCHWARZ
MICHAEL ALAN REVEY TRERK SCHWARZ
DIOJ/68, CLIVILS/O9 CLIVILS/O0
Description of Artificial Sequence:FLUORESCENTLY LABELLED
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Location/Qualifiers
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artificial sequences.

I (bases 1 to 8)
Reeve,M.A. and Schwarz,T.
Sequence determination by hybridization
Patent: JP 2002509701-A 50 02-APR-2002;
NYCOMED AMERSHAM PLC
OS Artificial Sequence
PN JP 2002509701-A/50
PD 02-APR-2002
PF 19-MAR-1999 JP 2000536888
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/organism="synthetic construct"
/mol type="genomic DNA"
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/db_xref="taxon:32630"
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JP 2002509701-A/50.
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BD217871
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S BD21783.2
S BD21783.1 GI:33027602
S Synthetic construct
ISM Synthetic construct
artificial sequences.

IS (base 1 to 8)
S Reeve, M.A. and Schwarz, T.
Sequence decrmination by hybridization
AL Patent: JP 2002509701-A 11 02-APR-2002;
NYCOMED AMERSTAM PLC
OS Artificial Sequence
PN JP 2002509701-A 11 02-APR-2002;
NYCOMED AMERSTAM PLC
OS ARTIFICIAL Sequence
PN JP 2002509701-A 11 02-APR-2002;
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PN 02-APR-2002

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PF 19-MAR-1999 UP 2000536888

PR 19-MAR-1999 GB 9805918.1

PI MCHAEL ALAN REEVE, TEREK SCHWARZ

PC C12Q1/68,C12N15/09,C12N15/09

CC Description of Artificial Sequence:HDS SPECIFIC CC

OLIGONUCLEOTIDE

FH Key Location/Qualifiers

FT source / Organism='Artificial Sequence'.
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/organism='Artificial Sequence'.
Location/Qualifiers
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synthetic construct
artificial sequences.

I (bases 1 to 8)
Reeve, M.A. and Schwarz, T.
Sequence determination by hybridization
Parent: JP 2002509701-A 12 02-APR-2002;
NYCOMED AMERSHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="synthetic construct"
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                                                  BD217832 8 bp DNA Sequence determination by hybridization. BD217832
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JP 2002509701-A/12.
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Best Local Similarity 100.
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RESULT 546
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                                                                                        /note="A lysine residue is linked to COOH-terminal of the PNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human-parathyroid hormone (human-PTH) producing hybrid vectors, human-parathyroid hormone gene, eucaryotic cells containing the hybrid vector and their use Patent: EP 0139076-A 15 02-MAY-1985, Gesellschaft (fuer Biotechnologische Forschung mbH (GBF) Location/Qualifiers

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Nucleotide sequence 15 from patent number EP0139076.
A06372.1 GI:411246
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/mol type="genomic DNA"
/db xref="taxon:32630"
/noTe="Peptide nucleic acid no. 1876"
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Method for identifying metastatic sequences
Patent: US 5783182-A 19 21.JUL-1998;
Location/Qualifiers
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AR018737.1 GI:3973851
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/organism="unknown"
/mol_type="unassigned DNA"
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artificial sequences.
1 (bases 1 to 10)
Mayer, H.
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Unclassified.
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Antibiotic-free bacterial strain selection with antisense molecules
Patent: Wo 02079467-A 31 10-OCT-2002;
Koebenharns Univesttet (DK)
Location/Qualifiers
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidee; Homo.
19-WAR-1998 GB 9805918.1
MICHAEL ALAN REEVE, TEREK SCHWARZ
C12Q1/68,C12N15/09,C12N15/00
Description of Artificial Sequence:FLUORESCENTLY LABELLED
CAPTURE
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Location/Qualifiers
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Alpha-2 adrenergic receptor polymorphisms
Patent: Wo 0.179561-A 5.25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Seguence 31 from Patent W002079467.
AX573621
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Sequence 5 from Patent WO0179561.
AX350493
AX350493.1 GI:18616095
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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19-UUN-1998 US 60/080921,19-UUN-1998 US 60/080853 PR 19-UUN-1998 US 60/080927,19-UUN-1998 US 60/080923 PR 60/080927,19-UUN-1998 US 60/080923 PR 60/080927,19-UUN-1998 US 60/080923 PR 60/080923 PR 19-UUN-1998 US 60/080923 PR 60/080929 PR 60/
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Cl2N1/21,Cl2N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,Cl2N5/00,Cl2N5/00,Cl2N15/00
Cl2N15/00,Cl2N5/00,Cl2N5/00,Cl2N5/00
C Preparation and use of superior vaccines
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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Preparation and use of superior vaccines.
BD238923
1 (bases 1 to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 216 15-OCT-2002,
GENZYME CORP
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/organism="Homo sapiens"
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                                                                                                                                                    Homo sapiens (human)
JP 2002534056-A/216
15-CCT-2002
18-JUN-1999 JP 2000554749
19-JUN-1998 US 60/090039
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JP 2002534056-A/341.
Homo sapiens (human)
Homo sapiens
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Lope-Nieto, C.Eduardo. and Nigam, S.Kumar.
Lopes-Shieto, C.Eduardo. and Nigam, S.Kumar.
Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis
Patent: US 6110667-A 13 29-AUG-2000;
Location/Qualifiers
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BD238798 10-JUL-200 BD238798.1 GI:33048568
JP 2002534056-A/216.
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens Subtazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hedgperth, J. Affonina, I.A., Kutyavin, I.V., Lukhtanov, E.A.,
Hedgperth, J. Affonina, I.A., Kutyavin, I.V., Lukhtanov, E.A.,
Belousov, E.S. and Meyer, R.B. Jr.
Hybridization and mismatch discrimination using oligonucleotides
conjugated to minor groove binders
conjugated to minor groove binders
Patent: US 6312894-A 3 06-NOV-2001;
Location/Qualifiers
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                                                                                                                                                                  Sequence 13 from patent US 6110667.
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/organism="unknown"
/mol_type="unassigned DNA"
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    .10
    /organism="unknown"
    /mol_type="unassigned DNA"

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       4 TGCCAGG 10
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AR176672
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FEATURES
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
2 (bases 1 to 10)
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4 (bases 1 to 10)
5 (bases 1 to 10)
6 (bases 1 to 10)
7 (bases 1 to 10)
8 (bases 1 to
                                        PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/56, G01N37/00, G01N37/00, C12N15/00, C12N15/00, C12N15/00, C12N5/00, C12N5
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C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15,
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1. .10
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/organism="Homo sapiens"
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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No. 2.9e+02;
0; Indels
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N JP 200234056-A/688

D 15-C72002

T 8-UUN-1998 US 60/090039,19-UUN-1998 US 60/08999, 19-UUN-1998 US 60/090078, 19-UUN-1998 US
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100.0%; Pred. No. 2.9
tive 0; Mismatches

    .10
    /organism="Homo sapiens"
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 7; Conservative
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PN 15-072534(PD 15-072534(PD 15-072534(PD 15-072534(PD 15-0725))
PR 19-070-1998 US 1
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CC CLONI,71, C1, C12NS/10, G01N33/15, G01N33/50, G01N33/53, G01N33/56,
G01N37/00,
CC T2N1S/00, C12NS/00, C12N1S/00
CC Preparation and use of superior vaccines
FH Key
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C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15,
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Pred. No. 2.9e+02;
0; Mismatches 0; Indels
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Preparation and use of superior vaccines.
BD238950
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JP 2002534056-A/368
15-OCT-2002
18-JUN-1999 UP 2000554749
19-JUN-1998 US 60/09003
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100.0%; Pred
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JP 2002534056-A/368.
Homo sapiens (human)
Homo sapiens
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Matches 7; Conservative
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BD238950/c
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G01N37/00,
C12N15/00, C12N5/00, C12N15/00
C12N15/00, C12N5/00, C12N15/00, C12N15/
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C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
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1 (bases 1 to 10)
Proberts, B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1299 15-OCT-2002;
GENZYME CORP
                                                                                                                                                           Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 10)

Roberts; B.L. and Shankara, S.

Preparation and use of superior vaccines
Patent: JP 2002534056-A 917 15-OCT-2002;
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60/0890973
60/0899991
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Location/Qualifiers
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/db_xref="taxon:9606"
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5. 2.9e+02;
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60/089997,19-UN-1998 US
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60/089999,19-UN-1998 US
60/090004,19-UN-1998 US
60/090044,19-UN-1998 US
60/090044,19-UN-1998 US
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Preparation and use of superior vaccines.
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Preparation and use of superior vaccines.
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Best Local Similarity 100.0%; Pred. No. 2.9
Matches 7; Conservative 0; Mismatches
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JP 2002534056-A/917
15-OCT-2002
18-JUN-1999 JP 2000554749
19-JUN-1998 US 60/090039
                                                      BD239499.1 GI:33049269
JP 2002534056-A/917.
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JP 2002534056-A/1299.
Homo sapiens (human)
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Homo sapiens
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BD239881
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C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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                              31.8%; Score 7; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels
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Preparation and use of superior vaccines
Key
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60/080997, 19-UUN-1998 US
60/080992, 19-UUN-1998 US
60/080801 19-UUN-1998 US
60/080801 19-UUN-1998 US
60/090000, 19-UUN-1998 US
60/090004, 19-UUN-1998 US
60/090008, 19-UUN-1998 US
60/0900078, 19-UUN-1998 US
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Best Local Similarity 100.0%; Pred. No. 2.9
Matches 7; Conservative 0; Mismatches
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JP 2002534056-A/754
15-0CT-2002
18-JUN-1999 UP 2000554749
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Homo sapiens
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19-UUN-1998 US 60/090044,19-UUN-1998 US 60/089844 PR
19-UUN-1998 US 60/080080,19-UUN-1998 US 60/089833 PR
19-UUN-1998 US 60/08994,19-UUN-1998 US 60/080017 PR
19-UUN-1998 US 60/080994,19-UUN-1998 US 60/090047 PR
19-UUN-1998 US 60/080078,19-UUN-1998 US 60/090045 PR
19-UUN-1998 US 60/080076,19-UUN-1998 US 60/080045 PR
06-UEC-1998 US 60/111718 SHANKARA
PC CLN15/09,CL2N15/09,A61K39/00,A61P35/00,A61P37/04,CL2N1/15, PC
CLN15/09,CL2N15/09,A61K39/00,A61P35/00,A61P37/04,CL2N1/15, PC
CLN1721,CL2N15/00,A61P35/00,A61P37/04,CL2N1/15, PC
GO1N37/00,
PC CLN15/00,CL2N5/00,CL2N15/00
PC Preparation and use of superior vaccines
PC PREPARATION TO LOCATION/QUALIFIERS /organism='Homo sapiens (human)'. Location/Qualifiers DB 1; Length 10; 2.9e+02; Query Match 31.8%; Score 7; DB 1 Best Local Similarity 100.0%; Pred. No. 2.5 Matches 7; Conservative 0; Mismatches 1. .10 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" 733 GAGAAAC 739 7 GAGAAAC 1 source FEEGE DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM source RESULT 564 BD240042/c LOCUS REFERENCE AUTHORS TITLE JOURNAL FEATURES COMMENT 8 à OS Homo sapiens (human)
PN JP 2002534056-A/1299
PD 15-CCT--2009
PP 19-CCT--209
PP 19-DUN-1999 US 60/090039,19-UUN-1999 US 60/090040 PR 19-UUN-1999 US 60/090031,19-UUN-1999 US 60/089993 PR 19-UUN-1999 US 60/089993 PR 19-UUN-1999 US 60/089993 PR 60/089999 US 60/089993 PR 19-UUN-1999 US 60/089999 US 60/089999 PR 19-UUN-1999 US 60/089999 US 60/089999 PR 60/089999 US 60/089999 US 60/089999 PR 19-UUN-1999 US 60/089999 US 60/08999 US 60/089999 US 60/08999 US 60/089 BD23958.1 GI:33049728
BD23958.1 GI:33049728
FOODS34056-A/1376.
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (basis 1 to 10)
Foperts; L. and Shankara; S.
Roberts; B.L. and Shankara; S.
Roberts; B.L. and Shankara; S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1376 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1376
PP 19-UN-1999 US 60/09003199 US 60/089853 PR 19-UW-1998 US 60/090041,19-UW-1998 US 60/090041,19-UW-1998 US 60/090041,19-UW-1998 US 60/090041 PR 19-UW-1998 US 60/090041,19-UW-1998 US 60/090041 PR 19-UW-1998 US 60/090042,19-UW-1998 US 60/090041 PR 19-UW-1998 US 60/090042 PR 19-UW-1998 US 60/090041 PR 19-UW-190041 PR 19-UW-190041 PR 19 PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC G01N37/00, C12N15/00, C12N15/00, C12N15/00, C12N15/00, C12N15/00 and use of superior vaccines

EN Key Location/Qualifiers ö Gaps .. 0 ce 1.10 / Organism='Homo sapiens (human)'.
Location/Qualifiers
1.10 / Organism="Homo sapiens"
/ organism="Homo sapiens"
/ db_xref="taxon:9606" Query Match
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RESULT 563 BD239958/c

TION Preparation and use of superior vaccines.

BD440042.1 GI:33049812

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BD540042.1 GI:33049812

Homo sapiens (human)

SISM Homo sapiens (human)

Ammalia; Hominidae; Homo.

(CE 1 (bases 1 to 10)

RS Roberts, B.L. and Shankara, S.

Preparation and use of superior vaccines

AL Patent: JP 2002534056-A 1460 15-OCT-2002;

GENERAL CORP PAT 17-JUL-2003 Γ PC PI BRUCE L ROBERTS, SRINIVAS SHANKARA PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, C12N1/19, PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, G01N37/00, PC C12N15/00,C12N3/00,C12N15/00 60/090040 60/08983 PR 60/089019 PR 60/089091 PR 60/089991 PR 60/089991 PR 60/089991 PR 60/089991 PR 60/089991 PR 60/08991 PR 60/08991 PR 60/08991 PR 60/08991 PR 60/08991 PR 60/111715 Homo sapien The 20025346 PR 15-000-1999 PR 19-000-1999 19-000-1998 US 19-000-1998 US

742 AACACCG 748

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Location/Qualifiers

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19-UN-1998 US 60/090041,19-UN-1998 US 60/089853 PR 19-UN-1998 US 60/08097,19-UN-1998 US 60/08097,19-UN-1998 US 60/08097 PR 60/08097 PR 60/08097 PR 60/08097 PR 60/08097 PR 60/08097 PR 19-UN-1998 US 60/08004 PR 60/08004 PR 19-UN-1998 US 60/08004 PR 60/08094 PR 60/08004 PR 60/08004 PR 60/08004 PR 60/08004 PR 60/08094 PR 60/
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G01N37/00,
C12N1S/00,C12NS/00,C12N1S/00
Preparation and use of superior vaccines
Key Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases I to 10)
3 Acberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1744 15-CCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1744
PD 11--CCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040
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Location/Qualifiers
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                                                                                                                                        10 bp DNA Preparation and use of superior vaccines.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                            BD240326.1 GI:33050096
JP 2002534056-A/1744.
Homo sapiens (human)
Homo sapiens
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BD240451/c
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BD240326
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AUTHORS
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G01N37/00,
C12N15/00,C12N5/00,C12N15/00
Preparation and use of superior vaccines
Key
Location/Qualifiers
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Roberts, B.L. and Shankara, S. Roberts, B.L. and Shankara, S. Prepartation and use of superior vaccines Patent: JP 2002534056-A 1476 15-OCT-2002,
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    /organism='Homo sapiens (human)'.

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002534056-A/1476
15-OCT-2002
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JP 2002534056-A/1476.
Homo sapiens (human)
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Best Local Similarity 100.
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1 (bases 1 to 10)
1 (bases 1 to 10)
Preparation and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 2131 15-OCT-2002,
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UP 2002534056-A/1889.

Homo sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens (human)

Rammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 10)

S Roberts, B. L. and Shankara, S.

Preparation and use of superior vaccines

L Patent: UP 2002534056-A/1889

DN UP 2002534056-A/1889

PD 15-OCT-2002;

PP 18-UJM-1999 UP 2000554749

PR 19-UJM-1998 US 60/090039,19-UJM-1998 US 60/090040 PR
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                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1869 15-OCT-2002;
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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Location/Qualifiers
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UP 2000279181-A/41.
Homo sapiens (human)
Homo sapiens
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Homo sapiens (human)
Homo sapiens
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2 CAGAACA 8
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E39646
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E39508
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EC-1998 US 60/111715
BRUCE L ROBERTS, SRINIVAS SHANKARA
C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
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C12N15/09, C12N15/09, C07H21/02, C07H21/04, C12Q1/68, G01N21/78, PC
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I (bases 1 to 10.)

Hedgpeth, J., Afonina, I.A., Kutyavin, I.V., Lukhtanov, E.A.,

Belousov, E.S. and Jr.R.B.M.

Hybridization and mismatch discrimination using oligonucleotides conjugated to minor groove binders

Patent: JP 2002527040-A 3 27-AUG-2002;

EPOCH BIOSCIENCES INC

OS BSCHPARICHES OIL

PN JP 2002527040-A/3

PD 27-AUG-2002
                                                               PC CL2N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, 1
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key
Location/Qualifiers
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03-APR-1998 US 09/054832
JOEL HEDGPETH,IRINA A AFONINA,IGOR V KUTYAVIN,EUGENY A
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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PC G01N33/584,
CC Hybridization and mismatch discrimination using oligonucleotides
CC conjugated to minor groove binders
FH Key Location/Qualifiers
1.10
/organism='Escherichia coli'.
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/db_xref="taxon:9606"
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JP 2002527040-A/3.
Escherichia coli
Escherichia coli
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Best Local Similarity 100.v
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PAT 31-JAN-2002
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1 (bases 1 to 10)

1 (bases 1 to 10)

1 Hashimoto, S., Matsushima, K. and Suzuki, T.
Genes with human denditic cell expression

Patent: JP 2000279181-A 41 10-OCT-2000;

SCIENCE TECH ACENCY

OS Homo sapiens (human)

PN JP 2000279181-A/41

PF 01-APR-1999 JP 1999095481
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I chases 1 to 10.

Hashimoto, S., Matsushima, K. and Suzuki, T.

Genes with human dendritic cell expression
Satent: 10 2000279181.A 179 10-0CT-2000;

Science & TECH AGENCY
OS Homo sapiens (human)
PD JP 2000279181-A/179
PD 10-0CT-2000
PP 01-APR-1999 JP 1999095481
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C12N15/09, C07K14/475, C07K16/18, C12N15/00
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    /organism='Homo sapiens (human)'.

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E39508 10 bp DNA Genes with human dendritic cell expression.
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Genes with human dendritic cell expression.
E39646
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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B39743.1 GI:18621834

D 2000279181-A/276.

Thomo sapiens (human)

Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 10)

Hashimoto, S., Matsushima, K. and Suzuki, T.

Genes with human dendritic cell expression

L P 2000279181-A 276 10-OCT-2000;

SCIENCE & TECH AGENCY

OS Homo sapiens (human)

PD 10-OCT-2000

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OS Homo sapiens (human)
PN JP 2000279181-A/224
PD 10-OCT-2000
PP 01-APR-1999 JP 1999095481
PR SHINICHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI PC CL2N15/09, C07K14/475, C07K16/18, C12N15/00
CC LP Key Location/Qualifiers
FH Key Location/Qualifiers
FT source (organism='Homo sapiens (human)'.
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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C12N15/09, C07K14/475, C07K16/18, C12N15/00
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FH Key Location'/
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/organism='Homo sapiens (human)'
Location/Qualifiers
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Genes with human dendritic cell expression.
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Best Local Similarity 100.v
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Genes with human dendritic cell expression.

Genes with human dendritic cell expression.

B 39448.1 GI:18621739

DS GENES GENES (Bunan)

NISM E39648.1 GI:18621739

Homo sapiens (human)

NISM Homo sapiens (human)

NISM Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

ICE 1 (bases 1 to 10)

RS Hashimoto, S., Marsushima, K. and Suzuki, T.

Genes with human dendritic cell expression

AL PATENT JD 2000279181-A 181 10-OCT-2000;

SCIENCE & TECH AGENCY

OS Homo sapiens (human)

PD 10-OCT-2000

PF 01-200-
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1 (bases 1 to 10)
Hashimoto,S., Matsushima,K. and Suzuki,T.
Hashimoto,S., Matsushima,K. and Suzuki,T.
Patent: JP 2000779181-A 224 10-OCT-2000;
SCIENCE & TECH AGENCY
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CC
FH Key
FT Source
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    .10
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xxef="taxon:9606"

    .10
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

     Location/Qualifiers
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Best Local Similarity 100.
Matches 7; Conservative
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E39691
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Unclassified.
1 (bases 1 to 10)
Plikaytis, B.B., Shinnick, T.M. and Crawford, J.T.
Rapid amplification-based subtyping of mycobacterium tuberculosis
Patent: US 5652106-A 14 29-JUL-1997;
Location/Qualifiers
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                                                     10 bp DNA
Human normal liver cell expression genes.
E54750
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Sequence 14 from patent US 5652106.
I58380
I58380.1 GI:2477618
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/organism="unknown"
/mol_type="unassigned_DNA"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2001211883-A/102.
Homo sapiens (human)
Homo sapiens
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                                                Eukaryofe, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 10)

Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.

Human normal liver cell expression genes
Patent: JP 2001211883-A 50 07-AUG-2001;

SCIENCE & TECH AGBNCY
OS Homo sapiens (human)
PN JP 2001211883-A/50
PN JP 2001211883-A/50
PP 31-JAN-2000 JP 2000023170
PP XOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO. TARO PT
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Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T. Human normal liver cell expression genes patent: JP 201211883-A 98 07-AUG-2001,

SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PD 07-AUG-2001
PP 31-JAN-2000 JP 2000023170
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KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
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                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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E54698.1 GI:22556181
JP 2001211883-A/50.
Homo sapiens (human)
Homo sapiens
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E54746.1 GI:22556229
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Best Local Similarity 100.0%;
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Homo sapiens (human)
Homo sapiens
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YAMASHITA
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E54746
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Unclassified.
Unclassified.
1 (bases 1 to 10)
Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
Androgen-regulated gene expressed in prostate tissue
Patent: US 6566130-A 22 20-MAY-2003;
Location/Qualifiers
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Unclassified.

I (bases 1 to 10)
Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
Androgen-regulated gene expressed in prostate tissue
Patent: US 6566130-A 29 20-MAY-2003;
Location/Qualifiers
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                 Query Match 31.8%; Score 7; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 2.9e+02;. Matches 7; Conservative 0; Mismatches 0; Indels
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AR409234.1 GI:40159877
                                                                                                                                                                          Sequence 22 from patent US 6566130. AR336847 GI:33722697
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Seguence 29 from patent US 6566130.
AR336854
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Best Local Similarity 100.
Matches 7; Conservative
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Unknown.
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AR336847/c
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AR409234/c
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Unknown.
Unclassified.
I (bases 1 to 10)
Shimmamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
Method for synthesizing cDNA from mRNA sample
Patent: US 654736-A 135 08-APR-2003;
Patent: Uccation/Qualifiers
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Shimamoto, A., Furuichi, Y., Shibata, Y., Funaki, H., Ohara, E. and
Watahiki, M.
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31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                     1 (bases 1 to 10)
Anastasio, A.E., Finkel, K., Koshy, B. and Lee, H.
Haplotypes of the AGTR1 gene
Patent: US 6521747-A 21 18-FEB-2003;
Location/Qualifiers
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Patent: US 6544736-A 319 08-APR-2003;
Location/Qualifiers
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Sequence 135 from patent US 6544736.
AR303410
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Sequence 319 from patent US 6544736.
AR303594.1 GI:31692370
 Sequence 21 from patent US 6521747.
AR282625
AR282625.1 GI:29719223
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/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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/wol_type="genomic DNA"
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Matches 7; Conservative
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AR303410/c
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AR303594/c
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AX113021/c
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AX152442/c
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Genes differentially expressed in tr1 cells and their use in the
manufacture of immunoregulatory compositions
Patent: WO 0127267-A 15 19-APR-2001;
ISIS INNOVATION LIMITED (GB)
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                                         l (bases 1 to 10)
Nielsen, P.B., Haaima, G. and Eldrup, A.B.
Peptide nucleic acid monomers and oligomers
Patent: US 6632919-A 52 14-OCT-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 10)
Nielsen, P.B., Haaima, G. and Eldrup, A.B.
Peptide nucleic acid monomers and oligomers
Patent: US 6632249-A 56 14-OCT-2003;
Location/Qualifiers
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Sequence 56 from patent US 6632919.
AR409238
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AX112968.1 GI:13939403
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Petent: WO 012767-A 68 19-APR-2001;
ISIS INNOVATION LIMITED (GB)
Location/Qualifiers
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Patent: WO 0138577-A 301 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
100.0%; Pred. No. 2.9e+02; rative 0; Mismatches 0;
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Sequence 68 from Patent WO0127267.
AX113021.1 GI:13939456
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Homo sapiens
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Best Local Similarity 100.
Matches 7; Conservative
  Best Local Similarity 100.
Matches 7; Conservative
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Human transcriptomes
Patent: WO 0138577-A 379 31-MAY-2001,
The Johns Hopkins University (US)
Location/Qualifiers
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AX152786/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0138577-A 378 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
                                                                                                                                                           Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0;
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Patent: WO 0138577-A 357 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
AX152442
Sequence 357 from Patent W00138577.
AX152442
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Seguence 378 from Patent WO0138577.
AX152463
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Sequence 379 from Patent WO0138577.
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AX152464.1 GI:14534115
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                                                     AX152442.1 GI:14534093
                                                                              Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 7; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0.138577-A 701 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Patent: WO 031-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0138577-A 1159 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Patent: WO 0138577-A 1160 31-MAY-2001;
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Patent: WO 0138577-A 1158 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Sequence 1159 from Patent WO0138577.
AX153244.1 GI:14534895
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                   AX153243.1 GI:14534894
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0138577-8
The Johns Hopkins University (US)
Location/Qualifiers
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Patent: WO 0138577-8 939 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Sequence 840 from Patent WO0138577.
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Sequence 939 from Patent WO0138577.

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AX152925.1 GI:14534576
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   Matches
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
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Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
                                                                                                           Sequence 1183 from Patent W00138577.
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Patent: WO 0138577-A 1183 31-MAX-2001;
The John HOpkins University (US)
Location/Qualifiers
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Sequence 1420 from Patent WO0138577.
AXIS3505.1 GI:14535156
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Homo sapiens
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733 GAGAAAC 739
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0138577-4 1182 31-MAY-2001;
The Johns Hopkins University (US)
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Patent: WO 0138577-4 1173 31-MAY-2001;
The Johns Hopkins University (US)
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The Johns Hopkins University (US)
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/organism="Homo sapiens"
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AX391458
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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Patent: WO 0138577-A 1420 31-MAY-2001;
The Johns Hopkins University (US)
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Patent: WO 0138577-A 1509 31-MAY-2001;
The Johns Hopkins University (US)
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Sequence 1509 from Patent WO0138577.
AX155594.1 GI:14535245
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Sequence 433 from Patent WO0185941.
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Antibiotic-free bacterial strain selection with antisense molecules Patent: WO 02079467-A 30 10-OCT-2002; Koebenhavns Univesitet (DK) Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    10
    /organism="synthetic construct"
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    /noTe="Peptide nucleic acid no. 1833"

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100.0%; Pred. No. 2.9e+02;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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LPS activated human monocyte expressing genes.
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LPS activated human monocyte expressing genes.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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2 CAGAACA 8
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ON LPS activated human monocyte expressing genes.

BD007771 GI:18636144

JP 2001069993-A/47.

Homo sapiens (human)

SM Homo sapiens (human)

Homo sapiens (human)

Manmalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Butsushima, K., Hashimoto, S. and Suzuki, T.

LPS activated human monocyte expressing genes

LPS activated human monocyte expressing genes

LPA activated human monocyte expressing genes

LPA activated human monocyte oxpressing genes

LPA activated human)

OS Homo sapiens (human)

PR 20-1069993-A/47

PD 21-MAR-2001

PP 28-APR-2000 JP 2000131079
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Composition and methods for the identification of lung tumor cells
Patent: ED 1310556-A 2 14-MAY-2003;
GENZYME CORPORATION (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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        /db_xref="taxon:32630"

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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synthetic construct
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                  735 GAAACAG 741
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DED07849.

BD007849.

Supplementary Control of September Supplementary Craniata, Vertebrata; Euteleostomi, Homo sapiens (human)

ISM Homo sapiens (human)

ISM Homo sapiens (human)

ISM Homo sapiens (human)

Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.

The Lates I (bases I to 10)

Matsushima, K., Hashimoto, S. and Suzuki, T.

I (bases I to 20)

Matsushima, K., Hashimoto, S. and Suzuki, T.

INS activated human monocyte expressing genes

AL Patent JP 2001069993-A 125 21-MAR-2001;

DE HOMO sapiens (human)

PR 26-APR-2000

PR 26-APR-2000 JP 2000131079

PR 26-APR-2000 JP 2000131079 NA BD0079491
BD0079491
GI:18636322
JP 2001069993-A/225.
Homo sapiens (human)
SM Homo sapiens (human)
SM Homo sapiens (human)
Manmalia, Butheria, Primates, Craniata, Vertebrata, Euteleostomi, Manmalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
El (Dases I to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
I.PS activated human monocyte expressing genes
DAPAN SCIENCE AND TECHNOLOGY CORP.
JAPAN SCIENCE AND TECHNOLOGY CORP.
SM UP 2001069993-A/225
PD 21-MAR-2001
PP 21-MAR-2001
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PP 21-MAR-2001
PP 21-MAR-2001
PP XOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC ô PAT 31-JAN-2002 linear PAT 31-JAN-2002 Gaps . 0 .ce 1. .10
/organism='Homo sapiens (human)'.
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Query Match 31.8%; Score 7; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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BD065275/c
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1 (bases 1 to 10)

Matsushima, K., Hashimoto, S. and Suzuki, T.

IPS activated human monocyte expressing genes patent: 19 Z001069993-A 255 21-MAR-2001,

OS Homo sapiens (human)

OS Homo sapiens (human)

PP 28-APR-2000 JP 2000131079
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C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
  C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00,
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LPS activated human monocyte expressing genes.
BD008032 GI:18636405
JP 2001069993-A/308.
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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    .10
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    /mol type="genomic DNA"
    /db_xref="taxon:9606"

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/organism="Homo sapiens"
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JP 2001069993-A/255.
Homo sapiens (human)
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I (bases 1 to 10)

I (bases 1 to 10)

Matsushima, K., Hashimoto, S. and Suzuki, T.

IPS activated human monocyte expressing genes

I Patent: JP 2001069993-A 308 21-MAR-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP

NA P 2001069993-A/308

PR 28-APR-2000

PR 201069993-A/308

PR 28-APR-2000

PR ASPR-2000

C 212N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC

A61P29/00,

R A61P31/00, C12P21/08, C12N15/00

C A61P31/00, C12P21/08, C12N15/00

C A61P31/00, C12P21/08, C12N15/00

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Location/Qualifiers
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Characterization of the yeast transcriptome.
BD065275

    10
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Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
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Human matured/activated dendritic cell expression genes.

BD083173.1 GI:22628783

BD083173.1 GI:22628783

JP 2001327293-A/94.

Homo sapiens (human)

EMARYOTCH; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Marmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Marmalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

Human matured/activated dendritic cell expression genes patent: JP 2001327293-A/94

PD APAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PD 27-NOV-2001

PF 22-MAY-2000 JP 2000150562

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI

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KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
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31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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JP 2001327293-A/100.
Homo sapiens (human)
Homo sapiens
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729 CCAGGAG 735
                   10 CCAGGAG 4
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                                                                  RESULT 616
BD083173
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VERGION
VERGYWORDS
SOUNCE
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bD092230.1 GI:22628840

BD093230.1 GI:22628840

JP 2001327293-A/151.

Homo sapiens (human)

SM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases it Ashimoto, S., Suzuki, T. and Nagai, S.

Human matured/activated dendritic cell expression genes

L Patent: JP 200132793-A 151 27-NVV-2001;

DAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2001327293-A/151

PP 22-MAY-2000 JP 2000150562

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
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Human matured/activated dendritic cell expression genes.
BD083361
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Matsuabima, K., Hashimoto, S., Suzuki, T. and Nagai, S.
Human matured/activated dendritic cell expression genes
Parent: JP 200132223-A 282 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PD J-NOV-2001
PP 22-MAY-2000 JP 2000150562
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/db_xref="taxon:9606"
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JP 2001327293-A/282.
Homo sapiens (human)
Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 10)
Nagai,S., Matsushima,K. and Hashimoto,S.
Human activated Th1 and Th2 cell expression genes
Human activated Th1 and Th2 cell expression genes
Daylor SCIENCE AND TECHNOLOGY CORP
OS Home sapiens (human)
PN JP 2002186482-A/66
PD 02-UUL-2002
PP 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
CLINIS/09,COYKA/4/47,COYKA/6/18,CL2D21/08,CL2N15/00 CC
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Human activated Thi and Th2 cell expression genes
Patent: JP 2002186482-A 160 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLGY CORP
OS Homo sapiens (human)
PD 02-JUL-2006
PP 19-DEC-2000 JP 2000385816
PP 19-DEC-2000 JP 2000385816
PI SHIGERORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
CL2NUS, 099 COPTA, 447, COPTA, 671, 801 mad Th2 cell expression genes FH Key
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

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JP 2002186482-A/160.
Homo sapiens (human)
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Matches 7; Conserv
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ACCESSION
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BD161338/c
LOCUS
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SOURCE
ORGANISM
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BD161404/c
LOCUS
     AUTHORS
TITLE
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TITLE
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                                                       C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
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JP 2002186482-A/66.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
          KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI
                                                                                                                                                                                                                                                                                                                        Gaps
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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BD161207
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Human activated Th1 and Th2 cell expression genes.
BD161244
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                                                                                                   Location/Qualifiers.
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JP 2002186482-A/29.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                        7; Conservative
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AUTHORS
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RESULT 621

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BD161244

ACCESSION

REFERENCE

Matches

FEATURES

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schultz1-727.rge

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PAT 17-JAN-2003
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C12P21/08,
C12N15/00
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No BD166678.1

BD166678.1

BD166678.1

GD127872490

Unidentified

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SOND SALENCE AND INCIDIOLOGIC CORF

PN JP 2002209591-A/84

PD 30-UUL-2002

PF 19-JAN-2001 JP 2001012328

PF 19-JAN-2001 JP 2001012328

PC C12N15/09, C07X14/47, C07X16/18, G01N33/15, G01N33/50//C12P21/08

PC C12N15/00

PC C12N15/00

CC Human liver disease-expressing genes

FH Key Location/Qualifiers

FT source 1..10

PT //organism='Homo sapiens (human)'.
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1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
Human liver disease-expressing genes
Patent: JP 2002209591-A 84 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo seapiens (human)
PN JP 2002209591-A/84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism='Homo sapiens (human)'. Location/Qualifiers
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31.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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Human liver disease-expressing genes.
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BD166539.1 GI:27872351
JP 2002209591-A/84.
unidentified
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PD 30-JU
PF 19-JA
PI KOJI
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                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

B. (Abses 1 to 10)
S. Matsuahima, K. and Hashimoto, S.
Human activated Thl and Th2 cell expression genes
L. Patent: JP 200216482-A 226 02-JUL-2002,
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (Human)
PN JP 2002186482-A/226
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC
C12N15/09.COTX14/47, COTX16/18, C12P21/08, C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
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E (Asses I to 10)

S (Asses I to 10)

Nagai,S., Matsushima,K. and Hashimoto,S.

Human activated Th1 and Th2 cell expression genes

L Patent: UP 2002186482-A 294 02-UUI-2002;

JAPPAN SCIENCE AND TECHNOLOGY CORP

OS HOMO sapiens (human)

PN 19-DEC-2000 JP 2000385816

PF 19-DEC-2000 JP 2000385816

PI SHIGENORIN NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC

C12NIS/09,COTX14/47,COTX16/18,C12P21/08,C12NIS/00 CC

LOCATION/Qualifiers

FT source

//organism='Homo sapiens (human)'.
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Location/Qualifiers
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BD161472
BD161472. GI:27867230
JP 2002186482-A/294.
Homo sapiens (human)
BDNessure.
Human activated Th1 and Th2 cell expression genes. BD161404
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100.0%; Pred. No. 2.9e+02,
iive 0; Mismatches 0

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                                                        ED161404.1 GI:27867162
JP 2002186482-A/226.
Homo sapiens (human)
Homo sapiens
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Matches 7; Conservative
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736 AAACAGA 742
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S Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.

Human liver disease-expressing genes

Patent: JP 2002209591-A 239 30-JUL-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homon sapiens (human)

PD 30-JUL-2002

PP 19-JAN-2001 JP 2001012238

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHĪ KANEKO, TARO PI

YAMASHITA

PC C12P1/09, COTK14/47, COTK16/18, GOIN33/15, GOIN33/50//C12P21/0, PC
C12P1/08,
PC C12P1/08,
PC C12P1/08,
PC C12P1/09

CC Human liver disease-expressing genes

FH Key Loadion/Qualifiers

FT SOURCE

/organism='Homo sapiens (human)'.

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                                         /organism='Homo sapiens (human)'. Location/Qualifiers
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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Human liver disease-expressing genes
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/db_xref="taxon:32644"

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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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RS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.

Human liver disease-expressing genes

AL PACENT: JP 2002209591-A 420 30-UUL-2002;

JAPAN SCIRNE AND TECHNOLOGY CGRP

OS Home sapiens (human)

PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328

PF 19-JAN-2001 JP 2001012328

PF 19-JAN-SHITA

PC 012N1S/09

CC 12N1S/09

CC Human liver disease-expressing genes

FH Key

Location/Qualifiers

FT source

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unclassified.
1 (bases it to 10)

Matsushima K., Hashimoto,S., Kaneko,S. and Yamashita,T.

Human liver disease-expressing genes

Human liver disease-expressing genes

AD 7002209591-A435

NO 2002209591-A435

PF 19-JAN-2001 JP 2001012328

PF 201015/09, CO7K14/47, CO7K16/18, G01N33/15, G01N33/50//C12P21/02, PC C12N15/09, CO7K14/47, CO7K16/18, G01N33/15, G01N33/50//C12P21/02, PC C12N15/09

CC Human liver disease-expressing genes

FF Source Location/Qualifiers

FT Source Location/Qualifiers

FT Source (human)'.
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C12N1S/00
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JP 2002209591-A/435.
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PAT 17-JAN-2003

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synthetic construct
artificial sequences.
1 (bases 1 to 10)
Jen,J., Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
Methods for the diagnosis and treatment of lung cancer
Batent: JP 2002509706-A 8 02-APR-2002;
GENZYME CORP,JOHN HOPKINS UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 31.8%; Score 7; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:32644"

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JP 2002509706-A/8.
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Number liver disease-expressing genes.

BD167149.

BD167149.

BD167149.1 GI:27872961

BD167149.1 GI:27872961

SD167149.1 GI:27872961

SD167149.1 GI:27872961

SM unidentified

Unclassified.

E 1 (bases I to 10)

Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.

Human liver disease-expressing genes

Aparts: JP 2002209591-A 694 30-JUL-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2002209591-A/694

PD 30-JUL-2002

PP 19-JAN-2001 JP 2001012328

PR COJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
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Human liver disease-expressing genes.
BD167093

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PC C12P21
PC C12N19
CC Human
FT SOURCE
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PC C12N1.
PC C12P2
PC C12N1
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BD167093/c
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BD225320.1 GI:33035090

BD225320.1 GI:33035090

TP 2002509707-A/2.

synthetic construct
synthetic construct
artificial sequences.

[ (bases 1 to 10)
Beaudry (A.A., Madden, S.L. and Bertelsen, A.H.

Compositions and methods for the identification of lung tumor cells Patent: JP 2002509707-A 2 02-APR-2002;

GBNZYME CORP

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OS Artificial Sequence

PN JP 202509706-A/8

PD 02-APR-2002

PF 30-MAR-1999 JP 2000540746

PR 31-MAR-1999 US 60/080044

PI JIN JEN GARY A BEAUDRY, STEPHEN L MADDEN, ARTHUR H BERTELSEN PC C12N15/09, A61K45/00, A61K48/00, A61P35/00, C12O1/68, G01N33/50, PC C12N15/00

CC Description of Artificial Sequence: SAGE tags FH Key
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PN JP 2002/09707-A/2
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541180
PR 31-MAR-1999 US 60/080037
PR GARY A BEAUDRY, STEPHEN L MADDEN, ARTHUR H BERTELSEN PC C12N15/09, A01K67/027, C07H21/04, C07K14/47, C07K16/18, C12N1/15, PC C12N1/21, C12N5/10, C12P21/08, C12Q1/68, G01N33/15, G01N33/53, PC C13N3/566//
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Location/Qualifiers
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ALIGNMENTS		RESULT 1	AAL49614/C TD AAL49614 standard: DNA: 21 BP.		AC AAL49614; xx	DT 27-NOV-2002 (first entry)	XX DE Tumour differentiation effecting protein TL4 related PCR			human; PCR; primer.	XX OS Unidentified.		PN W0200266049-A1.	DD 29-AIIG-2002.		PF 21-FEB-2002; 2002WO-JP001536.	PR 23-FEB-2001; 2001JP-00049450.		PA (TAKE) TAKEDA CHEM IND LTD.	PI Hikichi Y, Shintani Y, Matsui H;		WFI; Z002-6/4894/1Z.	Plasmic change agents and ar	of tumours of muscle tissue and of	PS Example 1; Page 127; 136pp; Japanese.	present invention relates to plasmic change	differentiation activity containing protein TL4. These	ion and diagnosis of rhabdosarcoma	C primer used in the exemplification of the invention		Sequence 21 BP; 1 A; 5 C; 6 G; 9 I; 0 U; 0 Otner;	95.5%; Score 21;	vative 0; Mi			Db 21 TGCCAGGAGAACCACC 1		RESULT 2	ABTUSU81/C ID ABT05081 standard; DNA; 18 BP.		AC ABT05081;	DT 11-OCT-2002 (first entry)	XX DE TNED1 expression modulation related antisense olido SEO		KW Antisense compound, tumour necrosis factor receptor 1, 1, xw mNED1. hensetitie. liver injury. hyperproliferative dispring.	nepacitis; liver injury; hyperproliterative ds.	AA OS Homo sapiens.	WO200	
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2 1 ABI65	2 1 ABI80	2 1 ABH68	2 1 ABI20	2 1 ABH75	2 1 ABI28	2 1 ABH80	2 1 ABH80 2 1 ABI05	2 1 ABI06	2 1 ABI32 2 1 ABH84	2 1 ABI13	2 1 ABH90 2 1 ABI15	2 1 ABI49	2 1 ABI52	2 1 ABI52	2 1 ABI76	2 1 ABI78	2 1 ABI66	2 1 ABI82	2 1 ABI17	2 1 ABH94	2 1 ABH95	2 1 ABH71 2 1 ABH72	2 1 ABI23	2 1 ABH74	2 1 ABI26	2 1 ABI02	2 1 ABI28	2 1 ABH79	2 1 ABIOS	2 1 ABI06	2 1 ABI09 2 1 ABH88	2 1 ABH88	2 1 AB141 2 1 AB145	2 1 ABI46	2 1 ABI49	2 1 ABI54	2 1 ABI57	2 1 AAF92	2 1 AAL37 2 1 AAL37	2 1 ABS71	2 1 ABQ75	2 1 ABK99	2 1 ABK15	2 1 ABQ77	2 1 ABQ77	12 1 ABX79734	2 1 ADA18 2 1 ADC22	2 1 ADC18	
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1421	C1422	C1424	1425	1427	1428	01430	c1431 c1432	c1433	C1434 C1435	1436	1437	1439	C1440	1447 1447	C1443	C1444	C1445	1447	1448	c1450	C1451	1452	1454	1455	1457	1458	c1460	1461	1462	C1464	1465 1466	1467	1468 C1469	C1470	1472	c1473	1475	1476	C1477 C1478	1479	C1480	1482	C1483	1485	1486	1488	1489 C1490	1491	

with cell
e can be used in the
leiomyosarcoma,
equence is a PCR osis and treatment arcoma; rat; ss; change; TL4; R primer #18. 0; Gaps liver disease; order; cancer; Q ID No 111. 21; 18 PN WO200248168-A1.

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Pred. No. 23;
0; Mismatches 0; Indels
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                                                                                                                                                                  Dean NM;
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                                                                                                                                                                  Zhang H,
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ABT05082/C
XX
AC
ABT05082;
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ACCT-2001;
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ACCT-2001;
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ACCT-2000;
ACCT
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100.0%;
                                     22-OCT-2001; 2001WO-US051224.
                                                                                24-OCT-2000; 2000US-00695451
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Best Local Similarity 10v...
Best Local 8; Conservative
                                                                                                                                                                  Cowsert LM,
                                                                                                                        (ISIS-) ISIS PHARM INC
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20-JUN-2002
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sis factor receptor 1 (TNFR1), useful for treating humans having
necrosis factor receptor 1 (TNFR1), useful for treating humans having disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
                                                                                                                                                                                                                               The invention relates to an antisense compound 8 to 30 nucleotides in length targeted to nucleic acid molecule encoding tumour necrosis factor acceptor 1 (TMFR1), where the antisense compound inhibiting the expression of TMFR1. The antisense compound is inhibiting the expression of TMFR1 in cells or tissues. The antisense compound is also useful for reating an animal (preferably human) having a disease or condition associated with TMFR1, e.g. a liver disease (such as hepatitis, or liver injury) or a hyperproliferative disorder such as cancer, by inhibiting diagnostics, therapeutics, prophylaxis and as research reagents and kits. This polymuleotide sequence represents a human oligonucleotide relating the target of the compound of the computer of the compute
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red. No. 23;
Mismatches 0
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Pred. No.
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100.0%;
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ABT05083/c
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Novel antisense compound targeted to nucleic acid molecule encoding tumor necrosis factor receptor 1 (TNFR1), useful for treating humans having disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
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                                                                                                                                                                             Antisense compound; tumour necrosis factor receptor 1; liver disease; INFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
                                                                                                                                               INFR1 expression modulation related antisense oligo SEQ ID No 47.
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                                          ABT05017 standard; DNA; 18 BP
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                                                                                                              (first entry)
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                                                                                                              11-OCT-2002
                                                                                                                                                                                                                      human; ds.
                                                                              ABT05017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides antisense compounds targeted to human tumour necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds can be used in a method of inhibiting the expression of TNFR1 human cells or tissues. The antisense compounds specifically hybridize with one or more nucleic acids encoding TNFR1 modulating the function of nucleic acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1 produced. The antisense compounds and method are useful as research reagents and diagnostics, and in the treatment and prophylaxis of infection, inflammation or tumour formation. Sequences AAZ4812-565 represent antisense oligos used for inhibition of the human TNFR1 mRNA
                        and kits.
the expression of TNFR1. The antisense compound is useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. This polynucleotide sequence represents a human oligonucleotide relating to the TNFR1 of the invention
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                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour necrosis factor receptor type 1; TNFR1; antisense; infection; inflammation; tumour formation; TNFR1; anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense inhibition of tumor necrosis factor type 1 expression for diagnosis, treatment and prevention of disease, particularly tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
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                                                                                                                             81.8%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 23; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                             Sequence 18 BP; 0 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                    731 AGGAGAAACAGAACACCG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Col 25; 34pp; English.
                                                                                                                                                                                                                                   18 AGGAGAAACAGAACACCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                             Query Match 81.8
Best Local Similarity 100.
Matches 18; Conservative
         8X8688
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Dean NM;

Zhang H,

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                                                          Gaps
                                                          .,
                        Score 17; DB 1; Length 18; Pred. No. 33; 0; Mismatches 0; Indels
Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                          Primer #1 for sWSS2359 human obesity gene.
                                                          ..
                                                                                        748
                                                                                                                                                                                                  BP.
                           77.3%;
                                                                                                           18 GGAGAAACAGAACACCG
                                                                                        732 GGAGAAACAGAACACCG
                                                                                                                                                                                                  AAT16398 standard; DNA; 18
                                                                                                                                                                                                                                                             (first entry)
                          Query Match
Best Local Similarity 100.
Matches 17; Conservative
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in ~

732 GGAGAACAGAACACCG 748

à

18 GGAGAACAGAACACCG 2

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Homo sapiens
                       US6124448-A.
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                                                                                                                                                                                                                                   adiposity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OB gene; h
PCR prime:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA12315;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
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                                                                                                                                                                                                                                                                                                                        AATI6392-T16429 represent amplification primers for the human obesity polypeptide (OBP) gene sequence (see AATI6373). These sequences were used to amplify the OBP gene sequence from the YAC contig containing the human CBP gene, in a series of sequence tagged-site (STS)-specific PCR assays. There were 19 STSs found within the YAC contig human OBP gene sequence. This sequence was used in conjuncture with AATI6399 to amplify the STS and its analogues are useful for modifying body weight (optionally combined with known medicaments), for treating diabetes, high blood pressure or high cholesterol. The OBP coding sequence (and sequences complimentary to it) can be used in gene therapy for modifying body weight. The protein can be used for reducing weight for health or cosmetic reasons in obese humans, or to produce leaner food animals. Antagonists of OBP (including antibodies) are useful for increasing body weight, e.g. for treating weight loss associated with cancer, or for commentic reasons in humans, or for production of Kobe beef or Fole gras in munoassays for the presence of OBP. The formation of Ab-OBP complexes enables in vitro evaluation of levels of OBP in a sample, especially to detect diseases associated with elevated or decreased levels, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; OB gene; obesity; adiposity; body weight; PCR primer; ss.
                                                                                                                                                                                                  Gajiwala K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                        Obesity polypeptide(s) able to modulate body wt. - useful for e.g. reducing wt. in treatment of diabetes, high blood pressure and high cholesterol and for cosmetic reasons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 18;
                                                                                                                                                                                               Zhang Y, Proenca R, Maffei M, Halaas JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human OB gene sequence tagged-site-specific PCR primer #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
 primer; amplify; polymerase chain reaction; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%; Score 15.4; D 94.1%; Pred. No. 59; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                        Example 10; Page 141; 304pp; English
                                                                                                                94US-00292345.
94US-00347563.
95US-00438431.
95US-00483211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            730 CAGGAGAAACAGAACAC 746
                                                                                           95GB-00016947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 CAGGAGAACACACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                           ROCKEFELLER
                                                                                                                                                                                                                                    WPI; 1996-099009/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 16; Conserv
                                                                                                                                                                                                  Friedman JM,
                                                                                                                                                                           (UYRQ ) UNIV
                                                                                           17-AUG-1995;
                                                                                                                  17-AUG-1994;
                                                                                                                              30-NOV-1994;
                                                                                                                                        10-MAY-1995;
07-JUN-1995;
                                               GB2292382-A
                                                                     21-FEB-1996
                                                                                                                                                                                                              Burley SK;
                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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The present sequence is a PCR primer which was used in an invention relating to the control of body weight of animals including humans. Mucleic acids of at least 10 nucleotides which are hyporidisable to a noncoding region of an OB nucleic acid have been created. The OB gene plays a critical role in the regulation of body weight and adiposity. The nucleic acids may be used as probes or as primers for PCR. They are useful for evaluating the presence of mutations in the human OB gene or for evaluating the level of expression of OB mRNA. Defects associated with OB gene expression result in obese phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             body weight; obesity; anorectic; adipose tissue; brain; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                             Nucleic acid primers and probes useful for detecting mutations in mammalian OB gene associated with regulation of body weight and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Zhang Y, Friedman JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.0%; Score 15.4; Di 94.1%; Pred. No. 59; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human OB DNA PCR primer sWSS2359 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Col 80; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              746
                                                                                                  94US-00292345.
94US-00347563.
95US-00438431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA12315 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00292345.
94US-00347563.
95US-00438431.
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                                               95US-00488208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                       UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                             Maffei M, Proenca R,
                                                                                                                                                                                                                                                                                                                WPI; 2000-601556/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer; ss.
                                                                                                  17-AUG-1994;
30-NOV-1994;
10-MAY-1995;
                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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10-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-1994;
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26-SEP-2000
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Zhang Y, Friedman JM;

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Best Loca
Matches
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                                                                                                                      This invention describes a novel method for modifying body weight of an animal which comprises administering mammalian obesity (OB) polypeptide. The products of the invention have anorectic activity. The OB polypeptide at a dose of 5 mg/g/day in 300 micro litres of PBS was injected intraperitoneally into mice. Control mice were injected with PBS dialysate of the recombinant protein. The body weight of the mice was noted. The results shows that recombinant the OB polypeptide is capable of reducing a body weight and is found to be effective when it is administered daily. The OB polypeptide acts as a part of the signalling pathway by which adipose tissue communicates with the brain and other organs. (I) is useful for modulating body weight of an animal especially humans. This sequence represents a PCR primer used in the amplification of a human OB protein described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antibody to mammalian obesity polypeptide useful for diagnosis and treatment of weight loss associated with disorders such as cancer, AIDS and anorexia nervosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, mouse, anabolic, cytostatic, immunostimulant,
OB polypeptide inhibitor; body weight, obesity, OB gene, cancer, AIDS,
anorexia nervosa, hypertension, heart disease, Type II diabetes,
                                        Modifying body weight of an animal comprises administering mammalian obesity polypeptide obtained from humans and murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a PCR primer which was used in an invention
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                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 70.0%; Score 15.4; DB 1; Length 18; Best Local Similarity 94.1%; Pred. No. 59; Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human OB gene sequence tagged-site-specific PCR primer #7.
                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                             Example 10; Col 133-134; 153pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Col 80; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proenca R, Zhang Y, Friedman JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    730 CAGGAGAAACAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-00292345.
94US-00347563.
95US-00438431.
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AAC62673 standard; DNA; 18
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               WPI; 2000-302788/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
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10-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC62673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
AAC62673/c
ID AAC62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New obese polypeptide useful for inducing reduction of body weight in an animal, for preparing a composition for treating obesity, disease associated with obesity such as hypertension, heart disease or type II
                                                                                                                                                                                            Ιij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; human; obese polypeptide; body weight; PCR; ob polypeptide; leptin; adipocyte; appetite reduction; cosmetic; primer; fat deposit reduction; improved body appearance; heart disease; obesity; agriculture; nutritional disorder; cancer associated weight loss; type II diabetes; obesity associated disease; AIDS associated weight loss; hypertension;
Attibodies against the mammalian obesity (OB) polypeptide have been identified. The antibodies are useful for modulating the activity of OB pathological The antibodies are useful for modulating the activity of OB to control body weight and fat content and/or to treat certain pathological conditions in which there is abnormal depression or elevation of body weight. The antibodies are used to treat weight loss associated with cancer, AIDS and anorexia nervosa. They are useful for the diagnosis of nutritional disorders such as obesity and diseases associated with obesity, such as hypertension, heart disease and Type I diabetes. The kits are used to determine the presence or amount of OB it he blood or plasma of an individual
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                             DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human sequence tagged specific PCR primer sWss2359 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halaas JL, Gajiwala K, Burley SK,
                                                                                                                                                                                                                                                                                Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                        70.0%; Score 15.4; D
94.1%; Pred. No. 59;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 10; Page 44; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-2000; 2000US-00736084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-00485943.
                                                                                                                                                                                                                                                                                                                                                Local Similarity 94.1%; es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    730 CAGGAGAAACAGAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 CAGGAGAAACACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX89547 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maffel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-722695/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002107211-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedman JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX89547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes
                                                                                                                                                                                                                                                                                                                             Query Match
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The invention

microsatellite markers used in the mapping of the human Ob gene onto chromosome 7. These genetic markers represent an important tool for studying the possible role of the Ob gene in inherited forms of human

Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

obesity

888888888888

70.0%; 94.1%;

DB 1; Length 18;

an animal comprising administering an obese gene (OB) polypeptide analogue, capable of modulating body weight and adiposity. The inventhas ancrectic and anabolic activity, ABC1415-ABL61468 represent PCR primers used in the detection of sequence tagged sites (5TS's) and

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conjugation with other cosmetic strategies e.g. surgery for its ossmetic effect; for identifying agonists or antagonists that affect its activity and has potential agicultural uses e.g. increasing the body weight of animals. Nucleic acid encoding the polypeptide is useful for identifying measurement of its encoded RNA and protein in nutritional disorders. A host cell transfected with a vector expressing the polypeptide is useful in the preparation of modulators of the polypeptide is useful in the preparation of modulators of the polypeptide is useful in the preparation of modulators of the polypeptide is useful in the preparation of modulators of the polypeptide in sample; for evaluating the presence of the polypeptide in a sample; for evaluating the presence of disease associated with elevated or decreased levels of ob polypeptide in a mannalian subject; for imagines ob polypeptide in subject; for imagines ob polypeptide is useful for reducing body weight of an animal, in particular humans. A composition comprising an antagonist of the polypeptide is useful for increasing body weight of an animal. Compositions containing the polypeptide and the antagonist are useful for reating obesity, weight loss associated with obesity such as hypertension, heart disease or type II diabetes. The present sequence represents a human sequence tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ob; human; obese; adiposity; body weight; anorectic; anabolic; PCR; primer; chromosome 7; STS; sequence tagged site; 7q31.3;
appetite or both and is used independently or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Ob gene STS sWSS2359 AFMa065zg9 PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 1 A; 3 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    70.0%; Score 15.4; 194.1%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL61421 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer; chromosome 7; STS;
microsatellite marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
tes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OB polypeptide; obese polypeptide; leptin; body weight; obesity; weight gain; protein therapy; weight loss; cancer; AIDS; human; acquired immunodeficiency syndrome; anorexia nervosa; PCR; primer; ss.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human or mouse OB polypeptide, also referred to as leptin polypeptide, which is capable of modulating body weight, useful for
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                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ob) gene associated PCR primer #7.
Score 15.4; DB
Pred. No. 59;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 10; Col 79-80; 153pp; English.
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                                                                                                                                           730 CAGGAGAAACAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                         ABX96407 standard; DNA; 18 BP
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94US-00347563.
95US-00438431.
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                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-298093/29
   Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-1994;
30-NOV-1994;
10-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6471956-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human obese
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX96407;
                                                                                                                                                                                                                                                                                                         RESULT 13
ABX96407/C
ID ABX96
XX
ACC ABX96
XX
DT 13-MA
DT 13-MA
DT 13-MA
DE Human
XX
OB PO
XX
C Homo
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DB 1; Length 18;

70.0%; Score 15.4;

Query Match

Modifying the body weight of an animal comprises administering an obese gene (OB) polypeptide analog.

94US-00292345. 94US-00347563. 95US-00438431.

17-AUG-1994;

10-MAY-1995;

(UYRQ) UNIV ROCKEFELLER.

Zhang Y,

Friedman JM,

WPI; 2002-412914/44.

This invention describes a novel method of modifying the body weight of

Example 10; Col 79-80; 152pp; English

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748
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732 GGAGAAACAGAACACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 GGAGAAGCAGAACACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tritz R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMI-) IMMISOF INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                          WO200130362-A2
                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robbins JM,
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19-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2001
                                                                                                                                                                                                                                                                                                                       Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV14108/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robbins JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%; Score 15.4; D
94.1%; Pred. No. 60;
ive 0; Mismatches
94.1%; Pred. No. 59; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclin B1 ribozyme binding site #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barber JR,
                                                                                         746
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                                                                                                                                                                                                                                                                                         BP.
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AAA85678 standard; DNA; 19
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                                                                                      730 CAGGAGAAACAGAACAC
                                                                                                                                            18 caggagaaacacaacac
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Best Local Similarity 94.1
Matches 16; Conservative
                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMU-) IMMUSOL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-412314/35.
     Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH60840;
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ID AAA88

AC AAA88

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DE CYCLI

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recognition site; anogh: thousand paining site; sequences, vinterary)

**Recognition site; anogh: thickness; skin disease; perciasis diabetic retinopathy;

**Revokies: initiamention; cell-cycle dependent kinase; cyclin, Why;

**Revokies: initiamention; cell-cycle dependent kinase; cyclin, Why;

**Revokies: initiamention; cell-cycle dependent kinase;

**Revokies: initiamentic accession; selection; selectinopathy; dest;

**Revokies: initiamentic accession; selectinopathy; cell-cycle dependent kinase;

**Revokies: initiamentic accession; selectinopathy; destinopathy; selectinopathy; selectinop
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Probe, hepatitis b virus, HBV detection, RT pol region, genetic analysis, preCore region, HBsAg region, genotype specific target, mutation detection, ss.
                                                                                                                                                                                          Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.
Probe HBPr274 for RT pol region of HBV.
                                                                                                                                                           ö
                                                                                                                                                            Maertens
                                                                                                                                                                                                                             Claim 5; Fig 1; 80pp; English.
                                                                                                         97WO-EP002002.
                                                                                                                          96EP-00870053
                                                                                                                                           (INNO-) INNOGENETICS NV.
                                                                                                                                                            Rossau R,
                                                                                                                                                                           WPI; 1997-535867/49.
                                              Synthetic.
Hepatitis B virus.
                                                                         WO9740193-A2.
                                                                                                                          19-APR-1996;
                                                                                                          21-APR-1997;
                                                                                        30-OCT-1997.
                                                                                                                                                            Stuyver L,
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This sequence represents a probe for the RT pol region of hepatitis b virus (HBV). This sequence can be used in the method of the invention for detection and/or generic analysis of hepatitis B virus (HBV) in a sample.

The method comprises: (a) optionally releasing, isolating or concentrating polynucleic acids (I) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 and the primer pair; (b) hybridising (I) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid 2 uncleotide probes, which are applied to known locations on a solid 2 uncleotide probes, which are applied to known locations on a solid 2 uncleotide probes, which are applied to known locations on a solid 3 cancype specific target sequences, or their complements or U for T comploques; (c) detecting the hybrids formed in step (B), and inferring the HBV genotype and/or mutuants present in the sample from the differential hybridisation signal (S). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, gene mutations selected by treatment with drugs, e.g. lamivudune and per gene mutations selected by treatment with drugs, e.g. lamivudune and per per proper precorne mutations to selected by treatment with drugs, e.g. lamivudune and per per proper precorne mutations and ST generic and selected by treatment with drugs, e.g. lamivudune and per per proper precorne mutations cornect OS field.)

Gaps ; 0 68.2%; Score 15; DB 1; Length 18; 100.0%; Pred. No. 68; O; Indels native 0; Mismatches 0; Indels Sequence 18 BP; 1 A; 6 C; 4 G; 7 T; 0 U; 0 Other; 728 GCCAGGAGAAACAGA 742 Conservative Query Match Best Local Similarity

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GCCAGGAGAACAGA 18

a

AAD22805 standard; DNA; 22 BP 26-FEB-2002 (first entry) AAD22805; AAD22805/c
ID AAD22
XX AC AAD22
XX
XX E-FE
XX
XX B-FE
XX
XX B-FE
XX
XX Humar
XX Humar
XX KW epide
XX RW menir
XW rheum

RESULT 17

Human EMR2 specific nested PCR primer, 3'-1.

Human; EGF-like molecule containing mucin-like hormone receptor-2; EMR2; epidermal growth factor; therapy; acute inflammation; injury; infection; meningitis; pneumonia; chronic inflammation; chronic tissue damage; rheumatoid arthritis; septic shock; atherosclerosis; autoimmune disease;

diabetes; Alzheimer's disease; autoimmunity; intravascular coagulation; clotting; fibrinolysis; thrombosis; embolism; wound repair; angiogenesis; meamatopoisesis; blood disorder; ameutropenia; agranulocytosis; migration; myeloid leukaemia; blood disorder; analfunction; congenital disease; wound healing; Marfan syndrome; hereditary haemorrhagic telangiectasia; huff; tumnour; infection; cancer; asthma; anorexia; parkinson's disease; bullimia; hypotension; acute heart failure; hypertension; osteoporosis; urinary refention; angina pectoris; myocardial infarction; allergy; ulcar; benign prostatic hypertrophy; neurological disorder; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; dyskinesia; Hutington's disease; Gilles dela Tourette's syndrome;

Homo sapiens.

WO200179296-A1

25-OCT-2001.

17-APR-2001; 2001WO-GB001729.

13-APR-2000; 2000GB-00009181.

(ISIS-) ISIS INNOVATION LTD.

Stacey M; Mcknight AJ, Gordon D, Lin H,

WPI; 2002-026015/03.

Novel human epidermal growth factor-like molecule containing mucin-like hormone receptor-2 polypeptide, useful for treating acute and chronic inflammation, chronic tissue damages and for wound healing.

Example; Page 49; 118pp; English.

Containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic acids encoding them. EMR2 sequences are useful for treating acute acids encoding them. EMR2 sequences are useful for treating acute inflammation caused by injury or infection (e.g. meningitis and premain acids encoding them. EMR2 sequences are useful for treating acute inflammation (e.g. rheumatoid arthritis), chronic inflammation (e.g. rheumatoid arthritis), chronic clissue damages, septic shock, atherosclerosis, repair and autoimmune disease processes, diabetes, Alzheimer's disease, processes such as medicion and effector mechanism of innate and acquired recruitment, induction and effector mechanism of innate and acquired autoimmunity. They are also useful for treating conditions involving clotting, fibrinolysis, intravascular coagulation, thrombosis and blood autoimmunity. They are also useful for treating conditions involving clotting, fibrinolysis, intravascular coagulation, thrombosis and compensation or deactivation of phagocytes, myeloid leukaemia, anemia, activation or deactivation of phagocytes, myeloid leukaemia, anemia, activation or deactivation of phagocytes, myeloid leukaemia, anemia, controlling atmour formation of phagocytes, myeloid leukaemia, anemia, controlling tumour formation of phagocytes, myeloid leukaemia, anemia, controlling tumour formation of granuloma. Sequences of the invention classic for treating macrophage controlling tumour formation or disease associated with EMR2 polypetide and in the preparation of a diagnostic agent for use in the method of diagnosis of condition or disease associated with EMR2 polypetide. Antibodies of the preparation of a diagnostic agent for use in the method of diagnosis of classic macrophage sections, particularly infections caused by thingal, proteonsion, acute heart failure, hypotrension, acute heart failure, hypotrension, and hand particularly mycoarders including anxiety, schizophrenia, mannic depression, and severe mental retardation, dyskinesias such as Huntington's disease or G patent discloses human epidermal growth factor (EGF)-like molecule

Sequence 22 BP; 2 A; 4 C; 8 G; 8 T; 0 U; 0 Other;

DB 1; Length 22; Score 14.6; I Pred. No. 85; 66.4%; Query Match Best Local Similarity

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The patent discloses human epidermal growth factor (EGF)-like molecule containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic acids encoding them. BMR2 sequences are useful for treating acute inflammation caused by injury or infection (e.g. meningitis and pneumonia), chronic inflammation (e.g. rheumatoid arthritis), chronic tissease processes, diabetes, Atherosclerosis, repair and autoimmune disease processes, diabetes, Atherosclerosis, repair and autoimmune climates and actoimmunity. Induction and effector mechanism of innate and acquired autoimmunity. They are also useful for treating conditions involving clotting, fibrinolysis, intravascular coagulation, thrombosis and autoimmunity. They are also useful for treating conditions involving choises such as aneutropenia, agranulocytosis, migration, retention activation or deactivation of phagocytes, myeloid leukaemia, anaemia, general disorders (connective tissue (e.g. vascular malfunction, wound healing) and congenital diseases such as hereditary haemorrhagic telangiectasia (HHT) and Marfan syndrome. They are also useful for
                                                                                                                                                                                                                                                                                                                                                                                     Human; EGF-like molecule containing mucin-like hormone receptor-2; EMR2;

we pidermal growth factor; therapy; acute inflammation; injury; infection;
meningits; preumonia; chronic inflammation; chronic tissue danage;
meningits; preumonia; chock; atherosclerosis; autoimmune disease;
diabetes; Alzheimer's disease; autoimmunity; intravascular coagulation;
clotting; fibrinolysis; thrombosis; embolism; wound repair; angiogenesis;
we meantopolesis; blood disorder; aneutropenia; agranulocytosis; migration;
myeloid leukaemia; naneemia; vascular malfunction; congenital disease;
wound healing; Marfan syndrome; hereditary haemorrhagic telangiectasia;
myeloid leukaemia; naneemia; vascular malfunction; congenital disease;
wulmar; infection; cancer; astham; anorexia; parkinson; s disease;
bulimia; hypotension; acute heart failure; hyportension; osteoporosis;
urinary retention; angina pectoris; myocardial infarction; allergy;
ulcer; benign prostatic hypertrophy; neurological disorder; anxiety;
ulcer; benign prostatic depression; delirium; dementia; mental retardation;
dyskinesia; Huntington's disease; Gilles dela Tourette's syndrome;
weeverse transcription; RT-PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human epidermal growth factor-like molecule containing mucin-like hormone.receptor-2 polypeptide, useful for treating acute and chronic inflammation, chronic tissue damages and for wound healing.
    Gaps
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0
    4; Indels
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                Human EMR2 specific RT-PCR primer #1.
                                            727 IGCCAGGAGAACAGAACACC 747
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                                                                            22 TCCCAGAAGACACAGAGCACC
                                                                                                                                                                                                           AAD22809 standard; DNA; 22 BP.
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17; Conservative
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                                                                                                                                                                                                                                                       AAD22809;
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  Matches
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controlling tumour formation and metastasis, for treating macrophage giant cells in bacterially-induced granuloma. Sequences of the invention are useful in the preparation of a medicament for use in a method of therapy of a condition or disease associated with EMR2 polypeptide and in the preparation of a diagnostic agent for use in the method of diagnosis of a condition or disease associated with EMR2 polypeptide. Antibodies against EMR2 are useful for treating infections such as bacterial, city and viral infections, parkinolarly infections caused by HIV-1 or HIV-2, pain, cancers, parkinolarly parkinson's disease, bulimia, hypotension, acute heart failure, hypertension, osteoporosis, urinary retention, angina pectoris, myocardial infarction, ulcers, allergies, benign prostatic hypertensis, myocardial infarction, ulcers, allergies, benign prostatic hypertensis, manic depression, delirium, dementia, severe mental retardation, dyskinesias such as Huntingcon's disease or Gilles dela Tourette's syndrome. The present DNA sequence is a reverse transcription (RT)-PCR primer which is specific for human EMR2 Human, EGF-like molecule containing mucin-like hormone receptor-2; EMR2;

epidermal growth factor; therapy; acute inflammation; injury; infection;

meningtis; preumonia; chronic inflammation; chronic tissue danage;

theumatoid arthritis; septic shock; atherosclerosis; autoimmune disease;

diabetes; Alzheiner's disease; autoimmunity; intravascular coagulation;

KW haematopoiesis; blood disorder; aneutropenia; agranulocytosis; migration;

KW haematopoiesis; blood disorder; aneutropenia; agranulocytosis; migration;

Wyeloid leukaemia; anaemia; vascular malfunction; congenital disease;

WHT; tumour; infection; aneure; astima; anorexia; parkinson; a disease;

WHI; tumour; infection; acute heart failure; hypertison; allergy;

Wulcar; benign prostatic hypertrophy; neurological disorder; anxiety;

W schizophrenia; manic depression; delinium; dementia; mental retardation;

dyskinesia; Huntington's disease, dilles dela Tourette's syndrome; ö Gaps ô Query Match 66.4%; Score 14.6; DB 1; Length 22; Best Local Similarity 81.0%; Pred. No. 85; Matches 17; Conservative 0; Mismatches 4; Indels Human EMR2 7 transmembrane domain identifying primer #1. Sequence 22 BP; 2 A; 4 C; 8 G; 8 T; 0 U; 0 Other; 727 IGCCAGGAGAACAGAACACC 747 22 TCCCAGAAGACACAGAGCACC BP 17-APR-2001; 2001WO-GB001729. 13-APR-2000; 2000GB-00009181. AAD22815 standard; DNA; 22 (first entry) cDNA sequences WO200179296-A1 Homo sapiens. 25-OCT-2001. 26-FEB-2002 AAD22815; RESULT 19 AAD22815, ଟ 셤

Novel human epidermal growth factor-like molecule containing mucin-like

Stacey M;

Gordon D, Mcknight AJ,

Lin H,

WPI; 2002-026015/03

(ISIS-) ISIS INNOVATION LTD.

(IMMU-) IMMUSOL INC.

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                                                            The patent discloses human epidermal growth factor (EGF)-like molecule containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic containing mucin-like hormone receptor-2 (EMR2) proteins and nucleic containing mucin-like hormone are useful for treating acute inflammation caused by injury or infection (e.g. meningitis and classae processes, diabetes, Albeimer's disease, processes such as filing of targets by degranulation, chemotraxis and leukocyte recruitment, induction and effector mechanism of innate and acquired recruitment, induction and effector mechanism of innate and acquired cutoimmunity. They are also useful for treating conditions involving clotting fibrinolysis; intravascular cosquitation, thrombosis and chotting fibrinolysis; intravascular cosquitation, thrombosis and condism, wound repair and angiogenesis, hadmatopoissis and blood disorders of connective tissue (e.g. vascular malfunction, wound activation or deactivation of phagocytes, myeloid leukaemia, anaemia, cativation and cativation of phagocytes, myeloid leukaemia, northing activation or deactivation of phagocytes, myeloid leukaemia, northing cutoin or deactivation of a medicament for use in a method of controlling tumour formation and metastasis, for treating macrophage giant cells in bacterially-induced granuloma, Sequences of the invention are useful for treating infections such as bacterial, or the preparation of a medicament for use in a method of crease associated with EMR2 polypeptide and in the preparation of disease associated with EMR2 polypeptide and in the preparation of disease associated with EMR2 polypeptide and in the cutoin and viral infections, particularly infections caused by unimary retention, acute heart failure, hypertension, acute heart failure, hypertension, acute heart failure, hypertension, acute heart failure, hypertension, dementia, severe mental retardation, dyskinesias such as Huntington's disease, benign proteated the propersion of 
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hormone receptor-2 polypeptide, useful for treating acute and chronic inflammation, chronic tissue damages and for wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22 BP; 2 A; 4 C; 8 G; 8 T; 0 U; 0 Other;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 TCCCAGAAGACACAGAGCACC 2
                                             Example; Page 51; 118pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         듸
                                                                                                                                                                                                                                                                                                                            designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in
                                                                                                                     cleaves
                                                                                                                  New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PCNA and Cyclin B1.
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                                                                                                                                                                                                                                                                                                     present invention relates to a hairpin or hammerhead ribozyme,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
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Robbins JM,
                                                                                                                                                                                                                                           Disclosure; Page 96; 109pp; English
Welch PJ, Barber JR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.5%;
93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        733 GAGAAACAGAACACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restenosis treatment
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                                                       WPI; 2000-412314/35.
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Tritz R,
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AAH60839/c
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RESULT 23
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ID AAH6
8888
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                                                      The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, anticlasborrheic, antidiabetic, antidiabetic, antidiabetic, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, squamous or basal cell carchnoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detechment, and for treating and preventing centing such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AAH57877 to AAH62099 represent sequences used in the cemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDX1, PCNA and Cyclin B1.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.5%; Score 14.4; DB 1; Length 19; 93.8%; Pred. No. 86; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 19 BP; 0 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robbins JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 100; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cdc 25 hs ribozyme binding site #49.
                      Example 1; Page 309; 408pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA85941 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US028772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 733 GAGAACAGAACACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAAGCAGAACACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 93.8
les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMU-) IMMUSOL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-412314/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA85941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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XX AAA8
XX AAA8
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XX MAD2C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (1) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, dermatological, vulnerary, keratolytic and virucide activities, and obthalmological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cyckine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermathis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic watt. They can also be used for treating proliferative eye diseases such as diabetic
inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                              64.5%; Score 14.2; DB 1; Length 19;
84.2%; Pred. No. 92;
ive 0; Mismatches 3; Indels
                                                                                                                                                              Sequence 19 BP; 0 A; 3 C; 5 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cdc25 hs ribozyme binding site SEQ ID NO:3527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 328; 408pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 729 CCAGGAGAACAGAACACC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 CCAGGAGAAAACAAAACC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-2000; 2000WO-US029500.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH61103 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                 Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tritz R;
                                                                               restenosis treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-300427/31.
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                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200130362-AZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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Gaps

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Indels

ъ, DB 1;

0, Mismatches Score 14.2; Pred. No. 96

64.5%; 84.2%;

Query Match
Best Local Similarity 84.2
Matches 16; Conservative

728 GCCAGGAGAACAGAACAC 746

21

GCCAGGAGGAGCAGAACCC

AAV14110 standard; DNA; 18 BP

AAV14110,

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The present invention relates to compositions and methods useful for the identification and detection of polycystic kidney disease (PKDI) gene mutations. The invention also relates to primers comprising a 5' region having a sequence that selectively hybridises to a PKDI gene sequence and coptionally, to a PKDI homologue sequence and an adjacent 3' region having a sequence that selectively hybridises to a PKDI gene sequence and not to a sequence that selectively hybridises to a PKDI gene sequence and not to a PKDI homologue sequence. Primer pairs of the invention are useful for detecting the presence or absence of a mutation in a PKDI polymucleotide in a sample, for identifying a subject at risk for a PKDI-associated disorder such as autosomal dominant polycystic kidney disease (ADPKD) or acquired cystic disease and for diagnosing a PKDI-associated disorder in a subject. They are useful for selectively amplifying a region of a PKDI gene. PKDI DNA fragments are useful detecting the presence of a mutant PKDI polymucleotide in a sample, as a probe for an amplification contact of the caction, in hybridisation or amplification assays of biological samples to an argument and for engineering transgenic the ansatt pkm, and the present sequence is a PCR primer used to detect mutation in the pares.
retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AAHS/5777 to AAHS(2099 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel primer for diagnosing polycystic kidney disease-associated disorder, comprises regions having sequence that selectively hybridizes to polycystic kidney disease gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, PKD1 gene, autosomal dominant polycystic kidney disease, ADPKD,
acquired cystic disease, transgenic animal; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                     DB 1; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PKD1 gene mutation detecting nested PCR primer, 5F1.
                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                  Sequence 19 BP; 0 A; 3 C; 5 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phakdeekitcharoen B;
                                                                                                                                                                                                                                                                                                                                            Pred. No. 92;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                 Score 14.2;
Pred. No. 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 100; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         729 CCAGGAGAACAGAACACC 747
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                                                                                                                                                                                                                                                                                                         64.5%;
84.2%;
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13-APR-2001; 2001US-0283691P.
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-179805/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200206529-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 24
AAD300255
IN AAD300255
XX AAD30
XXX Human
XXX Homo
XXX Homo
XXX Homo
XXX Homo
XXX I J-Ju
YX I J-Ju
YX I J-Ju
YX I J-Ju
XXX I J-Ju
XX I J-Ju
X
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Probe, hepatitis b virus; HBV detection; RT pol region; genetic analysis; preCore region; HBsAg region; genotype specific target; mutation detection; ss.

Synthetic. Hepatitis B virus.

WO9740193-A2

30-OCT-1997.

Probe HBPr276 for RT pol region of HBV.

(revised)
(first entry)

27-AUG-2003 19-MAY-1998

AAV14110;

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This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV). This sequence can be used in the method comprises: (a) optionally releasing, isolating on a sample. The method comprises: (a) optionally releasing, isolating on a sample. Concentrating polymucleic acids (1) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridising (1) with a combination of at least 2 nucleotide probes, which are applied known locations on a solid support and hybridise specifically to mutant target sequences chosen from the HBV RT pol gene region, HBV preCore region, HBSAg region and/or HBV compogues; (c) detecting the hybridis formed in step (b), and interring the HBV genotype and/or mutants present in the sample from the differential hybridisation signal(s). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, sepecifically genotype, preCore mutations, vaccine escape mutations and RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents a probe for the RT pol region of hepatitis b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lamivudune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%; Score 14; DB 1; Length 18; illarity 100.0%; Pred. No. 96; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specifically genotype, precore mutations, vaccine escape reper mutations selected by treatment with drugs, e.g. lamipenciclovir. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 1 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 14; Conserv
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Detection and/or genetic analysis of hepatitis B virus - specifically genotype, precore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.

Claim 5; Fig 1; 80pp; English.

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Rossau R,

Stuyver L,

WPI; 1997-535867/49.

INNO-) INNOGENETICS NV

97WO-EP002002. 96EP-00870053.

21-APR-1997; 19-APR-1996; .; 0

Gaps

. 0

Sequence 21 BP; 7 A; 6 C; 8 G; 0 T; 0 U; 0 Other;

95US-00577081 95US-00577081

YANG S Y. CEREB N.

ò g

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Testing a tissue sample to determine the allelic type of a human leukcytre antigen class I gene comprises amplification of nucleic acid polymers with primers which flank a region including an allelic variation of the HLA class I gene.
                         Tissue sample testing; allelic typing; human leukocyte antigen; PCR primer; probe; hybridisation; intron; amplification; ss; allelic variation; non-classical HLA class I gene; exon.
Hybridisation probe GE2-183 for typing HLA Class I genes
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 8; 90pp; English.
                                                                                                                                                                                                                                                                                                 WPI; 2000-223159/19
                                                                                                                                                                                                                                                                   Cereb N, Yang SY;
                                                                                                                                                                                                22-DEC-1995;
                                                                                                                                                                      22-DEC-1995;
                                                                                    Homo sapiens
                                                                                                             US6030775-A.
                                                                                                                                          29-FEB-2000.
                                                                                                                                                                                                                           (CERE/)
(YANG/)
 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV02716-V02738 are hybridisation probes used in a novel method for testing tissue samples to determine the allelic type of a human leukocyte artigen (HLA) class I gene in the sample. The HLA Class I gene is selected from among HLA-A, -B and -C genes. The method comprises of treating the tissue sample to obtain nucleic acid polymers suitable for amplification then combining these polymers with a first primer which hybridises with a portion of intron 1 or intron 3 of the HLA Class I gene and a second primer which hybridises with a different portion of the HLA Class I gene under conditions suitable for amplification to obtain an amplified product. The product is then evaluated to determine the Allelic type of the HLA-Class I gene. The method is useful for tissue matching HLA class I antigens between donors and recipients and hence for preventing graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-based human leukocyte antigen class I gene typing method - useful for tissue matching and prevention of graft versus host disease.
                                                                                                                                                                                                                donor;
                                                                                                                                                                                                             Human leukocyte antigen class I gene; allele testing; probe; d
tissue matching; recipient; graft rejection; class typing; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.7%; Score 13.8; DB 1; Length 18; Best Local Similarity 88.2%; Pred. No. 1e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               (SLOK ) SLOAN KETTERING INST CANCER RES
                                                                                                                                                                                 Human Class I HLA gene probe GE2-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 10; 89pp; English.
                                                                                                 BP
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 741
                                                                                                 AAV02721 standard; DNA; 18
                                                                                                                                                       (first entry)
 GCCAGGAGAAACAG
                              GCCAGGAGAAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Cereb N;
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         04-JAN-1996;
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                                                                                                                                                       19-MAY-1998
                                                                                                                                                                                                                                                                                                WO9723645-A1
                                                                                                                                                                                                                                                                                                                            03-JUL-1997,
                                                                                                                                                                                                                                                       Synthetic
                            18
                                                                                                                            AAV02721;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang SY,
 728
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The invention relates to a method (I) for testing a tissue sample to determine the allelic type of a human leukocyte antigen (HLA) class I gene in the sample, where the HLA class I gene is selected from HLA-A, Gene in the sample, where the HLA class I gene is selected from HLA-A, in HLA-B or HLA-C, by: (a) treating the tissue sample to obtain nucleic acid polymers with a primer which hybridizes with a portion of intron 1 or intron 3 of the HLA class I gene, and a second primer which hybridizes with a different portion of the HLA class I gene and performing with a different portion of the HLA class I gene and performing in a policiation, where the primers flank a region including at least one site of allelic variation in at least one of exons 2 or 3 of the HLA class I gene and where the first primer is a locus specific primer which hybridizes with intron 1 or 3 of only one of the HLA class I gene and where the first primer is a locus specific primer which hybridizes with intron 1 or 3 of only one of the HLA class I genes; and consumption of a classical or non-classical HLA class I gene in the sample The method is useful for testing a tissue sample to determine the allelic type of a classical or non-classical HLA class I gene in the sample. The sequences AAAII039-AAII22 represent consensus sequences of introns and exons of the HLA genes and primers and probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicament; agonist; melanocortin receptor type 3; ACTH; PMN; MC3-R; adrenocorticotrophic hormone; neutrophil chemoattractant; antigout; polymorphonuclear cell; septic shock; skin disorder; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.7%; Score 13.8; DB 1; Length 18; Best Local Similarity 88.2%; Pred. No. 1e+02; Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine melanocortin receptor MC3-R amplifying primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 7 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 AGGAGAAACAGAACACC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 28
AAZ57075/c
ID AAZ57075 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGAGACACGGAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Gaps

6

747

731 AGGAGAAACAGAACACC

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AGGAGACACGGAACACC

AAA11105 standard; DNA; 18

RESULT 27

AAA11105,

28-JUL-2000 (first entry)

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Novel antisense compound targeted to nucleic acid molecule encoding tumor necrosis factor receptor 1 (TNFR1), useful for treating humans having disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe, hepatitis b virus, HBV detection, RT pol region, genetic analysis, precore region, HBSAg region, genotype specific target, mutation detection, ss.
                                                                                                                                                            The invention relates to an antisense compound 8 to 30 nucleotides in length targeted to nucleic acid molecule encoding tumour necrosis factor exceptor 1 (TNFR1), where the antisense compound inhibites expression of TNFR1. The antisense compound is useful for inhibiting the expression of TNFR1 in cells or tissues. The antisense compound is also useful for treating an animal (preferably human) having a disease or condition associated with TNFR1. e.g. a liver disease (such as heparitis, or liver injury) or a hyperproliferative disease (such as heparitis, or liver injury) or a hyperproliferative disease (such as cancer, by inhibiting the expression of TNFR1. The antisense compound is useful for disquestics, therapeutics, prophylaxis and as research reagents and kits. This polynucleotide sequence represents a mouse oligonucleotide relating to the TNFR1 of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a probe for the RT pol region of hepatitis b
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 3 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.6; DB 1;
Pred, No. 1.2e+02;
0; Mismatches 4;
Dean NM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe HBPr273 for RT pol region of HBV.
                                                                                                                                   Example 21; Page 61; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stuyver L, Rossau R, Maertens G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      727 TGCCAGGAGAACAGAACAC 746
Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 TGTAAGGAGACTCAGAACAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Fig 1; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     61.8%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-EP002002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV14107 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INNO-) INNOGENETICS NV
 Cowsert LM,
                                 WPI; 2002-583481/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-535867/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-2003
19-MAY-1998
Baker BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV14107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 30
AAV14107/c
 TX4XTTTX8XX000000000000X8
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                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the use of a compound comprising an amino acid as equence His-Phe-Arg-Trp (HFRW) in the manufacture of a medicament and/or an agonist of melanocortin receptor type 3 (MC3-R) where the compound is not adrenocorticotrophic hormone (ACTH)1-39. The compounds are used to inhibit neutrophil chemoattractant production, polymorphomuclear cell (PMV) accumulation or reduction/treatment of inflammation. Especially, these compounds are agonists of the MC3-R. The inflammatory response/disease is selected from gout, gouty arthritis, rheumatoid arthritis, asthma, reperfusion injury or damage, stroke, myocardial infarction, septic shock, or a skin disorder. Sequences AA257073-80 represent PCR primers used for amplifying murine melanocortin receptors
 melanocortin receptor; anti-inflammatory; antiasmatic; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense compound; tumour necrosis factor receptor 1; liver disease; TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer; mouse; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                     Inhibition of neutrophil chemoattractant production, inhibition of polymorphonuclear cell accumulation or reduction/treatment of inflammation using compounds comprising the peptide sequence HFRW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR1 expression modulation related antisense oligo SEQ ID No 196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                       Flower R;
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 8; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                       (HARV-) HARVEY RES LTD WILLIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              732 GGAGAACAGAACACCG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABT05166 standard; DNA; 20 BP
                                                                                                                                       99WO-GB002392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.7%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGAACAGAAGACAG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2001; 2001WO-US051224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-2000; 2000US-00695451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.77
Best Local Similarity 88.2°
Matches 15, Conservative
                                                                                                                                                                                                                                       Perretti M, Getting S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                     WPI; 2000-182651/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200248168-A1
                                                                     WO200005263-A2
                                                                                                                                       22-JUL-1999;
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                                                                                                     03-FEB-2000
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                                   Mus sp.
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Gaps

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Length 20;

schultz1-727.rng

Page 25

virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or a concentrating polymudicic acids (i) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 collected probes, which are applied to known locations on a solid support and hybridise specifically to mutant target sequences chosen from the HBV RT pol gene region, HBV PR complements or U for T chem HBV protector region, HBSAG region and/or HBV chomologues; (c) detecting the hybridis formed in step (b), and inferring the HBV genotype and/or mutants present in the sample from the HBV genotype and/or monitor HBV mutants and/or genotypes in a sample, collagnose and/or monitor HBV mutants and/or genotypes in a sample, specifically genotype, precore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs, e.g. lamivudune and penciclovir. (Updated on 27-AUG-2003 to correct OS field.)

Sequence 18 BP; 1 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Gaps o' Query Match 60.9%; Score 13.4; DB 1; Length 18; Best Local Similarity 93.3%; Pred. No. 1.2e+02; Matches 14; Conservative 0; Mismatches 1; Indels

à d RESULT 31 AAV14104/c

AAV14104 standard; DNA; 18 (first entry) (revised) 27-AUG-2003 19-MAY-1998 AAV14104;

Probe HBPr270 for RT pol region of HBV.

Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis; preCore region; HBsAg region; genotype specific target; mutation detection; ss.

Synthetic. Hepatitis B virus.

WO9740193-A2

30-OCT-1997.

97WO-EP002002 21-APR-1997; 96EP-00870053. 19-APR-1996;

(INNO-) INNOGENETICS NV

Maertens G; Stuyver L, Rossau R,

WPI; 1997-535867/49.

Detection and/or genetic analysis of hepatitis B virus - specifically genotype, precore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.

Claim 5; Fig 1; 80pp; English.

This sequence represents a probe for the RT pol region of hepatitis b virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or concentrating polynucleic acids (I) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1

suitable primer pair; (b) hybridising (I) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid support and hybridise specifically to mutant target sequences chosen from the HBV RT pol gene region, HBV precore region, HBSAg region and/or HBV genotype specific target sequences, or their complements or U for T homologues; (c) detecting the hybridis formed in step (b), and inferring the HBV genotype and/or mutants present in the sample from the diagnose and/or monitor HBV mutants and/or genotypes in a sample, specifically genotype, precore mutations and/or genotypes in a sample, gene mutations selected by treatment with drugs, e.g. lamivudune and penciclovir. (Updated on 27-AUG-2003 to correct OS field.)

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Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Gaps ., Query Match 60.9%; Score 13.4; DB 1; Length 18; Best Local Similarity 93.3%; Pred. No. 1.2e+02; Matches 14; Conservative 0; Mismatches 1; Indels

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RESULT 32 AAV14106/c

AAV14106 standard; DNA; 18 BP.

AAV14106;

(first entry) (revised) 27-AUG-2003 19-MAY-1998

Probe HBPr272 for RT pol region of HBV.

Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis; preCore region; HBSAg region; genotype specific target; mutation detection; ss.

Synthetic. Hepatitis B virus.

WO9740193-A2.

30-OCT-1997.

97WO-EP002002. 21-APR-1997;

96EP-00870053 19-APR-1996;

(INNO-) INNOGENETICS NV

WPI; 1997-535867/49.

Stuyver L, Rossau R, Maertens

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Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.

Claim 5; Fig 1; 80pp; English

This sequence represents a probe for the RT pol region of hepatitis b virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or concentrating polymucleic acids (1) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridising (1) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid support and hybridise specifically to mutent target sequences chosen from the HBV RT pol gene region, HBV preCore region, HBSAg region and/or HBV genotype specific target sequences, or their complements or U for T

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Gaps . 0

Length 20; 1; Indels

Score 13.4; DB 1; Pred. No. 1.2e+02; 0; Mismatches 1;

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The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1. PCNA and Cyclin B1.
Representative examples of Tibozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 100; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    Cdc 25 hs ribozyme binding site #50.
60.9%; Scc.
93.3%; Pred
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%;
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                                                                                                             728 GCCAGGAGAAACAGA 742
                                                                                                                                                                                                                                                                             AAA85942 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2000 (first entry)
              Query Match
Best Local Similarity 93.33
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                        17 GCCAGGAGAAACGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-412314/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200032765-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-1999;
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                                                                                                                                                                                                                                                                                                                             AAA85942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pritz R,
                                                                                                                                                                                                                                                    AAA85942
                                                                                                                                                        g
                                                                                                                                                                                                                                                                                  The invention provides a highly sensitive method for detecting variation of viruses using a 2-step polymerase chain reaction (nested PCR) regime. The method comprises: (1) amplification of a predetermined region of viral DNA in the first round of PCR; (2) treatment of the amplified of product with a restriction enzyme capable of cleavage of a product a second round of PCR using a primer designed to introduce a mismatch a second round of PCR using a primer designed to introduce a mismatch base, to form a restriction enzyme recognition site in the amplified product with a restriction enzyme capable of cleavage of the amplified product with a restriction enzyme capable of cleavage of the amplified product derived from the viral mutant, (4) treatment of the amplified product derived from the viral mutant, (5) detection of mutation of viruses by investigation of the restriction pattern. The method allows simple and highly sensitive detection of mutation in viral genomes using 2-step nested PCR method in a short period of time. Sequences AAX77255-263 represent PCR primers used for the detection of lamivadine resistant hepatitis B virus by the method of the invention. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                RT
                      in step (b), and inferring
                                                                                                        specifically genotype, precore mutations, vaccine escape mutations and gene mutations selected by treatment with drugs, e.g. lamivudune and penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A highly sensitive detection method for detecting lamivudine resistant hepatitis B virus - using nested PCR.
                                                                                                                                                                                                                                                                                                      Gaps
                                       the HBV genotype and/or mutants present in the sample from the differential hybridisation signal(s). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain reaction; nested PCR; viral; mutation detection; resistance; hepatitis B virus; PCR primer; ss.
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                                                                                                                                                                                                                                                       Score 13.4; DB 1; Length 18;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus genomic DNA amplifying primer BF108.
                                                                                                                                                                                                          Sequence 18 BP; 2 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
                   (c) detecting the hybrids formed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 6; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX77255 standard; DNA; 20 BP
                                                                                                                                                                                                                                                         60.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                             Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                      GCCAGGAGAAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
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Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAYA/) SAYAMA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-1997;
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04-AUG-1999
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lamivudine
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RESULT 33
AAX 77255, XX
XX
XX
XX
XX
XX
DDT 27-N
DDB Hepal
DDB Hepal
XX

Robbins JM;

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                    Gaps
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0
Score 13.2; DB 1; Length 19;
Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                              Cdc 25 hs ribozyme binding site #48.
                                      729 CCAGGAGAACAGAACAC 746
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                                                         18 CCAGGAGAAAAACAAAAC
                                                                                                        AAA85940 standard; DNA; 19
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encoding a cyclin or cell-cycle dependent kinase other than CDK1,

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                                                                                                                                                                                                     The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1. PCKN and Cyclin B1. Representative examples of ribozyme recognition sites are given in RAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                    New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
                                                                                                                                                                                                                                                                                                                   Gaps
Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis;
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                                                                                                                                                                                                                                                                                                  60.0%; Score 13.2; DB 1; Length 19; 83.3%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                   Sequence 19 BP; 1 A; 3 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                     Robbins JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robbins JM
                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                       Disclosure, Page 100; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclin Bl ribozyme binding site #8.
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                                                                                                                     Barber JR,
                                                                                                                                                                                                                                                                                                                                    730 CAGGAGAAACAGAACACC 747
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                                                                   99WO-US028772.
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AAA85679 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                  restenosis treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-412314/35
                                                                                                  (IMMU-) IMMUSOL INC
                                                                                                                     Welch PJ,
                                                                                                                                    WPI; 2000-412314/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMI-) IMMISOL INC
                                                                                                                                                                                                                                                                                                           Local Similarity
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                                 WO200032765-A2
                                                                                   04-DEC-1998;
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                                                 08-JUN-2000
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                                                                                                                     Tritz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tritz R,
                                                                                                                                                                                                                                                                                                   Query Match
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                 Mammalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                        The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1. FORA and Cyclin B1.
Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.0%; Score 13.2; DB 1; Length 19; 83.3%; Pred. No. 1.38+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 0 A; 8 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cdc25 hs ribozyme binding site SEQ ID NO:3526.
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                                                                     Disclosure; Page 96; 109pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               728 GCCAGGAGAAACAGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 GCGGGGAGAAGCAGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .102/c
AAH61102 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 15; Conserv
PCNA and Cyclin B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200130362-A2.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, dermatcological, cytostatic, antiseborrheic, antidiabetic, antisickling, ophthalmological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, aquamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adiasion and hypertrophic or hypertrophic burn scarring such as keloid, adiasion and hypertrophic or hypertrophic burn scarring such as keloids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 1 A; 3 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exemplification of the present invention
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60.0%; Score 13.2; DB 1; Length 19; llarity 83.3%; Pred. No. 1.3e+02; Conservative 0; Mismatches 3; Indels 730 CAGGAGAACAGAACACC 747 19 CAGGAGAAAAACAAAACC 2 Query Match Best Local Similarity Matches 15; Conserv

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Gaps . 0

RESULT 38

Cdc25 hs ribozyme binding site SEQ ID NO:3528.

Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antisioriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; scaraolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma;

Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.

Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.

Robbins JM, Tritz R;

WPI; 2001-300427/31.

Example 1; Page 309; 408pp; English.

Example 1; Page 328; 408pp; English.

The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a

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ribozyme (1) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, ophthalmological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detechment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn sear. AAMS7577 to AAMS2099 represent sequences used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation, cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclin B1 ribozyme binding site SEQ ID NO:3265.
                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  729 CCAGGAGAACAGAACAC 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 ccaggagaaaaaaaaa
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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytokine involved in cill amation matrix metalloproteinase (MPM), cytolin, cell-cycle dependent kinase, growth factor or a reductase, or administering a concleic acid molecule (II) comprising a promoter operably linked to a concleic acid molecule (II) comprising a promoter operably linked to a concleic acid segment encoding [1]. ([1] can have antiposolatic, cophthalmological, vulnerary, keracloytic antidiabetic, antisickling, cophthalmological, vulnerary, keracloytic and virrode activities, and cleaves RNA encoding cytokine involved in inflammation. ([1] can be used (1] carcinome and viral or sebortheic wart. They can case therapy. ([1] and ([1] are useful for treating proliferative skin cleaves RNA encoding cytokine involved in inflammation. ([1] can be used ([2] carcinome and viral or sebortheic wart. They can case therapy. ([1] and ([1] are useful for treating proliferative skin case as socials of carcinome and viral or sebortheic wart. They can case therapy, virrecreting poliferative and in the relinopathy, virrecretinopathy, sickle cell retinopathy, retinopathy, virrecretinopathy, sickle cell retinopathy, virrecretinopathy, social design and hypertrophic or hypertrophic burn case semplification of the present invention

XX Sequence 19 BP; 0 A; 8 C; 3 G; 8 T; 0 U; 0 other;

Cy 728 GCGGGAGAAACACAACA 1

Best Local Similarity 83.3%; Pred; No. 1.3e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

MAZOSIO7

IN AAZOSIO7

AAZOSIO7;

AAZOSIO7;

AAZOSIO7;
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Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; notolusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORPS) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs encode polypeptides (see AAX1675+Y37499) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also
                                                                                                                                                                                                                                                                                                                                                PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of Chlamydia trachomatis.
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97FR-00016034.
98US-0107077F.
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                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9928475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-DEC-1997;
04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1997;
                                                                                                                                                                                                                                                               07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
RESULT 40
AAZO5107
ID AAZO5107
XX AAZO51
XX AAZO51
XX AAZO51
XX VACC11
XW VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, originalis, cervicitis, allinguis, perinapatitis, bartholinitis; penumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                        60.0%; Score 13.2; DB 1; Length 20; 83.3%; Pred. No. 1.38+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                    Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human HTPL scanning oligonucleotide SEQ ID 1254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 228; 718pp; English.
                                                                                                                                                                                                                                                                                  729 CCAGGAGAAACAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
33-JAN-2001; 2001WO-US000669.
33-MAY-2001; 2001WS-02800669.
                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2002; 2002EP-00001167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                        1 ccassasacraasaacac
                                                                                                                                                                                                                                                                                                                                                                                                                     ABV80008 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-676582/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AEOM-) AEOMICA INC
                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1229046-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV80008;
                                                                                                                                       diseases
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhan J;
                                                                                                                                                                                                                                                                                                                                                                         RESULT 41
ABV80008/c
ID ABV8000
                                                                                                                                                                                                                                              Matches
   8
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mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorders associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 2 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
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58.2%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 1.4e+02; ive 0; Mismatches 2; Indels 727 IGCCAGGAGAACAGA 742 Query Match Best Local Similarity 87.55 Matches 14, Conservative

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Gaps .

> recedercadacaca 2 17

ABV80009 standard; DNA; 17

(first entry) 03-JAN-2003 ABV80009;

Human HTPL scanning oligonucleotide SEQ ID 1255.

Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.

Homo sapiens

EP1229046-A2

07-AUG-2002

28-JAN-2002; 2002EP-00001167 30-JAN-2001;

30-JAN-2001, 2001WO-US000664. 30-JAN-2001, 2001WO-US000665. 30-JAN-2001, 2001WO-US000667. 30-JAN-2001, 2001WO-US000666. 30-JAN-2001, 2001WO-US000669. 31-MAY-2001, 2001US-00864761.

(AEOM-) AEOMICA INC

Zhan J;

WPI; 2002-676582/73.

Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.

Example 2; Page 228; 718pp; English

The present invention relates to human testis expressed Patched like protein (HTPL, see ABV97875). HTPL and ABP9519 to ABP9520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-6 (\$ for short) compared to HTPL- (I for long). HTPL shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar

÷ to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10p12.1 HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder sascotated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal livez, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention This invention describes novel tumor cells (I), with a combination of major histocompatibility (MHC) I and II genes occurring in humans. The tumor cells, tumor cell library or vaccine described in the invention can be used for the prophylaxis or treatment of tumor diseases. AAZ88790-Z88805 represent PCR primers used to amplify the human lymphocyte HLA molecules described in the method of the invention. Human, HLA; tumor cell, major histocompatibility complex; MHC; vaccine; prophylaxis; treatment; lymphocyte; HLA; PCR primer; ss. Tumor cells expressing human MHC I and II genes, methods of producing these and vaccines for immunotherapy of tumors. Gaps ö 58.2%; Score 12.8; DB 1; Length 17; llarity 87.5%; Pred. No. 1.4e+02; Conservative 0; Mismatches 2; Indels Sequence 17 BP; 2 A; 4 C; 4 G; 7 T; 0 U; 0 Other; Human HLA Cw*07 gene PCR primer Cw*07 forward. Example 3; Page 8; 17pp; German. 742 99WO-DE002280. 98DE-01032840 16 receasereaacaca 1 AAZ88792 standard; DNA; 19 727 TGCCAGGAGAACAGA 18-MAY-2000 (first entry) (KERK/) KERKMANN-TUCEK A. WPI; 2000-182538/16. Local Similarity hes 14; Conser Kerkmann-Tucek A; WO200004918-A2 Homo sapiens. 21-JUL-1999; 21-JUL-1998; 03-FEB-2000 AAZ88792; Query Match Best Loca Matches RESULT 43 886666666666888 à d

58.2%; Score 12.8; DB 1; Length 19; 87.5%; Pred. No. 1.5e+02; rative 0; Mismatches 2; Indels Query Match
Best Local Similarity 87.5
Matches 14; Conservative

Sequence 19 BP; 7 A; 5 C; 7 G; 0 T; 0 U; 0 Other;

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Gaps

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729 CCAGGAGAAACAGAAC 744

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Melanocortin 4 receptor; MC4R; G-protein coupled receptor; appetite; metabolic disorder; cachexia; anorexia; weaning-induced inappetance; growth; diabetes; cancer; renal failure; cardiac disease; endotooxaemia; fever; hepatic lipidosis; infection; inflammation; post partum sow; dairy cow; livestock; poultry; shipping stress; crowding stress; obesity; vaccine; PCR; primer; ss.

Melanocortin 4 receptor (MC4R) detection, reverse PCR primer.

(first entry)

08-MAY-2002 ABK15582;

ABK15582 standard; cDNA; 19 BP.

g

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ABK15582,
                                                                                                   The invention describes a substantially pure canine or feline melanocortin 4 receptor (MC4R) polypeptide (I). The polypeptide can be used in the treatment of appetite-related or metabolic disorders including cachexia, anorexia or weaning-induced inappetance and growth lag, diabetes, cancer, renal failure, cardiac disease, endotoxaemia, cever, hepatic lipidosis, infection or inflammation, in a post patrum sow, dairy cow, companion animal. livestock animal, poultry animal, obesse animal or a gravid animal. (I) is useful in the generation of contribodies, as reagents in diagnostic assays, identification of other cellular gene products involved in the regulation of appetite in animals, as reagents in assays for screening for compounds that can be used in the treatment of appetite disorders in animals. A ligand of MC4R is useful for elaborating the biological function of MC4R gene product and for ameliorating appetite disorders and metabolic disorders, in animals. This sequence represents the reverse primer used with primer ABK15584 to isolate feline and canine melanocortin 4 receptor (MC4R) clones, a G-protein coupled receptor described in the method of the invention
                                                                                                                                                                                                                                                                                                      Melanocortin 4 receptor; MC4R; G-protein coupled receptor; appetite; metabolic disorder; cachexia; anorexia; weaning-induced inappetance; growth; diabetes; cancer; renal failure; cardiac disease; endotoxaemia; fever; hepatic lipidosis; infection; inflammation; post partum sow; dairy cow; livestock; poultry; shipping stress; crowding stress; obesity; vaccine; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel canine or feline melanocortin 4 receptor polypeptide for screening modulator compounds useful for treating cachexia, anorexia, diabetes and
                                                                                                                                                                                                                                                                      Melanocortin 4 receptor (MC4R) isolation, reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robertson AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 10; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001; 2001EP-00305509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2000; 2000US-0213909P
CCGGGAGACACAGAAC 19
                                                                                                   585/c
ABK15585 standard; cDNA; 19
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houseknecht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-156598/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                           08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hickman MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JAN-2002.
                                                                                                                                                                           ABK15585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Felidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer.
                                                                                             ABK15585/
XXX ABK15585/
XXX ABK12
XXX ABK12
XXX Mela:
XXX Mela:
XXX Mela:
XXX ABC CO
XXX Cali;
X
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Novel canine or feline melanocortin 4 receptor polypeptide for screening modulator compounds useful for treating cachexia, anorexia, diabetes and

Robertson AS;

Hickman MA, Houseknecht KL,

WPI; 2002-156598/21.

cancer.

(PFIZ) PFIZER PROD INC.

26-JUN-2001; 2001EP-00305509. 26-JUN-2000; 2000US-0213909P.

EP1167386-A1. 02-JAN-2002.

Canidae.

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The invention describes a substantially pure canine or feline
melanocortin 4 receptor (MC4R) polypeptide (1). The polypeptide can be
used in the treatment of appetite-related or metabolic disorders
including cachexia, anorexia or wearing induced inappetance and growth

[19] diabetes, cancer, renal failure, cardiac disease, endotoxaemia,
[20] fever, hepatic lipidosis, infection or inflammation, in a post partum
[20] sow, dairy cow, companion animal, livestock animal, poultry animal,
[21] animal suffering from shipping or crowding stress, lactating animal,
[22] consea animal or a gravid animal. (1) is useful in the generation of
[23] antibodies, as reagents in diagnostic assays, identification of other
[23] callular gene products involved in the regulation of appetite in animals,
[24] cas reagents in assays for screening for compounds that can be used in the
[25] treatment of appetite disorders in animals. A ligand of MC4R is useful
[26] constants appetite disorders and metabolic disorders, in animals. This
[27] sequence represents the reverse primer used with primer ABK15581 to
[28] isolate felline and canine melanocortin 4 receptor (MC4R) clones, a G-
[26] protein coupled receptor described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.6; DB 1; Length 19;
Pred. No. 1.6e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Example 1; Page 27; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            728 GCCAGGAGAACAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 GCAAGGAGCTACAGATCAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.3%;
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AAS56856/c
ID AAS56856 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 78.9
Matches 15, Conservative
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BP.

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Gaps ; 0

57.3%; Score 12.6; DB 1; Length 19; 78.9%; Pred. No. 1.6e+02; ive 0; Mismatches 4; Indels

0;

Conservative

728 GCCAGGAGAACAGAACAC 746

GCAAGGAGCTACAGATCAC 1

19

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AAS56856;

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Sequences AAS56729-AAS56968 represent DNA encoding BRCA-1 regulators, ribozyme target recognition RNA sequences, DNA fragments encoding the RNA and primers used in the methods of the invention. Hybridisation of ribozymes to their targets results in cleavage of the RNA target. The ribozymes can be used to cleave regulators of the tumour suppressor BRCA-1, resulting in upregulation or downregulation of BRCA-1 in a cell. The mRNA targets include those encoding the BRCA-1 regulator BR1, inhibitor CHIRZ, AF6, BRZ and BR3. Regulation of BRCA-1 is useful for treating and diagnosing cancer and other proliferative disorders. The severity of an incleance of cancer can be lessened by regulating tumour proliferation through modulation of BRCA-1. The sequences of the invention are useful in the development of anti-cancer drugs
                                                                                                                    Human, BRCA-1 regulator, ribozyme, BR1, RNA target recognition, probe;
ycrostatic, RNA cleavage, tumour suppressor; PCR primer, CHLR2, AR6; BR2,
inhibitor dominant negative 4; breat basic conserved protein 1; BBC1;
BR3; ID4; cancer; proliferative disorder; tumour proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides that are the regulators of BRCA-1, useful for treating cancer and diagnosing the presence of neoplastic cells in biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance; mutation detection; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.4%; Score 12.4; DB 1; Length 16; 92.9%; Pred. No. 1.6e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HBV DNA polymerase gene L528M mutation probe HBPr293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16 BP; 0 A; 2 C; 6 G; 8 T; 0 U; 0 Other;
                                                                                   Validation ribozyme DNA sequence #30.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Barber J, Wong-Staal F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 8, 97pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-00536058.
                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US009559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              734 AGAAACAGAACACC 747
                                                 16-JAN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  (IMMU-) IMMUSOL INC. (BEGE/) BEGER C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-611503/70
                                                                                                                                                                                                                                          WO200170982-A2.
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    Beger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sample.
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The present sequence is a probe used in a method for monitoring antihepatitis B virus (HBV) drug resistance in a patient by genetic detection of any one of mutations 1528M, M552V/I and/or V/L/M551 in HBV DNA polymerase in a biological sample from the patient. The method is useful in the field of genetic detection of anti-HBV drug resistance during HBV therapy. The method is rapid, reliable and precise
                                                                                                                                                                                                                               Monitoring anti-HBV drug resistance by genetic detection of mutations in DNA polymerase of HBV in patient's sample, involves hybridizing the polynucleic acids of the sample with a probe and detecting the hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                       56.4%; Score 12.4; DB 1; Length 17; 92.9%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 1 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human HTPL scanning oligonucleotide SEQ ID 1257.
                                                                                                                                                                             Van Geyt C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;0
                                                                                                                                                                                                                                                                                       Claim 2; Page 9; 64pp; English
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2001WO-US000667
2001WO-US000667
2001WO-US000667
2001WG-US00669
2001UG-0327898P
                                                                                                           99EP-00870148.
99US-0143546P.
                                                                                 05-JUL-2000; 2000WO-EP006306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              728 GCCAGGAGAACAG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV80011 standard; DNA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GCCAGGAGAACGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 92.9
nes 13; Conservative
                                                                                                                                                                              Stuyver L, Maertens G,
                                                                                                                                                  (INNO-) INNOGENETICS NV
                                                                                                                                                                                                        WPI; 2001-138370/14
Hepatitis B virus.
                           WO200104358-A2
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30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                           08-JUL-1999;
13-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1229046-A2
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                                                       18-JAN-2001
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Best Local S
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23-MAY-2001; 09-OCT-2001;

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Gaps ö

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09-0CT-2001; 2001US-0327898P.
                                     (AEOM-) AEOMICA INC.
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                                                                                                                                                                                                                The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The chard structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL gene was important in regulating male germ cell development, and the HTPL gene was mappered to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, andlt and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention
                                                                                                         Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, gene therapy, tumour suppressor, HTPL, chromosome 10p12.1; human testis sypressed Patched like protein, testis, adrenal, liver, humen germ cell development, bone marrow, brain; kidney, lung, placenta, prostate, skeletal muscle, colon, male infertility, cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HTPL scanning oligonucleotide SEQ ID 1256.
                                                                                                                                                                                   Example 2; Page 228; 718pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 49
ABV800100/C
ID ABV80010 standard; DNA; 17 BP.
XX
AC ABV80010;
XX
DT 03-JAN-2003 (first entry)
XX
DT Human HTPL scanning oligonucleot.
XX
Human testis expressed Patched lix
XM
Human testis expressed Patched lix
XM
Male germ cell development; bone
XM
MORE Sapiens.
XX
FOMO Sapiens.
XX
N
D7-AUG-2002.
XX
PN
SPI229046-A2.
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PN
SPI229046-A2.
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SPI229046-A2.
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PN
30-JAN-2001; 2001W0-US000663.
PR
30-JAN-2001; 2001W0-US000664.
PR
30-JAN-2001; 2001W0-US000665.
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30-JAN-2001; 2001W0-US000666.
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30-JAN-2001; 2001W0-US000666.
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30-JAN-2001; 2001W0-US000666.
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30-JAN-2001; 2001W0-US000669.
PR
30-JAN-2001; 2001W0-US000669.
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30-JAN-2001; 2001W0-US000669.
PR
330-JAN-2001; 2001W0-US000669.
PR
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                                                                       WPI; 2002-676582/73.
(AEOM-) AEOMICA INC
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The present invention relates to human testis expressed Patched like correct invention relates to human testis expressed Patched like brotein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL constructions, with a few single base pair changes introduces a premature stop codon in HTPL-8 (S for short) compared to HTPL-10. Life long). HTPL codon in HTPL-8 (S for short) compared to HTPL-10. Life long). HTPL codon in HTPL-8 (S for short) compared to HTPL-10. Life long). HTPL codon in HTPL plays a role similar content of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome lopiz.1. HTPL and its coding sequence are consequent for diagnosting a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture with decreased expression or activity of human HTPL. Such disorders include disorders expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foctal liver, bone marrow, brain, kidney, lung, placenta, prostate, colinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention
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Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                          Example 2; Page 228; 718pp; English
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ID AAQ69166 standard; DNA; 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 92.9
Matches 13, Conservative
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14-FEB-1995 (first en
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07-JAN-1994;
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AAV14109;
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                                                                                                                                          The sequence is that of a PCR primer used for the amplification of a leucocyte derived growth factor 2 having mitogenic and/or chemctactic activity. LDGF2 reacts with PDGF receptors and can be used in wound healing, coagulation, inflammation, immune responses and cell growth. See also AAQ69162-73. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe, hepatitis b virus, HBV detection, RT pol region, genetic analysis, preCore region, HBsAg region, genotype specific target, mutation detection, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a probe for the RT pol region of hepatitis b virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or concentrating polynucleic acids (1) in the sample, and amplifying the selevant part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridising (1) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid
                                                       New leukocyte derived growth factor 2 - having mitogenic and/or chemotactic activity, partic. for connective tissue cells, used esp. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                           56.4%; Score 12.4; DB 1; Length 18; 92.9%; Pred. No. 1.76+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                  Seguence 18 BP; 1 A; 4 C; 3 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe HBPr278 for RT pol region of HBV.
                                                                                                                  Disclosure; Page 24; 58pp; English
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(first entry)
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Matches 13; Conservative
 lida N;
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                           WPI; 1994-249217/30.
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Hepatitis B virus.
 Grotendorst GR,
                                                                                      wound healing
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19-MAY-1998
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the HBV RT pol gene region, HBV precore region, HBSAg region and/or HBV genotype specific target sequences, or their complements or U for T homologues; (c) detecting the hybrids formed in step (b), and inferring the HBV genotype and/or mutants present in the sample from the differential hybridisation signal(s). The composition can be used to specifically genotype, Precore mutants and/or genotypes in a sample, specifically genotype, Precore mutantions, vaccine escape mutations and RT gene mutations selected by treatment with drugs, e.g. lamivudune and penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a probe for the RT pol region of hepatitis b virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or concentrating polymucleic acids (1) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridising (1) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid support and hybridise specifically to mutant target sequences chosen from the HBV RT pol gene region, HBV precore region, HBSA; region, HBSA; region and/or HBV genotype specific target sequences, or their complements or U for T homologues; (c) detecting the hybrids formed in step (b), and inferring the HBV genotype and/or mutants present in the sample from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe, hepatitis b virus, HBV detection, RT pol region, genetic analysis, preCore region, HBsAg region, genotype specific target, mutation detection, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.
                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                        56.4%; Score 12.4; DB 1; Length 18; 92.9%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV14109 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                             Query Match 56.4
Best Local Similarity 92.9
Matches 13; Conservative
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Hepatitis B virus.
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19-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRC8; Translocation in Renal cancer from Chromosome 8; fused DNA; 3,2; FHIT/TRC8 fusion DNA; sporadic renal cell carcinoma; TRC8/FHIT; TRC8FHIT; human chromosomal translocation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel Translocation in Renal cancer from Chromosome 8 genes, useful for detection of tumors, comprises rearrangements in the t(3;8) (p14.2;q24.1) chromosomal translocation which occurs in renal and thyroid carcinomas.
differential hybridisation signal(s). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, specifically genotype, precore mutations, vaccine escape mutations and gene mutations selected by treatment with drugs, e.g. lamivudune and penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                 Gaps
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                                                                                                                                                       56.4%; Score 12.4; DB 1; Length 18; 92.9%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                    Seguence 18 BP; 1 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 19 BP; 2 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRC8 related PCR primer SEQ ID No 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 10; 49pp; English
                                                                                                                                                                                                                                                                                                                                  02-JUL-2001; 2001US-00898533
                                                                                                                                                                                                                                        728 GCCAGGAGAACAG 741
                                                                                                                                                                                                                                                                          GCCAGGAGAACGG 5
                                                                                                                                                                                                 13; Conservative
                                                                                                                                                                            Similarity
                                                                                                                                                       Query Match
Best Local 8
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                                                                                                                                                                                               Matches
    88888888
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56.4%; Score 12.4; DB 1; Length 19;

Query Match

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                                                                                                                                                                                                                                                                                     Human, ss; translocation in renal cancer from chromosome 8; 4F; TRC8; fragile histidine triad; FHIT; renal cell carcinoma; t(3; 8); esingle-stranded conformational polymorphism; thyroid tumour; PCR; primer; SSCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a polypeptide (which is the product of the expression in a host cell of a DNA) TRC8 (Translocation in Renal Cancer from Chromosome 8). Also included are a polypeptide product of the expression in a host cell of a DNA, comprising (a) culturing a host cell of a DNA, comprising (a) culturing a host cell opolypeptide comprising TRC8 and (b) recovering the polypeptide. The gene encoding TRC8 is located in the chromosomal translocation region t(3;8), resulting in a fusion with the fragile histidine triad gene, FHIT. This region id associated with renal and thyroid tumours (especially renal call carcinoma, RCC). The polypeptide is useful for diagnosing tumours, particularly for determining if the TRC8 gene is expressed in samples. The present sequence is an single-stranded conformational polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New TRC8 (Translocation in Renal Cancer from Chromosome 8) polypeptide, useful for diagnosing tumors, particularly for determining TRC8 gene expression in samples.
               Gaps
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               Indels
 92.9%; Pred. No. 1.7e+02;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 2 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                   Human TRC8 coding region SSCP PCR primer 4F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sporadic renal cell carcinoma samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Col 17; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0077723P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00268140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYTE-) UNIV TECHNOLOGY CORP.
                                                 727 TGCCAGGAGAACA 740
                                                                                                                                RESULT 54
ABK10445/c
ID ABK10445 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             727 TGCCAGGAGAACA 740
                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drabkin HA;
                                                                        16 TGCCAGGACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-224110/28.
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Best Local Similarity
Matches 13; Conserv
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                 21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2001.
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                                                                                                                                                                                                   ABK10445;
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AAZ70293/c
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A265654 to AA269578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AA265579 to AAA7740 represent amplification primers for the biallelic markers. The biallelic markers of the invention primers for the biallelic markers. The biallelic markers of the invention can are genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel biallelic markers used to construct a high density disequilibrium
                                                                                                   Human biallelic marker upstream amplification primer SEQ ID NO:4649
                                                                                                                            Human genome, biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genomic SNP allele specific oligonucleotide SEQ ID NO:188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.5%; Score 12.2; DB 1; Length 18; 82.4%; Pred. No. 1.8e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 1222; 2745pp; English.
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                                                                                                                                                                                                                                                                                                                                          99WO-IB000822.
                                                                                                                                                                                                                                                                                                                                                                         98US-0082614P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 AGGAGAACAGAGGAAC 1
AAZ70293 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA36131 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-2000 (first entry)
                                                                    (first entry)
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nes 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-013267/01.
                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                             21-APR-1998;
                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                         WO9954500-A2
                                                                                                                                                                                                                                                                                                                                          21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                           23-NOV-1998;
                                                                 10-SEP-2001
                                                                                                                                                                                                                                                                                                        28-OCT-1999
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                                  AAZ70293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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ID AAA36
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AC AAA36
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DT 26-JI
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A method has been developed for detecting the presence or absence of a single nucleotide polymorphism (SNP) allele in a genomic sample. The method comprises preparing a reduced complexity genome (RCG) from the genomic sample and analysing the RCG for the presence or absence of a SNP allele. The method can be used to characterise a tumour, to generate a genomic pattern for an individual genome or to generate a genomic classification code for a genome. The method can be used to assess whether a subject is at risk for developing a disease or to identify a set of SNP alleles associated with a disease. The method can also be used to perform linkage analysis. AAA35944 to AAA35947 represent sequences used in the exemplification of the present invention. AAA35948 to
                                                                                                                                                                                                                                                                                                                                             Detection of single nucleotide polymorphisms in genomes by preparation and analysis of reduced complexity genomes, useful for genotyping, fingerprinting and determining allele frequency of SNPs.
Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis; allele specific ollogonucleotide; ASO; reduced complexity genome; RCG; genomic classification; identification; DNA fingerprinting; tumour characterisation; hybridisation; SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gastric acid production inhibiting oligonucleotide SEQ ID NO: 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gastric acid disturbance, gastric reflux, gastritis, dyspepsia, stomach ulcer, duodenal ulcer, Helicobacter pylori, antisense, DNA-RNA hybrid, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA36632 represent nucleotide sequences containing SNPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 1 A; 2 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                               Charest A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.5%; Scor.
100.0%; Pred. No. 1...
                                                                                                                                                                                                                                                  (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                               Housman DE,
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 59; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF16608 standard; DNA; 17 BP.
                                                                                                                                                                                                                  98US-0101757P.
                                                                                                                                                                                  99WO-US022283
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Best Local Similarity 100.'
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                                                                                                                                                                                                                                                                                 Landers JE, Jordan B,
                                                                                                                                                                                                                                                                                                                WPI; 2000-293181/25.
                                                                                                                   WO200018960-A2
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                                                                                      Homo sapiens
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                                                                                                                                                  06-APR-2000.
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AAF16608
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24-MAY-2000; 2000WO-AU000498.

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Page

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ACC54250 standard; DNA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPI; 2003-250498/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                  ACC54250;
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                                                                                                                                         The present invention provides oligonucleotides, and methods for their use, which are useful in modulating the action of proteins involved in gastric acid production. The target protein is preferably the histamine Hz receptor or one of the proteins which form part of the gastric protein pump. The sequences and methods of the invention are useful in the treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers, duodenal ulcers and other gastric acid disturbances, most of which are caused by Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, gene therapy, tumour suppressor, HTPL, chromosome 10p12.1; human testis expressed Parched like protein, testis; adrenal; liver, male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                           Treating gastric acid disturbance by administering an oligonuclectide which modulates the activity of a polypeptide involved in gastric acid production or secretion.
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                        53.6%; Score 11.8; DB 1; Length 17; 86.7%; Pred. No. 2e+02; 2; Indels cive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                     Sequence 17 BP; 10 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human HTPL scanning oligonucleotide SEQ ID 1253.
                                                                                                                      Example 3; Page 149; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                        ABV80007 standard; DNA; 17 BP
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30-JAN-2001, 2001WO-US000664.
30-JAN-2001, 2001WO-US000665.
30-JAN-2001, 2001WO-US000668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00669.
23-MAY-2001; 2001US-00864761.
09-OCT-2001; 2001US-0327898P.
99AU-00000510
                                                                                                                                                                                                                                                                                                   734 AGAAACAGAACACCG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002EP-00001167
                                                                                                                                                                                                                                                                                                                      3 AGGAACAGAACACAG 17
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Best Local Similarity bo...
Best Local 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-676582/73
                                                           WPI; 2001-025093/03
                  (TACH/) TACHAS G.
24-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1229046-A2
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                                                                                                                                                                                                                                                                                                                                                                                             ABV80007;
                                       Tachas G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhan J;
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL have isoforms, with a few single base pair differences between the cut. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the patched protein. The shares an overall structure organisation with the patched protein. The codon in HTPL-S and is a potential tumour suppressor. HTPL gene was important in regulating male germ cell development, and the HTPL gene was compared to human chromosome 10pl2.1. HTPL and is coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and fortune in the inverse of colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an account of an analysis of analysis of an analysis of an analysis of an analysis of an analy
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for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.6%; Score 11.8; DB 1; Length 17; Best Local Similarity 86.7%; Pred. No. 2e+02; Matches 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 17 BP; 1 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                               Example 2; Page 228; 718pp; English
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The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence with, after optimal alloament, at least 80 % identity to the 17 mer sequence that of any of them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic caids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti) sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the production of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alaheimer's disease and central analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diseases. The polypeptides can also be used to generate antibodies, and
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       The
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with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
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                                                                                                                                                                                                                                                                                                                         53.6%; Score 11.8; DB 1; Length 17;
86.7%; Pred. No. 2e+02;
live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                        Sequence 17 BP; 3 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABT35836 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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ACT35836/A
ACT36836/A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligomucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; se.
                                                                                                                                     Gaps
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                                                                                                       1; Length 17;
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                                                                                                                                     Indels
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                                                                           Seguence 17 BP; 1 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                           HBV hammerhead ribozyme substrate sequence #137.
                                                                                                      Score 11.8; DB 1
Pred. No. 2e+02;
0; Mismatches
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                                                                                                      53.6%;
86.7%;
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08-UUN-2001, 2001US-00877478.
08-UUN-2001, 2001US-0296876P.
24-OCT-2001, 2001US-0335059P.
05-DEC-2001, 2001US-0337055P.
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Roberts E;
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MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
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                                                                                                    Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis B virus.
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LEE P.
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(MACE/)
(MCSW/)
(MORR/)
(PAVC/)
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(ROBE/)
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and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, inozymes, zinzymes, amberzymes, and G-claaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecule, Hepatitis C virus, HCV; Hepatitis B virus, HBV; RNA stability; RNA expression, RNA synthesis; antisense; enzymatic nucleic acid, harmer/head ribozyme; DNAzyme; inozyme; zinzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state, HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.
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                                                                                                                                                                                                                                                                                   Seguence 17 BP; 0 A; 5 C; 4 G; 0 T; 8 U; 0 Other;
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Matches
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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HVV) or Hepatitis B virus (HVV) and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene archive and expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, inozyme, zinzyme, DNAzyme or amberzyme sequences
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                                    Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.6%; Score 11.8; DB 1; Length 17; Best Local Similarity 86.7%; Pred. No. 2e+02; Matches 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 1 A; 5 C; 4 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HBV inozyme substrate sequence #177.
                                                                                                                   Example 1; Page 138; 387pp; English
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ACD51996/c
ID ACD51996 standard; RNA; 17 BP.
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08-JUN-2001, 2001US-00877478.
08-JUN-2001, 2001US-0296876P.
24-OCT-2001, 2001US-0337055P.
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(BLAT/) BLATT L.
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17 GCCAAGAGAAACGGA 3
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WPI; 2003-229207/22
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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 68 identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies or viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides and polypeptides can be used to screen for their specific interactive molecules, and also be used to screen for their specific interactive molecules.
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                                                                                                                                                                  New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
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Pred. No. 2e+02;
0; Mismatches
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                                                                                                                                                                                                                                                                                        Disclosure; Page 756; 771pp; French.
                                                                           Tuijnder M;
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86.7%; Pred
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                      (MOLE-) MOLECULAR ENGINES LAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 rcccassasarcas 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 86.7 les 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INNO-) INNOGENETICS NV.
                                                                           Telerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9740193-A2
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19-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV14103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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AAV14103/
임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic molecules include antisense and enzymatic nucleic acids such as hammerada ribozymes, DNAzymes, anceid acoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV genes and MBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression of HBV genes and MBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                        Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                            ٠<u>,</u>
                                                                                                                                                                                                               Lee
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Pred. No. 2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                            Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour suppression/reversion associated nucleotide #6198.
                                                                                                                                                                                                            Mcswiggen J, Morrissey D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 0 A; 6 C; 3 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 153; 387pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disclosed in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.6%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-2002; 2002WO-IB004219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       728 GCCAGGAGAAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-2001; 2001FR-00011981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCAAGAGAAACGGA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                            Macejak D,
Roberts E;
                      MCSWIGGEN J.
MORRISSEY D.
PAVCO P.
LEE P.
DRAPER K.
ROBERTS E.
                                                                                                                                                                                                                                                                                        WPI; 2003-229207/22.
  MACEJAK D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003040369-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2003
                                                                                                                                                                                                         Blatt L, N
Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                   infection.
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                                                                                                    (LEEP/)
(DRAP/)
(ROBE/)
MACE/)
                         (MCSW/)
(MORR/)
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Gaps

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DB 1; Length 17; 2; Indels

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This sequence represents a probe for the RT pol region of hepatitis by virus (HBV). This sequence can be used in the method of the invention for detection and/or generic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releasing, isolating or concentrating polynucleic acids (I) in the sample, and amplifying the concentrating polynucleic acids (I) in the sample with at least 1 suitable primer pair; (b) hybridising (I) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid support and hybridises specifically to mucant rarget sequences chosen from the HBV RT pol gene region, HBV procore region, HBSAg region and/or HBV genotype specific target sequences, or their complements or U for T complements (c) detecting the hybrids formed in step (b), and inferring the HBV genotype and/or mutants present in the sample from the differential hybridisation signal (s). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, gene mutations selected by treatment with drugs, e.g. lamivudune and pencicleovir. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis; preCore region; HBsAg region; genotype specific target; mutation detection; ss.
                                                                  Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.6%; Score 11.8; DB 1; Length 18; 86.7%; Pred. No. 2.1e+02; live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 1 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe HBPr271 for RT pol region of HBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maertens G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maertens
                                                                                                                                       Claim 5; Page 32; 80pp; English
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Best Local Similarity 86.7°
Matches 13, Conservative
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 Stuyver L, Rossau R,
                                   WPI; 1997-535867/49.
qq
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Gaps

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This sequence represents a probe for the RT pol region of hepatitis b virus (HBV). This sequence can be used in the method of the invention for detection and/or generic analysis of hepatitis B virus (HBV) in a sample.

The method comprises: (a) optionally releasing, isolating or concentrating polymucleic acids (I) in the sample, and amplifying the concentrating polymucleic acids (I) in the sample, and amplifying the cultable primer pair; (b) hybridising (I) with a combination of at least 1 suitable primer pair; (b) hybridising (I) with a combination of at least 2 uncleotide probes, which are applied to known locations on, a solid consport and hybridise specifically to metent target sequences chosen from the HBV RT pol gene region, HBV precore region, HBAG region and/or HBV genotype specific target sequences, or their complements or U for T changouse; (c) detecting the hybrids formed in step (D), and inferring the HBV genotype and/or mutants present in the sample from the differential hybridisation signal (S). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, confice stationally genotype, precore mutations, vaccine escape mutations and RT generalizally genotype, precore mutations, vaccine escape mutations and RT generalizally contract on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated HIV-1 Group O env polypeptides - used for the detection of anti-HIV antibodies and for the production of antibodies for use in detection, purification and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes (A) an isolated HIV-1 Group O env polypeptide. Also described are: (1) an isolated HIV-1 Group O env
genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV; human immunodeficiency virus; antigen; detection; antibody; differentiation; Group O; env; immunogen; immunoassay; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.6%; Score 11.8; DB 1; Length 18; 86.7%; Pred. No. 2.1e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 2 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1 Group O env PCR primer SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 69; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                             Claim 5; Fig 1; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            742
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              728 GCCAGGAGAACAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-AUG-1997;
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Detection and/or genetic analysis of hepatitis B virus - specifically

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used as immunogens to produce antibodies. The antibodies can l
purify HIV polypeptides, for therapy and for detection of HIV
                                                                                                                   Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                  Hickman RK,
Devare SG;
                                                                                                                                                                                                                                                            antibody; assay; PCR primer; ss.
                                                                                                                                                                                                    AAX37184 standard; DNA; 18 BP
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                                                                                                                                                         730 CAGGAGAAACAGAAC 744
                                                                                                                                                                     CAGCAGGAACAGAAC 17
                                                                                                                                                                                                                             (first entry)
                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                         primer Seq ID No: 42.
                                                                                                                                                                                                                                                                                                                                                   Hackett JR,
                                                                                                                                                                                                                                                                                                                                                         Brennan CA,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-190224/16
                                                                                                                                                                                                                                                                                                                                     (ABBO ) ABBOTT LAB.
                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                         Golden AM,
                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                 AAX37184;
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                                                                                                                                 Query Match
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Matches
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change at the capture reagent site on the strip wherein the capture reagent for HIV-1 group O comprises a polypeptide shown in AAY06997-80 and AAY06993-84, and that for HIV-1 group M comprises a polypeptide shown in AAY06992, and that for HIV-2 comprises the polypeptide shown in AAY06991. The invention is used to screen patients for antibodies to HIV-1 types O and M, and HIV-2. The invention will be particularly useful in places and situation where equipment and/or electricity is not available. The invention provides a screening method which is faster and requires less equipment than prior art methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a polymorphic variant of a reference sequence for the solute carrier family 6 neurotransmitter transporter, serotconin member 4 (SLC644) gene or a fragment of it or a sequence complementary to the first sequence. The invention is used in producing a recombinant organism that can be used to express SLC644 for protein structure analysis and binding studies. A composition comprising a genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solute carrier family 6 neurotransmiter transporter; sectonin 4; SLC6A4; genotyping; allele specific oligonuclectide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide comprising a polymorphic variant for the solute carrier family 6 neurotransmitter transporter, serotonin member 9 gene for identifying drugs for treating disorders related to expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stephens JC;
                                                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SLC6A4 allele-specific oligonucleotide primer #20.
                                                                                                                                                                                                                                                           Sequence 18 BP; 7 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                           Score 11.8; DB 1;
Pred. No. 2.1e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nandabalan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 21; 152pp; English.
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                                                                                                                                                                                                                                                                                                         53.6%;
86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     730 CAGGAGAAACAGAAC 744
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Best Local Similarity 86.73
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-123317/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF73900;
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          8X66666666688
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  polypeptide comprising an immunoreactive portion of a polypeptide as in (A): (2) a polymorlectide (PN) encoding a polypeptide as in (A) or (1); (3) an antigen construct comprising a polypeptide as in (A) or (1); (3) an antigen construct comprising a fusion of at least one HIV-1 Group 0 env polypeptide; (a) an antigen construct comprising a fusion of at least one HIV-1 Group 0 env polypeptide with at least one HIV-1 group 0 env polypeptide with at comprising a fusion of a first HIV-1 env polypeptide, a second HIV-1 env polypeptide, a second HIV-1 env polypeptide, (6) an antigen construct comprising a first HIV-2 env polypeptide fused to a second HIV-2 env polypeptide; (7) a PN encoding an antigen construct as in (B) an expression vector comprising a PN as in (7); (9) a host cell transformed by an expression vector as in (B); and (10) an immunoassay kit for the detection of antibodies to HIV-1 comprising an immunoassay kit for the detection of antibodies in test samples. They can also be used as immunogens to produce antibodies. The antibodies can be used to used as immunogens to produce antibodies. The antibodies can be used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV-1; HIV-2; immobilised capture reagent; capillary action; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New rapid assay for antibodies to HIV-1 groups O and M, and HIV-2 - cabe used in field assay, requiring no electricity and less specialised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Varitek V, Necklaws EC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.6%; Score 11.8; DB 1; Length 18; 86.7%; Pred. No. 2.1e+02; ive 0; Mismatches 2; Indels
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Gaps

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51.8%; Score 11.4; DB 1; Length 15; illarity 92.3%; Pred. No. 2.2e+02; Conservative 0; Mismatches 1; Indels

Query Match Best Local Similarity Matches 12; Conserv

The invention relates to a rapid assay for simultaneous detection and differentiation of antibodies to HIV-1 groups O and M, and HIV-2. The method comprises (a) contacting the sample with a strip containing at least one immobilised capture reagent per analyte and on which the sample moves from the proximal to the distal end by capillary action, under conditions sufficient to form capture reagent/analyte complexes, and (b) determining the presence of analyte(s) by detecting a visible colour

Example, Page 50, 104pp; English.

equipment.

729 CCAGGAGAAACAG 741

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Sequence 15 BP; 1 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

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Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
                                                                                                                                                                                                                                                                                                                                                                                                                              Primer I (507-32) is based on amino acids 5-10 of an isolated peptide (AAN16546) of a 50 kDa cellulase (AAN16543) of Melanocarpus albomyces ALKO4237. It was used with primer 2 (AAT66548) to amplify the 50K-cellulase gene (AAT66542) by PCR using ALKO4237 genomic DNA as template. The enzyme is useful for bio-stoning and bio-finishing cotton fabrics. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDR, hammerhead ribozyme, hairpin ribozyme, cleavage, rumour angiogenesis, psoriasis, rheumatoid arthritis, ocular disease, fms-like tyrosine kinase 1, kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                             DNA encoding 20K, 50K and 50K B cellulase and facilitating protein useful for bio-stoning and bio-finishing cotton fabrics, especially denim, and as detergent for treating cellulosic fibre containing
                                                                                                                                                                                                                                        Miettinen-Ginonen A, Londesborcugh J, Vehmaanperae J, Haakana F
Maentylae A, Lantto R, Blovainio M, Joutsjoki V, Paloheimo M;
Suominen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #182.
   Thielavia albomyces; primer; PCR; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.8%; Score 11.4; DB 1; Length 17; 64.3%; Pred. No. 2.3e+02; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                       Example 21; Page 71; 204pp; English.
                                                                                                                                                95US-0005335P.
95US-0007926P.
96US-0020840P.
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96US-00584040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                             (PRIM-) PRIMALCO LID.
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                                                           WO9714804-A1
                                                                                                                     17-OCT-1996;
                                                                                                                                                  17-OCT-1995;
04-DEC-1995;
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                                                                                                                                                                              28-JUN-1996;
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11-JAN-1996;
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                                                                                         24-APR-1997
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a polymorphic variant of a reference sequence for the solute carrier family 6 neurotransmitter transporter, serotronin member 4 (SLC6A4) gene or a fragment of it or a sequence complementary to the first sequence. The invention is used in producing a recombinant organism that can be used to express SLC6A4 for protein structure analysis and binding studies. A composition comprising a genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50%-cellulase; endoglucanase; bio-stoning; bio-washing; denim; detergent; textile; pulp; paper; Melanocarpus albomyces; Myriococcus albomyces;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide comprising a polymorphic variant for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 gene for identifying drugs for treating disorders related to expression
                                                                                                                                                                                                            Solute carrier family 6 neurotransmiter transporter, sectonin 4; SLC6A4; genotyping; allele specific oligonuclectide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.8%; Score 11.4; DB 1; Length 15; 92.3%; Pred. No. 2.2e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                               Human SLC6A4 allele-specific oligonucleotide primer #18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 15 BP; 0 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50K-cellulase gene PCR primer 1 (507-128)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nandabalan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 21; 152pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                        PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                          99US-0146290P
                                                                                         AAF73898 standard; DNA; 15
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                                                                                                                                                   (first entry)
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                 CCAGAAGAACAG
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(GENA-) GENAISSANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Denton RR, Duda A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-123317/13
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nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the protein.
                                                                                                                                                                                                                                                                                     WO200109161-A1.
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25-NOV-1997
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                                                                                                                     AAF73898;
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Matches
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Claim 1; Page 638; 798pp; French.
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                                                                                                                                            The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (WEGF). A patient (preferably human) having a condition associated with the level of the fims-like tyrosine kinase 1 (fll-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67575 to AAX75782 represent specific examples of nucleic acid molecules from the present invention
                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                 Nucleic acid molecule modulating VEGF receptor(s) gene expression or stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
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                                         Escopedo J;
                                                                                                                                                                                                                                                                   Sequence 17 BP; 9 A; 1 C; 3 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human HTPL scanning oligonucleotide SEQ ID 1258.
                                         Stinchcomb D,
                                                                                                                            Claim 4; Page 128; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001, 2001WO-US000664.
30-JAN-2001, 2001WO-US000665.
30-JAN-2001, 2001WO-US000667.
30-JAN-2001, 2001WO-US000669.
33-JAN-2001, 2001WG-US00669.
09-OCT-2001, 2001US-03278999.
                                                                                                                                                                                                                                                                                                                                                                                                           ABV80012 standard; DNA; 17 BP
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         RIBOZYME PHARM INC. CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                  733 GAGAAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                        GAGAAUAGAACA 14
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Matches 12; Conservative
                                         Mcswiggen J,
                                                             WPI; 1997-259017/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
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         (RIBO-) 1
(CHIR ) (
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                                         Pavco P,
                                                                                                                                                                                                                                                                                        Query Match
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV7875 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (Sior short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was majortant in regulating male germ cell development, and the HTPL gene was important in regulating a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of course disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foctal liver, bone marrow, brain, kidney, lung, placenta, prostate, skelled muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention
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Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
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                                                                                                                                                                                          Example 2; Page 228; 718pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCCAGGTGAAAC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-DEC-2002.
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The invention relates to a novel isolated 17 mer mucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated mucleic acids, e.g. as one cidentifying, quantifying and/or amplifying a mucleic acid, e.g. as one component of a gene chip, in vitro as (anti) sense reagents, and for production of recombinant polypeptides. Any of the mucleic acids, polypeptides, vectors containing the mucleic acids, cells containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
                                                                         The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                           This sequence represents an isolated nucleic acid sequence associated with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour suppression related human fukutin oligo SEQ ID No 4191.
                                                                                                                                                                                                                                                                                                                                                                                               51.8%; Score 11.4; DB 1; Length 17; 92.3%; Pred. No. 2.38+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 1 A; 4 C; 3 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 523; 720pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-2002; 2002WO-IB004208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               730 CAGGAGAAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABT38554 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-313353/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003025175-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telerman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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ABT38551
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ABT3855
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patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynuclectide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Human Creaml protein coding sequence exon 25/intron 25 junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New retinoblastoma protein binding protein, its preparation and
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                                                                                                                                                                             1; Indels
                                                                                                                                              Length
                                                                                                                Sequence 17 BP; 2 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 16 BP; 4 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
50.9%; Score 11.2; DB 1;
Best Local Similarity 81.2%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 3;
                                                                                                                                           Score 11.4; DB 1;
Pred. No. 2.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SHAN-) SHANGHAI INST CYTOBIOLOGY CHINESE ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 3B; 35pp; Chinese.
                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-2000; 2000CN-00111426.
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                                                                                                                                             Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                          AAI64977 standard; DNA; 16
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                                                                                                                                                                                                             733 GAGAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                          17 GTGAAACAGAACA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yan X, Qian M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-566148/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   application.
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                                                                                                                                                                                                                                                                                                                                                          AAI64977;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 77
                                                                                                                                                                                                                                                                                          RESULT 76
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ID AAT1
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schultz1-727.rng

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Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; MSD; hammearhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid archritis; coular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                    Integrin inhibitor; B-Dex; neutrophil; leukocyte; trans-migration; cell adhesion; tick-derived antiinflammatory protein; Ixodes pacificus; Amblyomma americanum; polymerase chain reaction; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Degenerate sense PCR primers (AAT16990-94) are based on the 5' end of a sequence coding for a peptide fragment of novel tick-derived antiinflammatory protein E-Dex (see also AAR81794). They were used with antisense primers (AAT16995-99) complementary to the 3' end of the sequence for the RT-PCR amplification of tick salivary gland mRNA. Parrial cDNA clones were obtd. and used to screen a cDNA library to obtain a full-length cDNA clone (AAT16988) coding for E-Dex
                                                                                                                                                                                                                                                                                                                                                                                       Tick derived anti-inflammatory proteins E-Dex and Y/A-Dex - used to inhibit leukocyte trans-migration and in the treatment of inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.9%; Score 11.2; DB 1; Length 17; larity 71.4%; Pred. No. 2.5e+02; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 8 A; 1 C; 4 G; 1 T; 0 U; 3 Other;
                                                         E-Dex integrin inhibitor 1 PCR primer No. 1771.
                                                                                                                                                                                                                                                                                                                              Basi
                                                                                                                                                                                                                                                                                                  (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                Keim PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Fig 3A; 76pp; English
                                                                                                                                                                                                                                         95WO-US010138
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AAX73286 standard; RNA; 17
                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               foetal liver kinase 1; ss
                                                                                                                                                                                                                                                                                                                              Yednock TA,
                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-139700/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 10, Conserv
                                                                                                                                                                                                                                         08-AUG-1995;
                            10-JUL-1996
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                                                                                                                                                                                                            22-FEB-1996
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                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                              Bard F,
                                                                                                                                                                                                                                                                                                                                                                                                                        disease.
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The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (WEGF). A patient (preferably human) having a condition associated with the level of the fims-like tyrosine kinase 1 (fl-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, pocular diseases, psoriasis and rhematoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                                                                                                                                  gene expression or mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide array, genotyping, single base extension reaction, SBE; PCR primer; polymorphic locus, single nucleotide polymorphism, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecule modulating VEGF receptor(s) gene expression or stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.9%; Score 11.2; DB 1; Length 17; 81.2%; Pred. No. 2.5e+02; artive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lander ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Forward primer #143 used in multiplexing PCR/SBE assay.
                                                                                                                                                                                                                                                           Escopedo J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 1 A; 6 C; 4 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hirschhorn JN, Huang X, Kaplan P,
                                                                                                                                                                                                                                                           Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WHED ) WHITEHEAD INST BIOMEDICAL RES (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 146; 218pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC73641 standard; DNA; 17 BP.
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   96WO-US017480
                                                                                           96US-00584040
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                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 GCCAGGAGACACGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Conservative
                                                                                                                                                                                                                                                           Pavco P, Mcswiggen J,
                                                                                                                                                                                                                                                                                                                     WPI; 1997-259017/23.
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Best Local Similarity
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                                                             26-OCT-1995;
11-JAN-1996;
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23-JUN-1999;
25-OCT-1996;
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Universal array of oligonucleotides tags attached to a solid substrate

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Local Similarity
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ID AAH4

AC AAH4

XXX AAH

XXX AAH4

XXX AH6at

XXX Heat

XXX AH6at

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                                                                                                                                                                      The present invention relates to an oligonucleotide array comprising oligonucleotide tags fixed to a solid substrate. The oligonucleotide array is useful for genotyping a nucleic acid sample at one or more loci via single base extension (SBE) reactions. A pair of primers is used to polymorphic locus in a sample e.g. a single nucleotide polymorphic locus in a sample e.g. a single nucleotide the method of the present sequence is one of the primers used in the method of the present invention to amplify a polymorphic sample in a SBE amplified nucleic acid product is then used as a template in a SBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reaction with an extension primer. The SBE reaction products are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid molecules, which downregulates expression of a checkpoint kinase-1 gene, useful for treating colorectal, lung, breast or prostate cancers.
along with locus-specific tagged oligonucleotides useful in genotyping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.9%; Score 11.2; DB 1; Length 17; 81.2%; Pred. No. 2.5e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 10 A; 2 C; 3 G; 0 T; 2 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Chkl ribozyme substrate SEQ ID NO: 1113
                                             using single base extension reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mcswiggen J,
                                                                                                             Example 7; Page 63; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 80; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           form the oligonucleotide array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FATTAEY A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-496922/54.
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nes 13; Conserv
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Matches
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                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A heat-resistant lysin biosynthetic system enzyme gene of a high temperature-resistant coryneform microbe.
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immunogenetic; transplantation; genetic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 50.9%; Score 11.2; DB 1; Length 17; Local Similarity 81.2%; Pred. No. 2.5e+02; les 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     .
88
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                          Heat-resistant; lysin biosynthesis; enzyme; coryneform; aspartate-semialdehyde dehydrogenase; lysA; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human HLA genotyping oligonucleotide SEQ ID NO 1196
                                                                                                                                                                                                                                                                                                                                                Corynebacterium thermoaminogenes lysA PCR primer #2
Pred. No. 2.5e+02;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 17 BP; 1 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium thermoaminogenes.
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AAH45387 standard; DNA; 17 BP.
81.2%;
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                                                                    731 AGGAGAAACAGAACAC
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                                                                                                           2 AGGAGAAACAAUAAAC
                           Conservative
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DB 1; Length 17;

50.9%; Score 11.2;

Query Match

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The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucleotides (AB180512-AB18109) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them, providing genetic information to decide compatibility of organ and tissue for transplantation e.g. of bone marrow, kidney, liver, pancreas, Langerhans islet in pancreas and cornea, susceptibility diagnosis of genetic diseases and identifying individuals
                                                                                                                                                                                                                                      Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of individuals e.g. by determining immunogenetic differences when transplanting between them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ4; MDZ4; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
                                                                                                                                                                           Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MD27 scanning oligonucleotide SEQ ID 4764.
                                                                                                                                                                                                                                                                                                      Claim 10; Page 320; 345pp; Japanese.
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                                                              01-JUN-2001; 2001WO-JP004662.
                                                                                             01-JUN-2000; 2000JP-00164798
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                                                                                                                           (NISN ) NISSHINBO IND INC (SYST-) SYSTEM RES INC.
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WO200192572-A1
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Local S.
13;
                                06-DEC-2001
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD212, MD212. MD23 is concoded at chromosome 7422.1, MD24 is encoded at chromosome 6721.3-22.2, MD27 is encoded at chromosome 6721.3-22.2, MD27 is encoded at chromosome 6721.2 and MD212 is encoded at chromosome 572.3 and MD212 sequences are useful in therapy, or immunifacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212, or MD212. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ4; MDZ4; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
                                                     New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 0 A; 8 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MDZ7 scanning oligonucleotide SEQ ID 4763.
                                                                                                                                                    Example 8; SEQ ID NO 4764; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB03777 standard; DNA; 17 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 GCCAGGAGAAGAAGGA 1
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                  WPI; 2003-423107/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB03777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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81.2%; Pred. No. 2.5e+02;
ative 0; Mismatches 3; Indels
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New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.

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Gaps

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94US-00218334-
94US-00228334-
94US-002283834-
94US-002284883-
94US-0024536-
94US-0024536-
94US-00292820-
94US-0029133-
94US-00291433-
94US-00391433-
94US-00391433-
94US-0031849-
94US-00318492-
94US-003184847-
94US-00331489-
94US-003184847-
                                                                                                                                                                                                                                                                                                                                                                                       730 CAGGAGAACAGAACA 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 caguagacacaaaaca 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT54804 standard; RNA; 15
                                                                                                                                           ribozymes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                              Local Similarity 81.2
hes 13; Conservative
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23.SEP-1994;
28.SEP-1994;
03.OCT-1994;
07.OCT-1994;
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17-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-1995
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29-MAR-1994,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-1994
16-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT54804;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 86
   88888888
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                                            The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is encoded at chromosome 7422.1, MD24 is encoded at chromosome 672.1.3-22.2, MD27 is encoded at chromosome 672.1.3-22.2, MD27 is encoded at chromosome 1601.2 and MD212 is encoded at chromosome 1601.2 and MD212 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are protein are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.9%; Score 11.2; DB 1; Length 17; 81.2%; Pred. No. 2.5e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 0 A; 7 C; 2 G; 8 T; 0 U; 0 Other;
Example 8; SEQ ID NO 4763; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human K-Ras DNAzyme substrate #133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           728 GCCAGGAGAACAGAA 743
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06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-2002
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Best Local {
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ABZ66021

ABZ66021

ABZ66021

ABZ66021

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ABZ60021

ABZ600
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HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64944 - ABZ65531, ABZ6520 - ABZ6524, ABZ6530 - ABZ65585 represent substrate/target sequences for the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogeneus leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial; Kawaeski disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Ameliorating the effects of a disorder, e.g. psoriasis, by administering
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                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 85.7
nes 12; Conservative
           Mcswiggen JA,
                                      WPI; 2000-062023/05
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            Blatt L,
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                      The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the nuclectide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NF-kappaB and is implicated specifically in the induction of inflammatory responses. Regions of the mRNA that do not form secondary folding structures and that contain operatial hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their contain cuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit relA expression, making them potentially useful for treating rheumatoid arthritis, restenosis and asthma as well as to increasing probrance to transplanted tissues. The potential immunosuppressive properties of a ribozyme that cleaves relA mRNA means that uses are limited to local delivery, acute indications or ex vivo
                                                               Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Grimm S, Karpelsky A, Kisich K, Matulio-Adamic J, Mcswiggen JA;
Modak A, Pavco P, Belgeman L, Sullivan SM, Sweedler D, Thompson JD;
Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage; cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
                                                                                                                                                          Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 1861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.1%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 2.7e+02; trive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                treatment. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 1 A; 6 C; 2 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                    Claim 2; Page 225; 407pp; English.
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99US-00257608.
99US-00274553.
94US-00363233.
95US-00380734,
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                                       (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.73
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease; ss.
                                                                                                                                 WPI; 1995-351090/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
23-DEC-1994;
30-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1998;
25-FEB-1999;
23-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cirrhosis;
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The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the Hepatitis of virus (HCV) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential cribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and hepatitis c virus (HCV) infection, other infectious diseases, autoimmune diseases, and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological; cardiant; virucide, ophthalmological; keloid; skin disorder, Insulin-like Growth Factor I receptor; IGFP-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba, keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; skin cancer; sclerotic disease;
                                                                                                                                                                       Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection.
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Macejak D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 2 A; 4 C; 3 G; 0 T; 6 U; 0 Other;
Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wraight CJ, Werther GA, Edmondson SR;
Roberts E,
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                                                                                                                                                                                                                                                                                                                           Claim 1; Page 71; 123pp; English.
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8; Page 67; 201pp; English.

Example

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisorders. The method comprises contacting the skin with an receptor, IGP binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, of inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the artisense oligonucleotide is useful for ameliorating the effects of psoriasis, passing in the method is useful for ameliorating the effects of psoriasis, nechthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hypernecvascular condition such as a neovascular condition of the retina, brain or skin, growth factor—mediated malignancies, other sclerotic disease, kidney disease, hyperplasia
UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 1 A; 4 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                 Example 8; Page 67; 201pp; English
                                                        inflammation
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49.1%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 2.7e+02; tive 0; Mismatches 2; Indels 730 CAGGAGAACAGAA 743 14 CAGAAGTAACAGAA 1 Conservative Local Similarity les 12; Conserv Query Match g

Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, Keloid, skin disorder, Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein, IGFB-2, IGFBB3; inflammation, psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; necotation of the retina; ss. AAFFOLLO Standard; DNA; 15 BP
AAFFOLLO,
XX
XX
XX
AAFFOLLO,
XX
XX

GAF50LLO,
XX
XX

GF-I oligonucleotide #1070.
XX

Mutisense therapy; antiprolife cytostatic; dermatological; cytostatic; condition; tytostatic; cytostatic; c

99US-0140345P 21-JUN-2000; 2000WO-AU000693

(MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR;

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligomuclectide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligomuclectide which can be used to design the antisense oligomuclectides of the present invention (see AAF45151 and AAF45153-6150muclectides of the present invention (see AAF45151 and AAF45153-6160thyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, inhoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, kidney disease, hyperprivessels or any other hyperplasia
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Sequence 15 BP; 2 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

Gaps ; 0 49.1%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 2.7e+02; 1ve 0; Mismatches 2; Indels Query Match
Best Local Similarity 85.7
Matches 12, Conservative

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730 CAGGAGAAACAGAA 743 15 CAGAAGTAACAGAA d ò

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Gaps ; 0

BP. ABX00871 standard; RNA; 15 ABX00871; RESULT 90 ABX00871, CXSXLLLXXBXBBBBXBXBXBXBXXXXXXXXXXXXXXCCXCX

23-DEC-2002 (first entry)

Hepatitis C virus substrate #653 for HCV hammerhead ribozyme #653

Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection, HCV ribozyme; HCV expression, HCV replication; cirrhosis; virucide; liver failure; hepatocellular carcinoma; HCV infection; drug therapy; type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon; hepatotropic; antiinflammatory; substrate; hammerhead ribozyme; HH ribozyme; ss.

Hepatitis C virus.

US2002082225-A1.

27-JUN-2002.

23-MAR-1999; 99US-00274553

99US-00274553 (BLAT/) BLATT L. (MCSW/) MCSWIGGEN J A. (ROBE), ROBERTS B. (PAVC/) PAVCO P A. (MACE/) MACEJACK D. 23-MAR-1999;

ä Macejack Pavco PA, Roberts B, Mcswiggen JA, Blatt L,

WPI; 2002-617759/66.

New ribozymes targeting RNA derived from hepatitis C virus inhibit vireplication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.

Claim 1; Page 40; 80pp; English

The present invention relates to enzymatic nucleic acids which

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useful as probes
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13-JUL-1999;
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                                                                                            12;
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                                                              Query Match
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                                                                                            Matches
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AC AAS9
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specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin cof (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV ribozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or condition associated with HCV infection in conjunction with one or more a condition associated with HCV infection in conjunction with one or more a condition alpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note: Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence and substrate the sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence.
                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a consensus sequence of methanol regulated promoters of methylotrophic yeast. The specification describes 5' regulatory sequences within the alcohol oxidase I (AOXI) promoter region. AOXI catalyses the oxidation of methanol to formaldehyde. The AOXI promoter is an inducible promoter, primarily induced by methanol and starvation, and repressed in response to glucose and ethanol. The AOXI sequences can be used to produce expression cassettes and vectors, which are useful for protein production. The regulatory sequences are useful for protein production. The regulatory variety of host cells, in a research setting to further characterize promoter function and to study peroxisome biogenesis. They are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast, alcohol oxidase 1; AOX1; AOX2; promoter; formaldehyde; methanol; protein production; peroxisome biogenesis; ss.
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel alcohol oxidase I regulatory nucleotide sequences useful for enhancing expression of genes of interest in a variety of host cells, especially yeast cells.
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                                                                                                                                                                                                                                                                       49.1%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 2.7e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                              Seguence 15 BP; 2 A; 4 C; 3 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 6; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benson AK,
                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2002; 2002WO-US012851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-2001; 2001US-0281861P
                                                                                                                                                                                                                                                                                                                                    735 GAAACAGAACACCG 748
                                                                                                                                                                                                                                                                                                                                                                15 GAAACAGTACACTG 2
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                                                                                                                                                                                                                                                                                      Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monitoring anti-HBV drug resistance by genetic detection of mutations in DNA polymerase of HBV in patient's sample, involves hybridizing the polynucleic acids of the sample with a probe and detecting the hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance; mutation detection; probe; ss.
                                                                                                               Gaps
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                                                 49.1%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 2.7e+02; Live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HBV DNA polymerase gene L528M mutation probe HBPr270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16 BP; 0 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
Sequence 15 BP; 1 A; 6 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΰ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 9; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS98698 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                   BP.
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99US-0143546P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2000; 2000WO-EP006306.
                                                                                                                                                                          728 GCCAGGAGAAACAG 741
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                                                                                                                                                                                                                                                                                                                                                                                   AAF56033 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutation detection; probe;
                                                                                                                                                                                                                                  15 gccaggaragacag 2
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                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maertens G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-138370/14.
                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis B virus.
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The invention describes a novel isolated polymuclectide (I) comprising a sequence which is a polymorphic variant (PV) of a reference sequence for colony stimularing factor I receptor (CSFIR) gane, found on The colony stimularing factor I receptor (CSFIR) gane, found on The polypeptide are useful for improving the discovery and development of drugs for treating diseases associated with CSFIR activity, e.g., and inflammatory discorders and the haplotypes can be used to validate CSFIR as a candidate target for treating a specific condition or disease predicted to be associated vith CSFIR activity. Genotyphing the CSFIR gene of an individual can also be used in studying the expression and function of CSFIR, and in colony of the variation on the biological activity of CSFIR, and in studying the expression and function of CSFIR, and in the variation on the biological activity of CSFIR, as well as on the binding affinity of candidate drugs targeting CSFIR, Antibodies are useful in a variety of diagnostic and prognostic formats and therapeutic methods. A transgenic animal is useful in studying expression of the cSFIR isogenes in vivo, for in vivo screening and testing of drugs care useful against CSFIR protein, and for testing the efficacy of therapeutic agants CSFIR protein, and for testing the efficacy of therapeutic agants CSFIR protein, and for assaying a polymorphism in the target region. Without requiring any a priori knowledge of the phenotypic effect of any particular CSFIR or haplotype the invention provides a method for identifying lead compounds that are more likely to show efficacy in clinical trials. This sequence is an allele specific coligonucleotide primar used for detecting CSFIR gene polymorphisms, coligonucleotide primar used for Novel polymorphic variants of colony stimulating factor I receptor useful in studying expression and function of the protein, useful for screening candidate drugs to treat diseases e.g. inflammatory disorders. Colony stimulating factor 1 receptor; CSF1R; polymorphic variant; cytostatic; gene therapy; malignant histlocytosis; isogene; myeloid malignancy; inflammatcry disorder; transgenic animal; haplotype; genotype; human; allele specific oligonucleotide; ASO; primer; ss. Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #64. Sequence 15 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 1 Other; Claim 15; Page 16; 164pp; English. (GENA-) GENAISSANCE PHARM INC 12-APR-2000; 2000US-0196411P. 12-APR-2001; 2001WO-US012044 (first entry) Choi JY, Koshy WPI; 2002-075058/10 WO200179225-A2 Homo sapiens. 26-MAR-2002 25-OCT-2001 Chew A,

Gaps ö 48.2%; Score 10.6; DB 1; Length 15; 90.9%; Pred. No. 2.9e+02; live 1; Mismatches 0; Indels Gest Match
Buet Local Similarity 90.3%,
"...hes 10; Conservative

731 AGGAGAAACAG 741

à В

RESULT 94 ABI99104/c ID ABI99104 standard; DNA; 15

BP.

The invention relates to haplotyping the protocadherin 2 (PCDH2) gene, comprising determining which of the haplotypes given in the specification defines one or both copies of the individual's proble gene. The polymorphisms are within a 30244 base pair sequence (ABA05413), fully defined in the specification. The polymorphic variants are useful in studying the expression and function of FCDH2, in expressing PCDH2 contains for candidate drugs to treat diseases such as cancer, related to PCDH2 activity, in studying the effect of the variation on the biological activity of PCDH2 and the binding affinity of variation on the biological activity of PCDH2 and the binding affinity of variation on the biological activity of PCDH2 and the binding affinity of variation of the biological activity of PCDH2 and the binding affinity of validating PCDH2 as candidate target for treating a specific condition or disease associated with PCDH2 activity or in the condition or disease associated with PCDH2 activity. The present sequence is that of a PCDH2 allele-specific oligonucleotide (ASO) PCR primer of New protocadherin 2 (PCDH2) polymorphic variants and encoding genes, useful in expressing PCDH2 protein for screening candidate drugs to treat diseases related to PCDH2 activity. Human, PCDH2, protocadherin 2, haplotyping, polymorphic variant; SNP single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31; allele-specific oligonucleotide; ASO; PCR primer; ss. Sequence 15 BP; 0 A; 3 C; 2 G; 9 T; 0 U; 1 Other Claim 16; Page 14; 127pp; English. Tanguay DA; (GENA-) GENAISSANCE PHARM INC. 06-JUN-2000; 2000US-0209564P. 06-JUN-2001; 2001WO-US018321. Kliem SE, Koshy B, WPI; 2002-097928/13 WO200194361-A2. the invention Homo sapiens. 13-DEC-2001.

Human PCDH2 ASO PCR primer SEQ ID NO 61.

27-FEB-2002 (first entry)

ABI99104;

Gaps . 0 48.2%; Score 10.6; DB 1; Length 15; 90.9%; Pred. No. 2.98+02; ive 1; Mismatches 0; Indels Query Match
Best Local Similarity 90.9
Matches 10; Conservative

733 GAGAACAGAA 743 Ŋ 15 GRGAAACAGAA 셤

(revised)
(first entry) 16-OCT-2003 15-JUL-1999 AAX56920;

AAX56920 standard; DNA; 12 BP

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HIV-1 proviral DNA fragment 3.

DNA-targeting

conjugate; anticancer drug; viral DNA-cleaving agent;

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ABIS4034 standard; DNA; 12 BP.
                                                                                                                                                                   06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                                                       07-APR-2000; 2000DE-01019173.
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                                                                                                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                      WPI; 2001-657177/75
                                                                                                                                                                                                                                                                                                                                                                                              methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 11; Conser
                                                                                      WO200177384-A2.
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                                                    Homo sapiens.
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                                                                                                                            .8-OCT-2001
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                                                                                                                                                                                                                                                                                olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABI54034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tinis invention describes novel derivatised solid supports of rormula S'-L' -Z-CH2CH2-R, where: S' = a solid support; in = a bond or an (in) organic linker; Z = SO2 or S-S; R = dH, an H-phosphonate, alkanephosphonate, phosphortiester, phosphoramidite diester, phosphoration or modified nucleotide (N'), or an optionally substituted or modified nucleotide (N'), or an optionate, phosphorate, alkanephosphorate, phosphoritester, phosphorited (Triseter, phosphorate, phosphorotiditate, phosphorotical or phosphoramidate or phosphoramidite group, OH, ORI, SRI or optionate, alkanephosphonate, phosphorotidister, phosphorotidister, phosphorotidister, phosphoramidate or phosphoramidate, phosphorotidithidate, phosphoramidates, a substitutional or phosphoramidate, phosphorotidithidate, phosphoramidates, a process for preparing an oligonucleotide 5'-phosphate, a process for preparing an oligonucleotide 3'-diphosphate. The claying or phosphate, a process for preparing an oligonucleotide 3'-diphosphate. The claying conjugates, e.g. with anticancer drugs or viral (e.g. HIV) DNActargeting conjugates, e.g. with anticancer drugs or viral (e.g. HIV) DNActargeting conjugates, e.g. with anticancer drugs or viral (e.g. HIV) DNActargeting conjugates, e.g. with anticancer drugs or viral (Equation 16-OCT-COCT) or phosphates is simple and suitable for use in automatic DNA synthesisers. This sequence represents a fragment of the HIV-1 provirus genome, used to describe the method of the invention. (Updated on 16-OCT-COCT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel derivatised solid supports of formula S'-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
                                                                                                                                                                                                                                                                                                                                                            Derivatised solid supports and reagents for oligo:nucleotide synthesis and new oligo:nucleotide phosphoramidate conjugates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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viral DNA-binding agent; solid support; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                           (SLOK ) SLOAN KETTERING INST CANCER RES.
(ZWBI-) ZW BIOMEDICAL RES AG.
                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 43; 68pp; English
                                  Human immunodeficiency virus 1
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                                                                                                                                                                                         13-MAY-1994;
                                                                          W09531434-A1
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                                                                                                              23-NOV-1995.
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 303291; 29pp + Sequence Listing; German.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oycosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 354007; 29pp + Sequence Listing; German
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                                             Berlin K;
                                             Piepenbrock C,
(EPIG-) EPIGENOMICS AG
                                                                                             WPI; 2001-657177/75
                                             olek A,
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ö 47.3%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 2.8e+02; ive 0; Mismatches 1; Indels Query Match 4.7.2 Best Local Similarity 91.77 Matches 11; Conservative 733 GAGAAACAGAAC 744 ઠે

1 GAGAAAGAGAAC 12 g

ABH94559 standard; DNA; 12 BP. (first entry) 22-FEB-2002 ABH94559; RESULT 98 ABH94559/c CXSXAXBXBXBXAXBXAXBXBXBXBXBXCXX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 294552 for detecting SNP TSC0016175.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Olek A, Piepenbrock C,

set of oligonuclectides, useful for diagnosis and cell typing, i designed to detect single-nuclectide polymorphisms and cytosine methylation status. WPI; 2001-657177/75.

Berlin K;

Claim 1; SEQ ID NO 294552; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic

acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABE99989, ABC0010-ABE99989 and ABI0010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at 0

Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;

Gaps ; 0 Query Match 47.3%; Score 10.4; DB 1; Length 12; Best Local Similarity 91.7%; Pred. No. 2.8e+02; Matches 11; Conservative 0; Mismatches 1; Indels

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99 RESULT 95 ABH40265

BP. ABH40265 standard; DNA; 13

ABH40265;

(first entry) 22-FEB-2002

0

Oligonucleotide SEQ ID NO 240242 for detecting SNP TSC0058589.

SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS

Olek A, Piepenbrock C,

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WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 240242; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oycosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at

Sequence 13 BP; 6 A; 6 C; 1 G; 0 T; 0 U; 0 Other;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                Oligonucleotide SEQ ID NO 173167 for detecting SNP TSC0006888.
                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2001; 2001WO-IB000713.
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                                                                           22-FEB-2002 (first entry)
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ABH40264/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                           Length 13;
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                                                                           1; Indels
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                         47.38;
91.78;
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                                                  Similarity
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                         Query Match
Best Local S
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                                                                              Matches
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10 A BF 73171
11 A A C A BF 73171
12 A A C A BF 73171
13 A BF 73171
14 A C A BF 73171
15 A BF 73171
16 A C A BF 73171
18 A C A BF 73171
18 A BF 731
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                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 173167; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 13 BP; 1 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
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Best Local Similarity 91.7%
Matches 11, Conservative
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0; Gaps

ABF73170/c ID ABF73170 standard; DNA; 13 BP.

RESULT 101

736 AAACAGAACACC 747

8

AAACATAACACC

11; Conservative

Matches

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oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligoners described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                  40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 58+02; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                     13 AAACAAAACATC 2
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                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
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                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 233767 for detecting SNP TSC0057055.
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Pred. No. 5e+02;
0; Mismatches 2; Indels
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                              Mismatches
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83.3%;
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Best Local Similarity 83.3'
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ABH34756/c
ID ABH3475
XX
AC ABH3475
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ABH33790
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40.0%; Score 8.8; DB 1; Length 13;

Query Match

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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                        Claim 1; SEQ ID NO 87428; 29pp + Sequence Listing; German.
                                                  06-APR-2001; 2001WO-IB000713.
                                                                 07-APR-2000; 2000DE-01019173
                                                                                              Piepenbrock C,
                                                                               (EPIG-) EPIGENOMICS AG
                                                                                                            WPI; 2001-657177/75
                                                                                                                                           methylation status.
                    WO200177384-A2
       Homo sapiens.
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Berlin K;

ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Gaps . 0 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; 2; Indels rative 0; Mismatches 2; Indels Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences 10; Conservative Query Match Best Local Similarity Matches

ABH24319 standard; DNA; 13 BP. RESULT 559 ABH24319

ABH24319;

22-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 224296 for detecting SNP TSC0054650.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABC0010-ABC99899, ABC0010-ABC99899, ABC0010-ABC99899, ABC0010-ABC99989, and ABL0010-ABC9989 and ABL0010-ABC99989, as obtained in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
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Piepenbrock C,
                                        WPI; 2001-657177/75
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RESULT 560

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ABF49924 standard; DNA; 13 BP. ABF49924/ ID ABF4

ABF49924;

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 149921 for detecting SNP TSC0037827.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

16-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 149921; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pct_sequences
                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                               Oligonucleotide SEQ ID NO 9291 for detecting SNP TSC0002459.
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                               ABC09300 standard; DNA; 13 BP
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                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                             40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels
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                               Sequence 13 BP; 10 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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                               40.0%; Score 8.8; DB 1; Length 13;
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Seguence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
                                                 Pred. No. 5e+02;
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ABC01519 standard; DNA; 13
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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07-APR-2000; 2000DE-01019173
                                                                                                                                                                                                           Piepenbrock C,
                                                                                                     (EPIG-) EPIGENOMICS AG
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0; Gaps
Score 8.8; DB 1; Length 13;
Pred. No. 5e+02;
0; Mismatches 2; Indels
   40.0%;
                Local Similarity 83.3
es 10; Conservative
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734 AGAAACAGAACA 745 AAAAACATAACA 1 (first entry)

BP.

Oligonucleotide SEQ ID NO 1510 for detecting SNP TSC000521.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

Berlin K; Piepenbrock C, Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disonders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic formet from WIPO at

Claim 1; SEQ ID NO 29872; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Pred. No. 5e+02;
0; Mismatches 2; Indels
Claim 1; SEQ ID NO 1510; 29pp + Sequence Listing; German.
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83.3%;
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Oligonucleotide SEQ ID NO 254057 for detecting SNP TSC0061944.
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                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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83.3%; Pred. No. 5e+02;
tive 0; Mismatches
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                                                                                   ABH48475 standard; DNA; 13
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Best Local Similarity 83.3
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                       1 AAACACCACACC 12
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                nethylation status
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734 AGAAACAGAACA 745 ATAAACATAACA 2

ABC87410 standard; DNA; 13

(first entry) SNP; single peptide nucle

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide SEQ ID NO 87427 for detecting SNP TSC0021983.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Piepenbrock C,

WPI; 2001-657177/75.

set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 87427; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

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Query Match

40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels

ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF0010-ABF99889, ABH00110-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. ö Oligonucleotide SEQ ID NO 242916 for detecting SNP TSC000966. Claim 1; SEQ ID NO 242916; 29pp + Sequence Listing; German. 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; 2; Indels ive 0; Mismatches 2; Indels Sequence 13 BP; 6 A; 6 C; 0 G; 1 T; 0 U; 0 Other; Seguence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other; was obtained in electronic format from Wiftp.wipo.int/pub/published_pct_sequences ftp.wipo.int/pub/published_pct_sequences Berlin K; ABH42939 standard; DNA; 13 BP 06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173 (first entry) 734 AGAAACAGAACA 745 10; Conservative 12 AAAAACACAACA 1 Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. Sest Local Similarity WO200177384-A2 Homo sapiens. 22-FEB-2002 18-OCT-2001 ABH42939 Query Match olek A, Matches ABH42939 RESULT 8888888888 ઠ

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPD at
                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                          06-APR-2001; 2001WO-IB000713
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                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine methylation status.
                                                                                          Oligonucleotide SEQ ID NO 242915 for detecting SNP TSC0000966.
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                                                                                                                                                           Oligonucleotide SEQ ID NO 32973 for detecting SNP TSC0010416.
40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02;
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                   0; Mismatches
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

Oligonucleotide SEQ ID NO 248451 for detecting SNP TSC0060719.

ABH48474 standard; DNA; 13 BP.

RESULT 547 ABH48474

736 AAACAGAACACC 747 Local Similarity 83.3

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13 AAACACCACACC 2

22-FEB-2002 (first entry)

ABH48474;

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Gaps

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1; Length 13; 2; Indels

Score 8.8; DB 1 Pred. No. 5e+02; 0; Mismatches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomorleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABR00010-ABF9989, ABR00010-ABF9989, and ABI00010-ABF82073 data for this partent did not form par of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ilarity 83.3%;
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ABH42938/c ID ABH42938 standard; DNA; 13 BP.

Sequence 13 BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

RESULT 546

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(EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at
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Berlin K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
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Olek A, Piepenbrock C,
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                                                                   WPI; 2001-657177/75
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Matches
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(first entry)

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Oligonucleotide SEQ ID NO 6145 for detecting SNP TSC0001931.
                                                                              ABC06154 standard; DNA; 13 BP.
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                                                                                                                   ABC06154;
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                                       RESULT 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide SEQ ID NO 23162 for detecting SNP TSC0004665.
                                                                                                                   40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 23162; 29pp + Sequence Listing; German.
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                                                                            Sequence 13 BP; 6 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                      Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                       Query Match
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 5e+02;
0; Mismatches 2; Indels
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les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, designed to detect single
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                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligoners described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                             Berlin K;
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                                                                                           Olek A, Piepenbrock C,
                                                                 (EPIG-) EPIGENOMICS AG
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75

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                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 94314 for detecting SNP TSC0023541.
Claim 1; SEQ ID NO 254058; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF9989, ABH0010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                            Oligonucleotide SEQ ID NO 243229 for detecting SNP TSC0059331.
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22-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                              SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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BC1111-121-18

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 202493; 29pp + Sequence Listing; German. Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other; WPI; 2001-657177/75

40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; cive 0; Mismatches 2; Indels AAACAGAACACC 747 query Match Best Local Similarity 83.3 Matches 10; Conservative 736 ò

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ABF82674 standard; DNA; 13 22-FEB-2002 ABF82674; ABESULT:
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BP

(first entry)

Oligonucleotide SEQ ID NO 182671 for detecting SNP TSC0045147.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin Piepenbrock C, olek A,

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WPI; 2001-657177/75

bet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 182671; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomera ealso used for detecting cell type differentiation. ABC00100-ABC99989, ABC00100-ABF99889, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences 88888888888888

Sequence 13 BP; 0 A; 0 C; 4 G; 9 T; 0 U; 0 Other;

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Best Local Similarity 83.35
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736 AAACAGAACACC 747 12 AAACACAAAACC 1 ò g

ABH34757 standard; DNA; 13 BP

ABH34757 ID ABH

ABH34757;

(first entry) 22-FEB-2002

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Oligonucleotide SEQ ID NO 234734 for detecting SNP TSC0057297.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin Olek A, Piepenbrock C,

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WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and call typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 234734; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosize methylation status in chemically pretreated generic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pot_sequences

Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; Query Match Best Local Similarity

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metebolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPO at
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Matches 10; Conservative
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                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ftp.wipo.int/pub/published_pct_sequences
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide SEQ ID NO 202493 for detecting SNP TSC0049770.
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RESULT 530

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            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coingomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Matches 10; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymoxphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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                                                                                                                                       Oligonucleotide SEQ ID NO 127766 for detecting SNP TSC0031989.
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              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                     (EPIG-) EPIGENOMICS AG
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Best Local Similarity
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Claim 1; SEQ ID NO 32974; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of oligonucleotides, useful for diagnosis and cell typing, igned to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                   Oligonucleotide SEQ ID NO 159003 for detecting SNP TSC0040037.
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                                                                                            ABF59006 standard; DNA; 13 BP.
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                                                                                                                                                     (first entry)
    Olek A, Piepenbrock C,
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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; oytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                     Query Match
40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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                                                                                          Sequence 13 BP; 1 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
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Best Local Similarity
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ABH29485
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleicated (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, azdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typ.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically precreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
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Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                     Claim 1; SEQ ID NO 123385; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                      Score 8.8; DB 1; Length 13;
Pred. No. 5e+02;
0; Mismatches 2; Indels
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83.3%;
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Best Local Similarity 83.3
Warches 10; Conservative
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                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 29871; 29pp + Sequence Listing; German.
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Matches 10; Conservative
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                    Oligonucleotide SEQ ID NO 24690 for detecting SNP TSC0005920.
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                            (first entry)
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                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; ive 0; Mismatches 2; Indels
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                                                    736 AAACAGAACACC 747
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                            Conservative
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                                                                            AAACCCAACACC 13
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            Local Similarity
hes 10; Conserv
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF8003 fata for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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nes 10; Conservative
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Score 8.8; DB 1; Length 13; Pred. No. 5e+02; 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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Best Local Similarity 83.3
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                    WPI; 2001-657177/75
                                             methylation status.
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF0010-ABF99989, ABH0010-ABH99998 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                         Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
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Best Local Similarity 83.3%;
Matches 10; Conservative 0
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                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 173769; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; ative 0; Mismatches 2; Indels
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                                            Piepenbrock C,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                           Oligonucleotide SEQ ID NO 240238 for detecting SNP TSC0058589.
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central nervous system; gastrointestinal; respiratory; immune; metabolic
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                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                  Oligonucleotide SEQ ID NO 219967 for detecting SNP TSC0053525.
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KW SNP;
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                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 148661; 29pp + Sequence Listing; German.
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Local Similarity 83.3%; Pred. No. 5e+02;
les 10; Conservative 0; Mismatches
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Berlin
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF39989, ABF00010-ABF99989, ABH00010-ABF99989, ABF900010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABF909899, ABH00010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF90
                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
                               SEQ ID NO 37942; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH0010-ABF9989, ABF9989, ABH0010-ABF9989, ABH0010-ABF9989, ABH0010-ABF9989, ABH0010-ABF9989, ABH0010-ABF9989, ABH0010-ABF9989, ABH0010-ABF9989, ABF9989, ABF998
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                                                                                          Sequence 13 BP; 7 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
was obtained in electronic format from WIPO at
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2001WO-IB000713.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 82398; 29pp + Sequence Listing; German.
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                               07-APR-2000; 2000DE-01019173.
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Best Local Similarity 83.3
Matches 10; Conservative
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                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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             Oligonucleotide SEQ ID NO 107386 for detecting SNP TSC0026896.
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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Score 8.8; DB 1; Length 13; Pred. No. 5e+02; 0; Mismatches 2; Indels

40.0%;

736 AAACAGAACACC 747

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABC37925 standard; DNA; 13 BP.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2.

18-OCT-2001

Homo sapiens

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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABF0010-ABF99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at figure.
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Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                               Sequence 13 BP; 1 A; 0 C; 2 G; 10 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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Matches 10, Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                   ABF07388 standard; DNA; 13 BP
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736 AAACAGAACACC 747
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21-FEB-2002 (first entry)

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schultzl-727.rng

WPI; 2001-657177/75.

ABC24672 standard; DNA; 13 BP. 733 GAGAACAGAAC 744 13 GAGAAACGGTAC 2 à B This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABB99989 and ABI0010-ABI82073 and act for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences of oligonucleotides, useful for diagnosis and cell typing, is igned to detect single-nucleotide polymorphisms and cytosine Claim 1; SEQ ID NO 202494; 29pp + Sequence Listing; German. Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other; Berlin 07-APR-2000; 2000DE-01019173 06-APR-2001; 2001WO-IB000713 Piepenbrock C, (EPIG-) EPIGENOMICS AG methylation status. WPI; 2001-657177/75 WO200177384-A2 18-OCT-2001 olek A,

Oligonucleotide SEQ ID NO 48978 for detecting SNP TSC0013898. 961/c ABC48961 standard; DNA; 13 (first entry) AAAAAAAACACC 13 21-FEB-2002

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2. Homo sapiens 18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Piepenbrock C, olek A,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                    Claim 1; SEQ ID NO 48978; 29pp + Sequence Listing; German.
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Best Local Similarity 83.3
Matches 10; Conservative
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SNP, single nucleotide polymorphism, human; diagnosis, PNA, cancer, CNS, peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide SEQ ID NO 24689 for detecting SNP TSC0005920. WO200177384-A2. Homo sapiens. 18-OCT-2001.

(first entry)

20-FEB-2002

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40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels

736 AAACAGAACACC 747 Conservative

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Query Match Best Local Similarity Matches 10; Conservat

Berlin K; Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 24689; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

Query Match

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ABF43128;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of oligonucleotides, useful for diagnosis and cell typing, igned to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                      Oligonucleotide SEQ ID NO 143126 for detecting SNP TSC0035899.
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standard; DNA; 13 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                     Query Match
40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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Sequence 13 BP; 10 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                         ABF43128 standard; DNA; 13 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2002 (first entry)
                                                                                                                                         734 AGAAACAGAACA 745
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                      2 ATAAACAAAACA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-657177/75.
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Gaps

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Homo sapiens

RESULT 501 ABF43129/c

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                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                          Claim 1; SEQ ID NO 9290; 29pp + Sequence Listing; German.
                                                          Berlin K;
                                                          Olek A, Piepenbrock C,
                     (EPIG-) EPIGENOMICS AG.
                                                                                                  WPI; 2001-657177/75
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ö Gaps ; 0 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; cive 0; Mismatches 2; Indels Sequence 13 BP; 8 A; 5.C; 0 G; 0 T; 0 U; 0 Other; Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative ઠે

736 AAACAGAACACC 747 AAACACAAAACC 13

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ABC64866 standard; DNA; 13 BP (first entry) 21-FEB-2002 ABC64866;

Oligonucleotide SEQ ID NO 64883 for detecting SNP TSC0017098.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

ĸ Berlin Piepenbrock C, olek A,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 64883; 29pp + Sequence Listing; German

71

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The cligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at 88888888888888888

Seguence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;

Gaps .; 0 DB 1; Length 13; 2; Indels Query Match
40.0%; Score 8.8; DB 1;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches

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736 AAACAGAACACC 747 ||||| |||| | 12 AACAAAACATC 1

ABF24769 standard; DNA; 13 BP. ABF24769; RESULT 49 ABF24769 ID ABF2

Oligonucleotide SEQ ID NO 124766 for detecting SNP TSC0031192. (first entry) 21-FEB-2002

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin Olek A, Piepenbrock C,

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WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 124766; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent din ot form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 8.8; DB 1; Length 13;
Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 9289; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                          Berlin K;
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                                                                                                                                                                                                                                      06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                                                                                                                               07-APR-2000; 2000DE-01019173.
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83.3%;
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                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                           WO200177384-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200177384-A2
                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                          olek A,
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ABC09299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o;
                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                         Oligonucleotide SEQ ID NO 76071 for detecting SNP TSC0019478.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. Se+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 76071; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                        BP
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                                                                                                                     ABC76054 standard; DNA; 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
    AGAAGCAGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-657177/75.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200177384-A2.
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Gaps

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schultz1-727.rng

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Locked nucleoside analogue; LNA; bicyclic; tricyclic; diagnosis;
PCR application; strand displacement oligomer; polymerase; substrate;
nucleotide based drug; diagnostic probe; antisense therapy; antiviral;
                                                                                                                                                                                                                                                                                       New oligonucleotides containing polycyclic, locked nucleoside analogs, useful e.g. as diagnostic probes or in antisense therapy.
                                                                                                                                                                                                                                                                                                               Example 161; Page 186; 269pp; English
                                             Locked nucleoside analogue oligomer.
ВР
                                                                                                                                                                 97DK-00001054.
97DK-00001492.
98DK-00000061.
98DK-0000585.
98DK-0000585.
98DK-0000750.
                                                                                                                                                   98WO-DK000393
AAX56496 standard; DNA; 13
                               (first entry)
                                                                                                                                                                                                                                                        Wengel J, Nielsen P;
                                                                                                                                                                                                                                                                       WPI; 1999-337376/28.
                                                                                                                                                                                                                                        (EXIQ-) EXIQON AS.
                                                                                     antitumour; ss
                                                                                                                                                                12-SEP-1997;
19-DEC-1997;
16-JAN-1998;
03-MAR-1998;
29-APR-1998;
08-JUN-1998;
28-JUL-1998;
                               27-JUL-1999
                                                                                                                    WO9914226-A2
                                                                                                                                                   14-SEP-1998;
                                                                                                                                   25-MAR-1999.
                                                                                                     Synthetic.
                AAX56496;
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The present invention describes novel modified oligonucleotides (I)

Containing at least one locked nucleoside analog (LNA). Monomeric LNA's

(II) are also described. (I) to bind to target sequences in

double-stranded DNA or RNA (by strand displacement or triplex formation);

(ii) as ribozymes; (iii) as therapeutic antisense, antigene or gene

activating agents, specifically for recruitment of RNASS H; (iv)

diagnostically for isolation, purification, detection, identification,

primers; (v) as aptamers for therapy, diagnosis, RNA-mediated catalytic

processes and for specific binding to antibodies, drugs etc., including

resolution of enantiomers; (vi) for labeling, then separating, cells; and

(vi) to hybridize to non-coding RNA. LNA are used in synthesis of (I);

as therapeutic and diagnostic agents; to equalize the meting point of

unmodified reference oligonucleotides and as enzyme substrates. Typical

therapeutic applications are as antiviral and antitumour agents. (I) have

increased specificity and/or affinity, i.e. higher melting point (TM),

cor complementary RNA or DNA than oligomers not containing LNA, and are

more resistant to nuclease. The present sequence represents an oligomer

used in an example from the present invention
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ö Gaps .; 0 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; Live 0; Mismatches 2; Indels Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other; 10; Conservative Local Similarity Query Match

RESULT 494

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The present sequence is the junction between the first and second exons of the wild-type agouti cDNA. The agouti locus is located on mouse chromosome 2. It regulates the differential production of black and yellow pigment granules which give rise to the agouti coat colour of the mouse. The cDNA sequence of the lethal yellow mich confers an all-type sequence at the junction between the first and second exons. The agouti locus also contributes to essential developmental processes unrelated to pigmentation. For example, the lethal yellow allele is associated with obesity, diabetes and the development of tunours in a wide variety of tissues. Embryonic lethality and hyperamylinaemia may also be associated with certain agouti alleles. The agouti gene may therefore be used to produce transgenic mice which can be used as animal models for the study of such disorders. Such as bulimia or anorexia, may be treat these disorders and others, such as bulimia or anorexia, may be tested using the animal models. Oligonucleotide probes derived from the agouti cDNA sequence may be used for the detection of the agouti gene and mutations in the gene. Antibodies to the agouti gene and mutations in the gene. Antibodies to the agouti gene product may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting Agouti protein, useful for screening for the risk of developing e.g. diabetes or obesity in animals, by contacting a biological sample with antibodies specific for the protein and detecting the resulting
                                                                                                                                                                       Mouse, agouti, chromosome 2, coat colour; diabetes; hyperamylinaemia, tumour, obesity; bulimia; anorexia; transgenic mouse; lethal yellow; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
                                                                                                                                     Mouse wild-type agouti cDNA exon junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LOCK ) LOCKHEED MARTIN ENERGY RES CORP.
                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 10; Fig 9B; 28pp; English.
93US-00064385.
95US-00462732.
97US-00899134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               734 AGAAACAGAACA 745
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Best Local Similarity 83.3
Matches 10; Conservative
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Locked nucleoside analogue; LNA; bicyclic; tricyclic; diagnosis;
PCR application; strand displacement oligomer; polymerase; substrate;
nucleotide based drug; diagnostic probe; antisense therapy; antiviral;
                                                         Locked nucleoside analogue oligomer FP2.
                                                                                                                      antitumour; ss
                                 27-JUL-1999
                                                                                                                                                                  WO9914226-A2
                                                                                                                                          Synthetic.
           AAX56464;
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invetion relates to the isolation of the mouse agouti locus cDNA sequence (AAV81341) from neonatal skin cells. Several mutant sequences were also isolated: the Is1-Gso and a(SNNU) mutations. The Is1-Gso mutation contains an inversion which causes the 3' half of the gene to be juxtaposed with the 1d gene in the opposite transcriptional orientation. The a(SNNU) mutation contains an intragenic 2.8 kb genomic deletion. Also isolated was a lethal yellow mutant A() which contains an alternatively splice 1st exon sequence (see AAV81342-V81350 for the sequences around the mutation breakpoints). This sequence represents the wild type sequence across the exon I and exon I junction. The agouti CDNA is claimed to be useful in method for detecting the agouti gene by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of Agouti gene by amplification or hybridisation assay - for diagnosis of diabetes or obesity.
                                                                                                                                                                                                                                                  Mouse, agouti; locus, neonatal skin cell; mutant; inversion, deletion; mutation; alternative splicing; breakpoint; detection; amplification; hybridisation; ss.
                                              Gaps
                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. Se+02; tive 0; Mismatches 2; Indels
                     40.0%; Score 8.8; DB 1; Length 13; llarity 83.3%; Pred. No. 5e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
Sequence 13 BP; 4 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                        (LOCK ) LOCKHEED MARTIN ENERGY SYSTEMS INC.
                                                                                                                                                                                                                              Mouse agouti wild type exon 1/2 junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Fig 9B; 31pp; English.
                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amplification or hybridisation
                                                                                                                                                                                                                                                                                                                                                                           95US-00463387,
                                                                                                                                                                                                                                                                                                                                                                                                  93US-00064385
                                                                                                                                                        AAV81348 standard; cDNA; 13
                                                                                                                                                                                                       (first entry)
                                                                     729 CCAGGAGAACA 740
                                                                                               CCTGGAGAGACA 13
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                                   Local Similarity
nes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1995;
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Best Local Simi
Matches 10;
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                                                                                                                                                                               AAV81348;
                         Query Match
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                                                 Matches
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The present invention describes novel modified oligonucleotides (I) containing at least one locked nucleoside analog (LNA). Monomeric LNA's containing at least one locked nucleoside analog (LNA). Monomeric LNA's (II) are also described. (I) are used: (i) to bind to rarget sequences in (ouble-stranded DNA or RNA (I) are used: (i) to bind to rarget sequences in (ii) as ribozymes; (iii) as therapeutic antisense, antigene or gene activating agents, specifically for recruitment of RNASS H; (iv) diagnostically for isolation, purification, detection, identification, quantitation or capture of (synthetic) nucleic acid, e.g. as probes or promers; (v) as aptemers for therapy, diagnosis, RNA-mediated catalytic processes and for specific binding to antibodies, drugs etc., including resolution of enantiomers; (vi) for labeling, then separating, calls; and (vii) to hybridize to non-coding RNA. LNA are used in synthesis of (I); as therapeutic and diagnostic agents; to equalize the meting point of unmodified reference oligonucleotides and as enzyme substrates. (I) have increased specificity and/or affinity, i.e. higher mediting point (TM), increased specificity and/or affinity, i.e. higher mediting point (TM), cor complementary RNA or DNA than oligomers not containing LNA, and are more resistant to nuclease. The present sequence represents an oligomer used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful e.g. as diagnostic probes or in antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 137; Page 152; 269pp; English
                                                                                                                                                                                                                                                     98DK-00000286.
98DK-00000585.
98US-0088309P.
                                                                                                                                                                               97DK-00001492
98DK-00000061
                                                                                                                                                                                                                                                                                                                                                                  98DK-00000750
                                                                      98WO-DK000393
                                                                                                                                                97DK-00001054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wengel J, Nielsen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-337376/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EXIQ-) EXIGON AS.
                                                                      14-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                              08-JUN-1998;
28-JUL-1998;
                                                                                                                                                                                      19-DEC-1997;
16-JAN-1998;
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25-MAR-1999
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RESULT 493 AAX56496/c

AAX56464 standard; DNA; 13 BP.

RESULT 492

AAX56464/c ID AAX56

734 AGAAACAGAACA 745 Conservative

AGAAGCAGCACA 2

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                                                                                                                                                                                                                                                                                                                       The present sequence represents a complementary target sequence for a bridged oligonucleotide derivative (AAV06762). The invention relates to C -5 thiol-substituted nucleoside derivatives which can be incorporated into an RNA or DNA strand during synthesis of oligonucleotides. These compounds can be in the form of cross-linked linear cross-linked hairpin or bridged circular oligonucleotides. The oligonucleotides may be used for detection and isolation of target nucleic acids, or for targeting drugs to specific cell types (e.g. for treatment of Alzheimer's disease, beta-thalassemia, osteogenesis imperfecta arthritis, sickle cell anaemia or viral infections). The presence of the nucleoside derivatives in a linear oligonucleotide allows the formation of covalent crosslinks
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                                                                                                                                           New C-5 thiol-substituted nucleoside derivatives - whose presence in oligo:nucleotide(s) allows formation of covalent cross-links between non-complementary DNA domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agouti locus; mouse chromosome 2; hair colour; embryonic lethality; obesity; diabetes; tumour development; transgenic mouse model; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between non-complementary DNA domains
                                                                                                                                                                                                                                                                    Example 11; Page 101; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       732 GGAGAAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAGAAAAAAA 12
                                                                                  WPI; 1997-245044/22.
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ID AAV42
AC AAV42
AC AAV42
AX AAV42
AX AAV42
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AX AAV42
AX AAV42
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AAV42361-62 represent the transition point of exon 1 from exon 2 in agoutti locus of chromosome 2 of mice (see AAV42361 for wild type sequence). The mutations for homozygous lethal yellow (AAV42362) and heterozygous lethal yellow (AAV42362) occur here. The agouti gene is

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responsible for hair colour in mice, as well as embryonic lethality, obesity, diabetes, and the development of tumours in a wide variety of tissues. A transgene encoding the agouti gene product is used to transform the germ and somatic cells to produce a transgenic mouse. The transgene includes in operable linkage a promoter necessary for transcription of the transgene in the mouse, and where the agouti gene product is ectopically expressed in the mouse at levels sufficient for the mouse to exhibit insulin-independent diabetes, obesity, hyperamilineemia or tumours. The mouse is used in animal models for the study of diabetes, obesity and tumours, and for the testing of potential therapeutic agents against these diseases
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR region, major histocompatibility complex; HLA-DR; HLA-typing;
HLA-DR beta consensus sequence; allelic polymorphism;
HLA-DR beta-allelic polymorphism; probe; bone marrow; transplant;
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                                                                                                                                                                                                                                                                                       Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe H30 used to identify HLA-DR sequences.
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Best Local Similarity 83.3
Matches 10; Conservative
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schultz1-727.rng

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The invention relates to an isolated nucleic acid (NI) comprising at least 20 but not more than 1500 consecutive nucleotides of the optineurin promoter promoter appearing as ADE13800. Also included are the optineurin promoter of perably linked to a heterologous nucleic acid, a nucleic acid capable of detecting a single nucleotide polymorphism (SNP) in the optineurin promoter, a host cell comprising the promoter operably linked to a heterologous sequence, diagnosing or promoter operably linked to a heterologous sequence, diagnosing or promoter operably linked to a heterologous sequence, diagnosing or promoter operably linked to a heterologous sequence, diagnosing or promoter region of the optineurin gene, associated with a glaucoma phenotype), detecting a SNP sequence variation in a sample containing DNA, detecting the presence of an optineurin promoter sequence variation in a sample containing DNA, determining the presence or increased susceptibility to glaucoma or to a progressive ocular hypertensive clasored resulting in loss of visual field in a patient (or the severity or progression of glaucoma in a patient, comprising providing or promoter and amplifying the DNA) and detecting a polymorphism (comprising obtaining a sample containing thum genomic DNA, providing a nucleic acid detecting the polymorphism. The invention is used to disorder, and progressint sequence is an optineurin promoter or mutative remision to progress the sequence is an optineurin promoter motif, repeat element or mutative remision is used to disorders. The progression tends of the promoter motif, repeat element or
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                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequences of the optineurin gene are useful to detect polymorphisms particularly single nucleotide polymorphisms in the optineurin promoter to diagnose, prognose and treat glaucoma and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
glaucoma related disorder; motif; repeat element; regulatory region.
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                                                                                                                                                               06-MAR-2002; 2002US-00091281
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                                                                                                                                                                                                                                                                                                                           Raymond V, Morissette J,
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                                                                                                                                                                                                                                           (SIEE/) SI E.
(RAYM/) RAYMOND V.
(MORI/) MORISSETTE J.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-864168/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          putative regulatory
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es 10; Conserv
                                                                              US2003190617-A1
                                         Homo sapiens
                                                                                                                       09-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders.
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Matches
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ID AAX7
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AC AAX7
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DT 17-A
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A novel method of typing the human leukocyte antigen (HLA) of the major histocompatibility complex (MHC), esp. for typing donors for bone marrow transplants, involves determining if the donor tissue HLA-DR alleles are selected from the gp.: HLA-DRWSZC, DR12a,b, DR3a,n, DR5a-e, DRNewl, DR8a-d, DRW33a-c, DR4a-f, DR7, DR9, DR2a-C B3, DR2a-G B1, DR10 and DR1a-c. The method uses PCR to amplify these regions followed by sequence-specific oligonucleotide probe hybridisation (SSOFH) using the probes AAX79365-X79429. SSOFH allows detection of polymorphisms that predict differences at a single amino acid level thus reducing errors and improving the chance of successfully matching tissues
Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR; major histocompatibility complex; bone marrow transplant; primer; amplification; polymerase chain reaction; probe; polymorphism; sequence-specific oligonucleotide probe hybridisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                   Improved method for HLA typing - by DNA amplification and sequence-specific oligo:nucleotide hybridisation, used to select bone marrow
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Pred. No. 5e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Target oligonucleotide for bridged DNA ligand.
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Col 19-20; 20pp; English.
                                                                                                                                                                                                                                         BLOO-) BLOOD CENT RES FOUND INC.
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Best Local Similarity
                                                                                                                                                                               08-APR-1993;
                                                                                                                                                                                                              27-JUN-1990;
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                                                                                                                    JS5468611-A.
                                                                                                                                                  21-NOV-1995,
                                                                                                                                                                                                                                                                        Gorski JA,
                                                                                       Synthetic
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                                                                                                                                                                                                                                                                                                                                                                   donors.
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(RESE) RESEARCH CORP TECHNOLOGIES INC.

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10; Conservative
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 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention comprises a method of purifying double-stranded DNA from a solution containing the double-stranded DNA mixed with other components, comprising passing the solution through a support comprising a covalently coupled oligonuclectide capable of forming a triple helix with the double-stranded DNA by hybridisation with a specific sequence present in the double-stranded DNA. The method is useful for purifying double-stranded DNA. The method is useful for purifying double-stranded DNA. The method is useful for purifying double-stranded DNA contained in a solution and mixed with other components. The new method is a simple, rapid and effective method for DNA purification, and makes it possible to obtain especially high purities with high yields. The method enables DNA to be purified from complex mixtures comprising other nucleic acids, proteins, endotoxins, nucleases and the like. The supports may be readily recycled, and the DNAs obtained display improved properties to pharmaceutical safety. Further, the method entails only one step contrarty to prior art. The present sequence represents an oligonuclectide which can be used to prepare a DNA triple-helix affinity gel
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purifying double-stranded (ds) DNA from a solution containing dsDNA and other components, comprises passing the solution through a support comprising a covalently coupled oligonucleotide able to form a triple helix with the dsDNA.
                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                    Oligonucleotide used to prepare a DNA triplex affinity gel
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                                                                                 Query Match

40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                               DNA purification, triple helix, plasmid purification, triplex affinity chromatography.
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                                                        Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wils P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clàim 1; Page 25; 40pp; English.
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AAS20481 standard; DNA; 12
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                                                                                                                                             736 AAACAGAACACC 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AVET ) AVENTIS PHARMA
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                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, optineurin, ds, ophthalmological; single nucleotide polymorphism; SNP; glaucoma; progressive ocular hypertensive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stimulus-responsive DNA organization of highly compatible functional material undergoing reversible formation/dissociation of supercoil or rotation in response to external stimulus, useful as e.g. artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parts or medical micromachines e.g. artificial muscles. This sequence represents an oligonucleotide used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                      ss; stimulus-responsive DNA organization; supercoil; rotation; external stimulus; medical micromachines; artificial muscle.
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83.3%; Pred. No. 4.9e+02;
ive 0; Mismatches 2; Indels
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                                                                                                                                                                                       ADD71434 standard; DNA; 12 BP.
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731 AGGAGAAACAGA 742
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                 12 AGGAAAAAAAGA
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methylation status.

06-APR-2001; 2001WO-IB000713.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fer wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                          of oligonucleotides, useful for diagnosis and cell typing, igned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 281819; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8.8; DB 1; Length 12;
Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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                                                                                                              Berlin K;
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83.3%;
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                                               07-APR-2000; 2000DE-01019173
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                                                                              (EPIG-) EPIGENOMICS AG
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                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                     Claim 1; SEQ ID NO 308660; 29pp + Sequence Listing; German.
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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Best Local Similarity 83.3%;
Matches 10; Conservative
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ABI15833
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(first entry)
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                                                                                   Homo sapiens.
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22-FEB-2002
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DX BX SX M M M X DX DX BX Y X D
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                                                                                                                                                                               SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Gaps
                                                                                                                                                           Oligonucleotide primer SEQ ID NO 326681 for detecting SNP TSC0033222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
0; Mismatches
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                                                                                                                                                                                                                                                                                          06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                                                                                                                                                              07-APR-2000; 2000DE-01019173
                                                                                            ABI26708 standard; DNA; 12
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                                                                                                                                       (first entry)
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                    732 GGAGAAACAGAA 743
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10; Conservative
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                                        GGAGAATTAGAA 1
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                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonuclectide primer SEQ ID NO 281401 for detecting SNP TSC0009722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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nes 10; Conservative
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Gaps

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Seguence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                    Conservative
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       WPI; 2001-657177/75.
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABC0010-ABB9989, ABH0010-ABB9989, ABH0010-ABB9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire Jub/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 347483 for detecting SNP TSC0045131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                               Score 8.8; DB 1; Length 12;
Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but type wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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Length 12;

Score 8.8; DB 1; Pred. No. 4.9e+02;

40.0%;

Query Match Best Local Similarity

This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nuclectide polymorphisms (SMP) and cytosine methylation status in chemically pretreated genomic DMA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single-nuclectide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 323675; 29pp + Sequence Listing; German.

Seguence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
                                                                                                                                                                                                                                                        Set of oligonuclectides, useful for diagnosis and cell typing, i designed to detect single-nuclectide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 367512; 29pp + Sequence Listing; German.
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discrders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                Oligonucleotide primer SEQ ID NO 346941 for detecting SNP TSC0044842.
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                 ABI46968 standard; DNA; 12
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide primer SEQ ID NO 365188 for detecting SNP TSC0054956.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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83.3%;
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                                                        Score 8.8; DB 1; Length 12;
Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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Sequence 12 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPD at
                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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ses 10; Conservative
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                                           (EPIG-) EPIGENOMICS AG
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               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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es 10; Conservat
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                                                                                                                                            WO200177384-A2
                                                                                                      Homo sapiens
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Query Match

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Gaps

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide primer SEQ ID NO 377461 for detecting SNP TSC0062342
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06-APR-2001; 2001WO-IB000713

WO200177384-A2

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                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent fod not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 358592 for detecting SNP TSC0051195.
                                                                                                                                  Gaps
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designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
                                                                                                        Score 8.8; DB 1; Length 12; Pred. No. 4.9e+02;
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                                                                              Seguence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
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Best Local Similarity 83.3%;
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Best Local Similarity
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                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 270444 for detecting SNP TSC0002138.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was obtained in electronic format from Wil
ftp.wipo.int/pub/published_pct_sequences
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ABH70467 standard; DNA; 12
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                                                                                                                        22-FEB-2002 (first entry)
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Oligonucleotide primer SEQ ID NO 271109 for detecting SNP TSC0002401.

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                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 298959; 29pp + Sequence Listing; German.
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                                                                                                                               Berlin
                                         06-APR-2001; 2001WO-IB000713.
                                                                      07-APR-2000; 2000DE-01019173
                                                                                                                            Olek A, Piepenbrock C,
                                                                                                (EPIG-) EPIGENOMICS AG
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               18-OCT-2001.
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Gaps
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Query Match

40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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Oligonucleotide primer SEQ ID NO 308956 for detecting SNP TSC0023294. 983/c ABI08983 standard; DNA; 12 BP. (first entry) Homo sapiens 22-FEB-2002 ABI08983;

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713 WO200177384-A2. 18-OCT-2001.

07-APR-2000; 2000DE-01019173

Berlin Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

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WPI; 2001-657177/75

Set of oligonuclectides, useful for diagnosis and cell typing, i designed to detect single-nuclectide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 308956; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at

Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;

Gaps ; 0 . Match 40.0%; Score 8.8; DB 1; Length 12; Local Similarity 83.3%; Pred. No. 4.9e+02; es 10; Conservative 0; Mismatches 2; Indels Query Match Best Local Matches

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732 GGAGAAACAGAA 743 ||| ||| ||| 12 GGATAAAGAGAA 1 ABI47139 standard; DNA; 12 BP.

22-FEB-2002 (first entry) ABI47139;

Oligonuclectide primer SEQ ID NO 347112 for detecting SNP TSC0044915.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 347112; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DMA. oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastroinfestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCO0010

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2 Homo sapiens.

18-OCT-2001.

Oligonucleotide primer SEQ ID NO 297177 for detecting SNP TSC0017472

22-FEB-2002

ABH97184;

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                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                    Gaps
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Score 8.8; DB 1; Length 12;
Pred. No. 4.9e+02;
); Mismatches 2; Indels
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity
Matches 10; Conserv
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WO200177384-A2.

ABH97184 standard; DNA; 12 BP.

ABH97184 ID ABH9 XX

RESULT 463

733 GAGAAACAGAAC 744

Matches

12 GATAACACAAC 1

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Gaps

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fup.wipo.int/pub/published_pct_sequences designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 330834; 29pp + Sequence Listing; German. Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other; Berlin Piepenbrock C, WPI; 2001-657177/75. Olek A,

Query Match
40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels

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ABH86305 standard; DNA; 12 BP 22-FEB-2002 ABH86305

(first entry)

Oligonucleotide primer SEQ ID NO 286298 for detecting SNP TSC0012661.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 286298; 29pp + Sequence Listing; German.

invention describes novel oligonucleotide primers or peptide nucleic (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) This

and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH99999 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences 88888888888888888

Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;

Gaps . 0 Query Match
Best Local Similarity 83.3%; Pred. No. 4.98+02;
Matches 10; Conservative 0; Mismatches 2; Indels

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736 AAACAGAACACC 747

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1 AAACAAAACCCC 12

ABI72010 standard; DNA; 12 BP.

ABI72010;

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Claim 1; SEQ ID NO 371983; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;

22-FEB-2002 (first entry)

0; Gaps

Oligonucleotide primer SEQ ID NO 371983 for detecting SNP TSC0059099.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitted specification, but ftp.wipo.int/pub/published_pct_sequences
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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80.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indel8
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                                                      Homo sapiens.
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                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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83.3%;
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Best Local Similarity 83.37
Marches 10; Conservative
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ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE99899, ABH00010-ABE99899 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABF00010-ABF9989, SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Oligonucleotide primer SEQ ID NO 311186 for detecting SNP TSC0024345. Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. ö Claim 1; SEQ ID NO 311186; 29pp + Sequence Listing; German. Query Match

40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels Claim 1; SEQ ID NO 270303; 29pp + Sequence Listing; German Seguence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other; 꿌 Berlin BP. 06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173 213/c ABI11213 standard; DNA; 12 (first entry) 734 AGAACAGAACA 745 1 AAAAACACAACA 12 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75. WO200177384-A2. 22-FEB-2002 Homo sapiens 18-OCT-2001. ABI11213; ABIII213/C IND ABIII 셤 ଚ

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                                                                                               Sequence 12 BP; 0 A; 2 C; 3 G; 7 T; 0 U; 0 Other;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                  Query Match
Best Local Similarity 83.2.
Best Local 10, Conservative
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AD122547,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Berlin K;

onucleotides, useful for diagnosis and cell typing, is detect single-nucleotide polymorphisms and cytosine

Set of oligonucleotides,

methylation status.

designed

WPI; 2001-657177/75

Berlin K;

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Piepenbrock

olek A,

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. Claim 1; SEQ ID NO 317597; 29pp + Sequence Listing; German.

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Gaps

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Length 12; Indels

Page 211

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
         Oligonucleotide primer SEQ ID NO 316187 for detecting SNP TSC0027326.
                                                                                                                                                                                                                         Set of oligonuclectides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 316187; 29pp + Sequence Listing; German.
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Matches 10; Conserv
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 4.9e+02;
0; Mismatches 2;
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

18-OCT-2001

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

Oligonucleotide primer SEQ ID NO 284322 for detecting SNP TSC0011780.

(first entry)

22-FEB-2002

ABH84329;

BP.

ABH84329 standard; DNA; 12

ABH84329/

736 AAACAGAACACC 747

12 AAACAAAACCCC 1

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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitted in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 topses this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABR99899, ABR0010-ABR99899 ABH0010-ABR99899 and ABI00010-ABR9989. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABIS2073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                  Claim 1; SEQ ID NO 353314; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.0%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 4.9e+02; tive 0; Mismatches 2; Indels
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WPI; 2001-657177/75.
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 the represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                      Oligonucleotide primer SEQ ID NO 307740 for detecting SNP TSC0022659.
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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ABI07767 standard; DNA; 12 BP
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                Score 8.8; DB 1; Length 12;
Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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Sequence 12 BP; 6 A; 5 C; 1 G; 0 T; 0 U; 0 Other;
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Best Local Similarity 83.3%;
Matches 10; Conservative
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABH73881 standard; DNA; 12 BP.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, azdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at fitte.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at fire printed specification, but fire wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 301683; 29pp + Sequence Listing; German.
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                                                                                                                 Berlin K;
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                                                                                                                 Piepenbrock C,
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                                                 (EPIG-) EPIGENOMICS AG
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Gaps

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734 AGAAACAGAACA 745

12 AAAAACAAAACA 1

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formmat from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                        Oligonucleotide primer SEQ ID NO 304356 for detecting SNP TSC0020884.
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ABI04383 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
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                                                                       22-FEB-2002
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                                   ABI04383;
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Claim 1; SEQ ID NO 273866; 29pp + Sequence Listing; German.

Berlin K;

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Page 206
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 322876 for detecting SNP TSC0031092.
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                                                                                                                             ABI22903 standard; DNA; 12 BP.
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Bust Local Similarity 83,33,
Bast Local Similarity 83,434,
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1 GGAGAAAAGGAA 12
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ABH76378
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Score 8.8; DB 1; Length 12; Pred. No. 4.9e+02; 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                       Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
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Best Local Similarity 83.3'
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AB180821
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                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they wipo.int/pub/published_pct_sequences
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              designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
                                                                                                                Claim 1; SEQ ID NO 367441; 29pp + Sequence Listing; German
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Matches 10, Conservative
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                                                  methylation status
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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 380794; 29pp + Sequence Listing; German.
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                                                                                                                                                          Berlin K;
07-APR-2000; 2000DE-01019173.
                                                                                                                                                          Piepenbrock C,
                                                                               (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                     WPI; 2001-657177/75.
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732 GGAGAAACAGAA 743

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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC0010-ABE9989, ABE00010-ABE9989, ABE00010-ABE9989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two will pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                              set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 288936; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.0%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 4.9e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
                                                         06-APR-2001; 2001WO-IB000713
                                                                                                               07-APR-2000; 2000DE-01019173
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                                                                                                                                                                      (EPIG-) EPIGENOMICS
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18-0CT-2001
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                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                 Oligonucleotide primer SEQ ID NO 275085 for detecting SNP TSC0003780.
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                           (first entry)
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Best Local Similarity 83.3
Matches 10; Conservative
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Gaps

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                      Oligonucleotide primer SEQ ID NO 367441 for detecting SNP TSC0007360
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                                                                                                                                                                                                                                                                                                                                      of oligonucleotides, useful for diagnosis and cell typing,
                                                                                                                                                                                                                                                                                           Berlin K;
                     ABI67468 standard; DNA; 12 BP.
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                                                                 (first entry)
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Indels

83.3%; Pred. No. 4.9e+02;

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10; Conservative

Best Local Similarity

Matches

731 AGGAGAAACAGA 742

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ABH75098

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC09989, ABC00010.ABH99889 and ABI00010.ABH82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at fibe printed specification, but ftp.wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
are used for diagnosis and/or prognosis of cancer and a
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                                                                                                                                                                            Score 8.8; DB 1; Length 12;
Pred. No. 4.9e+02;
0; Mismatches 2; Indels
                                                                                                                                               Sequence 12 BP; 6 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
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Best Local Similarity 83.3.
                                                                                                                                                                                                                                        737 AACAGAACACCG 748
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                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 274506 for detecting SNP TSC0003574.
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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12 AGGAGAGAGAGA 1
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                                                RESULT 434
ABH74521/c
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ABH75098/c
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Matches
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Mon Oct 18 14:40:07 2004
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40.0%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 4.9e+02; tive 0; Mismatches 2; Indels Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other; 727 TGCCAGGAGAA 738 Conservative Query Match Best Local Similarity Matches 10; Conserv

ABH89478 standard; DNA; 12 22-FEB-2002 ABH89478; RESULT 431 ABH89478

(first entry)

Oligonucleotide primer SEQ ID NO 289471 for detecting SNP TSC0013949.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                        Claim 1; SEQ ID NO 289471; 29pp + Sequence Listing; German.
Berlin K;
Piepenbrock C,
                                      WPI; 2001-657177/75
olek A,
Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                  07-APR-2000; 2000DE-01019173
                                                                                                                                                                   06-APR-2001; 2001WO-IB000713
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(EPIG-) EPIGENOMICS

WO200177384-A2.

18-OCT-2001

Homo sapiens,

WPI; 2001-657177/75

Gaps ; 0 Query Match 40.0%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 4.9e+02; Matches 10; Conservative 0; Mismatches 2; Indels

Seguence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from wipo at

Claim 1; SEQ ID NO 268591; 29pp + Sequence Listing; German.

ABI66990 standard; DNA; 12 BP. RESULT 432

(first entry) 22-FEB-2002 ABI66990;

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Gaps

; 0

Oligonucleotide primer SEQ ID NO 366963 for detecting SNP TSC0005306.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 366963; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 371355 for detecting SNP TSC0058727.
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                                          ABI71382 standard; DNA; 12
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Best Local Similarity 83.3
Matches 10, Conservative
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                   ABI71382,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 4.9e+02;
0; Mismatches 2; Indels
                                                                                   Query Match
40.0%; Score 8.8; DB 1; Length 12
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
                                          Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 83.3<sup>3</sup>
"a+rhes 10; Conservative
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ABENUT 42
ABI43959/
ABI4395/
ABIA395/
ABIA39

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Gaps

.; 0

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

12 AAAAACCGAACA 1

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Claim 1; SEQ ID NO 352169; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for derecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99899 and ABI00010-ABF80011 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                 Berlin
                 07-APR-2000; 2000DE-01019173.
                                                                                                 Piepenbrock C,
                                                        (EPIG-) EPIGENOMICS AG
                                                                                                                                        WPI; 2001-657177/75.
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0; Gaps Query Match
40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels

736 AAACAGAACACC 747 1 AAACCCAACACC 12 d င်

ABI52196 standard; DNA; 12 BP. 22-FEB-2002

Oligonuclectide primer SEQ ID NO 352169 for detecting SNP TSC0047706. (first entry)

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001,

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Gaps .. Length 12; Query Match
40.0%; Score 8.8; DB 1; Length 12
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels

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RESULT 427 ABH81189/c

ABH81189 standard; DNA; 12 BP.

ABH81189;

22-FEB-2002 (first entry)

Oligonuclectide primer SEQ ID NO 281182 for detecting SNP TSC0009516.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 281182; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oycomers for detecting single nucleotide polymorphisms (SNP) oligomers are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonuclectide primer SEQ ID NO 312002 for detecting SNP TSC0024799.
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                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 331032 for detecting SNP TSC0035932.
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                                                                                                                                                              ВЪ.
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                                                                                                                                                              ABI31059 standard; DNA; 12
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  736 AAACAGAACACC
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Matches

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ABI12029 ID ABI1 XX AC ABI1 XX DT 22-F

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scourtzi-/2/.rng

ö Gaps . 0 Score 8.8; DB 1; Length 12; Pred. No. 4.9e+02; 0; Mismatches 2; Indels Sequence 12 BP; 9 A; 1 C; 2 G; 0 T; 0 U; 0 Other; Match 40.0%; Local Similarity 83.3%; les 10; Conservative Query Match XX

734 AGAAACAGAACA 745

1 AAAAAGAGAACA 12

g

946/c AAA06946 standard; RNA; 12 BP.

(first entry) 03-JUL-2000 Human XIAP IRES wild-type polypyrimidine tract.

X-linked inhibitor of apoptosis protein; XIAP; IRES; internal riboscome entry site; human; cap-independent translation; drug screening; cancer; autoimmune disease; degenerative disease; immunorejection; game therapy; polypyrimidine tract; ss.

Homo sapiens.

WO200005366-A2

03-FEB-2000

99WO-IB001415 22-JUL-1999; 98US-00121979. 99US-00332319. 24-JUL-1998; 14-JUN-1999;

(UYOT-) UNIV OTTAWA.

Holcik M, Korneluk RG,

WPI; 2000-338644/29.

New isolated X-linked inhibitor of apoptosis internal ribosome entry site, used to develop agents for treating, e.g. cancer.

Example IV; Fig 5A; 87pp; English.

The invention relates to the identification of modulators of capindependent translation and apoptosis. The method comprises exposing a crest compound to an X-linked inhibitor of apoptosis protein (XIAP) internal ribosome entry site (IRES) reporter cistron, and determining the amount of translation from the unexposed XIAP IRES compound relative to the translation from the unexposed XIAP IRES reporter cistron. A relative increase in translation from the exposed XIAP IRES reporter cistron indicates a compound that increases XIAP IRES compound relative increases in translation from the exposed XIAP IRES caperter cistron indicates a compound that increases XIAP IRES capendent (rap independent translation of the method construction of Advantances and caspase-7. Compounds identified by the method which decrease XIAP IRES dependent translation (thus leading to reduced expression of XIAP and hence increasing apoptosis) can be used for treating cancer. The methods can also be used for the identification of treating cancer. The methods can also be used for the identification of agents that upregulate XIAP translation and hence inhibit apoptosis, which can be used to treat autoimmune diseases, degenerative diseases or immunorejection. Such agents may, for example, be used to inhibit apoptosis of neurons in conditions such as Altheimer's disease; isleet capinal and better retinopathy; and cardiomycytes after myocardial conference which encode the survival of call or capan transplants. XIAP IRES elements can also be uncorporated into expression constructs which encode XIAP or other IAPP (Inhibitor of apoptosis proteins, e.g., TIAPP: AAYB1440). Such constructs may be used in

for gene therapy to inhibit apoptosis in a cell. The present sequence represents the RNA sequence of the wild-type human XIAP IRES polypyrimidine tract which, along with mutant polypyrimidine tracts (AAAA06947-A06954), was used in an exemplification of the present invention to determine whether the polypyrimidine tract is important XIAP IRES function 888888888

Sequence 12 BP; 0 A; 2 C; 1 G; 0 T; 9 U; 0 Other;

Gaps .. 0 Query Match 40.0%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 4.9e+02; Matches 10; Conservative 0; Mismatches 2; Indels

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734 AGAAACAGAACA 745

12 AAAAAGAGACA 1

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ABH75798 standard; DNA; 12 BP.

ABH75798;

(first entry) 22-FEB-2002 Oligonucleotide primer SEQ ID NO 275791 for detecting SNP TSC0004001.

SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 275791; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at

Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ; Query Match

40.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels

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New isolated X-linked inhibitor of apoptosis internal ribosome entry site, used to develop agents for treating, e.g. cancer.
                                                                                                                         internal ribosome entry site; human; cap-independent translation; drug screening; cancer; autoimmune disease; degenerative disease; immunorejection; gene therapy; polypyrimidine tract; ds.
                                                                                                                 X-linked inhibitor of apoptosis protein; XIAP; IRES;
                                                                                                  Human XIAP IRES polypyrimidine tract.
                                                                                                                                                                                                                                                                                                               Disclosure; Page 31; 87pp; English.
                                                    AAA06941 standard; DNA; 12 BP.
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99US-00332319.
                                                                                  (first entry)
735 GAAACAGAACA 745
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             13 RAAACACAACA 3
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                                                                                                                                                                                                                                           (UYOT-) UNIV OTTAWA
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                                                                                   03-JUL-2000
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                                                                   AAA06941;
                                     RESULT 419
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Liston P;

independent translation and apoptosis. The method comprises exposing a internal ribosome entry site (IRES) reporter cistron, and determining the amount of translation from the XIAP IRES reporter cistron, and determining the compound relative from the XIAP IRES reporter cistron exposed to the compound relative to the translation from the unexposed XIAP IRES reporter cistron. A relative increase in translation from the exposed XIAP IRES reporter cistron indicates a compound that increases XIAP IRES reporter cistron indicates a compound that increases XIAP IRES role in the regulation of apoptosis by suppressing activation of downstream caspase-3 compounds identified by the method which decrease XIAP IRES dependent translation (thus leading to reduced apoptosis proteins, e.g., TIAP: AAY81440). Such constructs may be used in gene therapy to inhibit apoptosis in a cell. The present sequence represents the polypyrimidine tract of human XIAP IRBS, which is necessary for IRBS-dependent translation of XIAP witch decrease A. The Inc. dependent training and the seed for treating cancer. The methods can also be used for the identification of agents that upregulate XIAP translation and hence inhibit apoptosis, which can be used to treat autoimmune diseases, degenerative diseases or immunorejection. Such agents may, for example, be used to inhibit apoptosis of neurons in conditions such as Alzheimer's diseases or apoptosis of neurons in conditions such as Alzheimer's disease; islet cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis pigmentosa and diabetic retinopathy; and cardiomycoytes after myocardial infarction. They can also be used to enhance the survival of cell or organ transplants. XIAP IRES elements can also be incorporated into expression constructs which encodes XIAP or other IAPS (inhibitor of modulators of capinvention relates to the identification of

The Threnton Tetales to the Identification of monutators of cagindependent translation and apoptosis. The method comprises exposing a
test compound to an X-linked inhibitor of apoptosis protein (XIAP)
amount of translation from the XIAP IRES reporter cistron, and determining the
amount of translation from the XIAP IRES reporter cistron exposed to the
compound relative to the translation from the exposed
XIAP IRES reporter distron indicates a compound that increases XIAP IRES
compound regulater distron indicates a compound that increases XIAP IRES
dependent (cap independent) translation. XIAP protein plays a critical
CC dependent (cap independent) translation. XIAP protein plays a critical
CC dependent (cap independent) translation identified by the method
which decrease XIAP IRES-dependent translation (thus leading to reduced
compourned to XIAP and hence increasing apoptosis) can be used for
creating cancer. The methods can also be used for the identification of
squents that upregulate XIAP translation and hence inhibit apoptosis,
which can be used to reat autoimmune diseases, degenerative diseases or
immunorejection. Such agents may, for example, be used to inhibit
cap be used to treat autoimmune diseases, degenerative diseases or
immunorejection. Such agents may, for example, be used to inhibit
poptosis of neurons in conditions such as Alzheimer's disease; islet
cells in autoimmune diabetes mellitus; photoreceptor cells in retinitis
pigmentosa and diabetic retinopathy; and cardiomycorytes after myccardial
infarction. They can also be used to enhance the survival of cell or
expression constructs which encode XIAP or other IAPS (inhibitor of
apoptosis proteins, e.g., TIAP: AAY81440). Such constructs may be used in
gene therapy to inhibit apoptosis in a cell. The present sequence
created (AAA06941) of human XIAP IRES The invention relates to the identification of modulators of cap Disclosure; Page 31; 87pp; English. Sequence 12 BP; 0 A; 2 C; 1 G; 9 T; 0 U; 0 Other;

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                                                                                                                                                                    X-linked inhibitor of apoptosis protein; XIAP; IRES; tinternal tribosme entry site; human; cap-independent translation; drug screening; cancer; autoimmune disease; degenerative disease; immunorejection; gene therapy; polypyrimidine tract; antisense; ss.
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                                                                                                                                                    Human XIAP IRES polypyrimidine tract antisense oligonucleotide.
Score 8.8; DB 1; Length 12;
Pred. No. 4.9e+02;
0; Mismatches 2; Indels
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                                                                                                AAA06942 standard; DNA; 12 BP.
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99US-00332319.
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        83.3%;
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                                                    12 AAAAAGAGAACA 1
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         Best Local Similarity
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                                                                                                                                                                                                                  Homo sapiens,
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Query Match
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                  Matches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                               of oligonuclectides, useful for diagnosis and cell typing, is igned to detect single-nuclectide polymorphisms and cytosine
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                                                                                                   Claim 1; SEQ ID NO 68284; 29pp + Sequence Listing; German
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100.0%; Pred. No. ...
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WPI; 2001-657177/75.
                                                                   methylation status.
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABR00010-ABC99989, ABR00010-ABC99989, ABR00010-ABC99989, ABR00010-ABC99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, oardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide SEQ ID NO 134133 for detecting SNP TSC0033441.
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Pred. No. 4.7e+02;
1; Mismatches 1; Indels
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                                                                                                                                                    Seguence 13 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 1 Other;
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Pred. No. 4.7e+02;
1; Mismatches 1;
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Similarity 81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 181150; 29pp + Sequence Listing; German.
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es 9; Conservative
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                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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iive 1; Mismatches 1
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABC68267 standard; DNA; 13 BP
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Sequence 13 BP; 7 A; 0 C; 3 G; 2 T; 0 U; 1 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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81.8%; Pred. No. 4.7e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                       Oligonucleotide SEQ ID NO 68283 for detecting SNP TSC0017813.
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Claim 1; SEQ ID NO 181152; 29pp + Sequence Listing; German
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                     WPI; 2001-657177/75.
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Best Local Similarity
Matches 9; Conserv
                                                                       WO200177384-A2.
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                                                  Homo sapiens
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                                                                                                18-OCT-2001
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                                                                                                                                                                                               Olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABH00010-ABH99889 and ABI00010-ABIS2073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                            set of oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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                                                                                                                                                                                             Claim 1; SEQ ID NO 181151; 29pp + Sequence Listing; German.
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es 9; Conservative
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WPI; 2001-657177/75.
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SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 80033 for detecting SNP TSC0020318.

(first entry)

21-FEB-2002

ABC80016;

BP

ABC80016 standard; DNA; 13

1 RAAACCGAACA 11

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RESULT 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI0010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                      40.9%; Score 9; DB 1; Length 13; 81.8%; Pred. No. 4.7e+02; Live 1; Mismatches 1; Indels
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                                                               Sequence 13 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 1 Other;
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                                                                                 Query Match
Best Local Similarity 81.8
....hes 9; Conservative
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Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713.

WO200177384-A2 Homo sapiens.

18-OCT-2001.

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                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The cligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, axidovascular and metabolic disorders. The coingomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                     Claim 1; SEQ ID NO 80033; 29pp + Sequence Listing; German.
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les 9; Conservative
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Best Local Similarity Matches 9; Conserv

Query Match

Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 134132; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
                                06-APR-2001; 2001WO-IB000713.
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                                                                                               (EPIG-) EPIGENOMICS AG
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Matches
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40.9%; Score 9; DB 1; Length 13; 81.8%; Pred. No. 4.7e+02; ive 1; Mismatches 1; Indels

81.8%;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two was obtained in electronic formmat from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                              Claim 1; SEQ ID NO 124037; 29pp + Sequence Listing; German.
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Pred. No. 4.7e+02;
1; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073

Berlin K;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 134131 for detecting SNP TSC0033441.

(first entry)

21-FEB-2002

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The invention relates to characterising cell based toxins, where the cell possessing luminescent reporter molecules (biosensors) are provided on a mirrochip, and are treated with fluorescence based molecular reagents.

The cells are photographed with fluorescence optics, and the optical information is converted into digital data. The presence of the toxin in a reagent, is detected using the digital data. The presence of the toxin in closalisation, distribution structure of identifier, detector and closalisation, distribution structure of identifier, detector and closalisation storing a cell based toxin characterisation program, and a kit for cell based toxin detection. The method is used for characterising or detecting a biological cell based toxin that affect particular biological functions and for preparing molecular biochemical arrays for new drug discovery paradigm. It is also used in automated DNA sequencing, PCR application, positional cloning, hybridisation arrays and bioinformatics crising cell based quantity and speed molecular reagents, thereby crising cell based quantity and speed molecular reagents, thereby cresulting in increased quantity and speed of data collection, shortened cycle times and faster evaluation of promising drug candidates. The method also provides increased throughput while decreasing the volumes of cycle times and faster evaluation of promising drug candidates. The capacit and test compounds required in each assay. The biosensor comprises a signal component (fluorescent protein (fused e.g. NAP4, teager domain (localising the biosensor to a particular cellular cellular companies and the invention of a capacit of a protease recognition site (e.g. for a capacit ellular cellular cellular companies and the invention of a protease recognition site (e.g. for a capacit ellular cellular cellula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell based toxin characterization method for e.g. in drug discovery paradigm, involves treating cells possessing luminescent reporter molecules with fluorescence based molecules reagents to detect presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10; SEQ ID NO 75; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for a biosensor of the invention.
                                                                                             27-FEB-1997; 97US-00810983.

26-FEB-1998; 98US-00031271.

26-FEB-1999; 99US-0123399P.

08-MAR-1999; 99US-0123399P.

12-JUL-1999; 99US-0151797P.

17-SEP-1999; 99US-0151797P.

17-SEP-1999; 99US-016408P.

25-FEB-2000; 2000US-0151783.
                                                 19-MAR-2002; 2002US-00100957
                                                                                                                                                                                                                                                                                                                                                                                        (CELL-) CELLOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Giuliano K, Kapur R;
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P-PSDB; ADC18388.
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2

18-OCT-2001.

Homo sapiens.

Claim 1; SEQ ID NO 134131; 29pp + Sequence Listing; German.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 4.7e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABF34135 standard; DNA; 13 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    735 GAAACAGAACA 745
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13 RAAACATAACA 3
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Gaps . 0

ABF34134/c ID ABF34134 standard; DNA; 13 BP. XX AC ABF34134;

RESULT 403

g à

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The present invention relates to a method of diagnosing neurodegenerative diseases, comprising determining the concentration of a protein in a body sample, where the protein may be M30 or a variant thereof, M31, M32 or M33. The method is used to diagnose neurodegenerative diseases, particularly stroke but also e.g. fragile X syndrome, Huntington's, particularly stroke but also e.g. fragile X syndrome, Huntington's, particularly stroke but also e.g. fragile X syndrome, Huntington's, particularly acaneer. The proteins can be used to identify specific ligands, potentially useful for treating neurodegeneration, immune-system disorders (e.g. autoimmune diseases, allergy, viral infection, leukaemia, inflammation etc.), carcinoma and sarcoma. Inhibitors of the interaction between the proteins and the protein kinase IRAK-1 can be used to treat
                                                                                                                                                                             Diagnosis of neurodegenerative disease comprises detecting level of M30-
                                                                                                                                                                                                                                                                                                                                                                                                                                    neurodegeneration. The present sequence is a fragment of the M33 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; cell based toxin; luminescent reporter molecule; biosensor; microchip; drug discovery; MAP4; epitope; affinity tag; protease recognition site; caspase; target domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 BP; 1 A; 3 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protease recognition site for caspase-3 DNA.
                                                                                                      Rossner M,
                                                                                                                   Lanahan A,
                                                                                                                                                                                                                        Example 11; Page 47; 130pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC18373 standard; DNA; 12 BP
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98US-00031271.
99US-0123152P.
99US-0123399P.
99US-00352171.
              07-SEP-2001; 2001WO-EP010366.
                                            07-SEP-2000; 2000US-00657479.
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                                                                       (AXAR-) AXARON BIOSCIENCE
                                                                                                      Hiemisch H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                    Kuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         734 AGAAACAGA 742
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                                                                                                                                                 WPI; 2002-292287/33.
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es 9; Conserv
                                                                                                                                                                                             family proteins.
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                                                                                                     Schneider A,
Eisenhardt G,
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26-FEB-1999
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31-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 401
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The invention relates to characterising cell based toxins, where the cell possessing luminescent reporter molecules (biosensors) are provided on a microchip, and are treated with fluorescence based molecular reagents.

The cells are photographed with fluorescence optics, and the optical information is converted into digital data. The presence of the toxin in a readent, is detected using the digital data. The presence of the toxin in classifier in each cell. Also included are a computer readable storage callsafier in each cell. Also included are a computer readable storage medium storing a cell based toxin characterisation program, and a kit for cell based toxin detecting bloogram) and a kit for cell based toxin detecting a biological coll based toxin that affect particular biological functions and for preparing molecular blochemical arrays for new drug discovery paradigm. It is also used in automated DNA sequencing, PCR application, positional cloning, hybridisation arrays and bioinformatics using cell based scanning and screening system. The method improves the target validation and candidate optimisation by combining many cell screening formats with fluorescence based molecular reagents, thereby resoluting in increased quantity and speed of data collection, shortened cycle times and faster evaluation of promising drug candidates. The method also provides increased throughput while decreasing the volumes of centenally ing it to microtubules) or detectable signal (epitope or affinity tage), a protease recognition site (e.g. for a caspase protein) and a test omparant fluorescent seasons to a particular cellular comparion of the biosensor to a particular cellular comparion.
                                                                                                                                                                                       Cell based toxin characterization method for e.g. in drug discovery paradigm, involves treating cells possessing luminescent reporter molecules with fluorescence based molecules reagents to detect presence of toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Match 40.9%; Score 9; DB 1; Length 12; Local Similarity 100.0%; Pred. No. 4.6e+02; es 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease recognition site for procaspase-8 DNA
                                                                                                                                                                                                                                                                                                  Example 10; SEQ ID NO 61; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for a biosensor of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC18387 standard; DNA; 12 BP.
25-FEB-2000; 2000US-00513783.
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                                           (CELL-) CELLOMICS INC.
                                                                                      Giuliano K, Kapur R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AGAAACAGA 11
                                                                                                                            WPI; 2003-786988/74.
                                                                                                                                                   P-PSDB; ADC18374.
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                                                                                                                                                 , Klugmann M, Naim J;
Worley P, Spielvogel D, Scheek S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.9%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 4.6e+02; ative 0; Mismatches 0; Indels
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Gaps

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ds; cell based toxin; luminescent reporter molecule; biosensor; microchip; drug discovery; MAP4; epitope; affinity tag; protease recognition site; caspase; target domain.

US2003096322-Al Unidentified

(GIUL/) GIULIANO K. (KAPU/) KAPUR R.

Giuliano K, Kapur R;

WPI; 2002-634730/68. P-PSDB; ABG94452.

or or Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes luminescent reporter molecules such as detectors, classifiers o

identifiers.

Example 10; Fig 29B; 214pp; English.

The invention describes methods of automated detection, classification and identification comprising treating cells containing luminescent reporter molecules (I) in array of locations with a test substance, where (I) are detectors, classifiers or identifiers, imaging cells in each coation to obtain luminescent signals and converting optical information into digital data to interpret presence of toxins in the test substance. The method are useful for detection of toxins in the test substance. Thosylating toxins, cytotoxic phospholipases, and exfoliative toxins. Thosylating toxins, cytotoxic phospholipases, and exfoliative toxins. The actors, classifiers and identifiers are described and serve as reporters of toxic threat agents. The first two levels of characterisation ensure a rapid readout of toxin class without characterisation characterisation whither a rapid readout of toxin class without secrificing the ability to detect many new mutant toxins or dissect several complex mixtures of known toxins. This sequence encodes a several complex mixtures of known toxins. This sequence encodes a process of the complex mixtures of known toxins. This sequence encodes a serveral complex mixtures of known toxins. This sequence encodes a serveral complex mixtures of known toxins.

Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Gaps . 0 Query Match

40.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred, No. 4.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels

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734 AGAAACAGA 742 3 AGAAACAGA 11 ò

AAL46301 standard; DNA; 12 BP.

19-JUL-2002 (first entry)

AAL46301;

Human M33 protein coding sequence intron 1 fragment.

Neurodegenerative disease; M30; M31; M32; M33; stroke; fragile X syndrome; Huntington's disease; Parkinson's disease; Alzheimer's disease; multiple sclerosis; ovarian cancer; neurodegeneration; immune disorder; autoimmune disease; allergy; infection; leukaemia; inflammation; neuroprotective; cerebroprotective; immunosuppressive; cytostatic; nootropic; antiparkinsonian; antiallergic; virucide; antiinflammatory; gene; ds.

WO200221138-A2

14-MAR-2002

17-SEP-1999; 29-OCT-1999; 01-DEC-1999; 31-AUG-1999;

schultz1-727.rng

Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes of luminescent reporter molecules such as detectors, classifiers or Example 10; Fig 29B; 214pp; English 99US-0151797P. 99US-00398965. 99US-00430656. 99US-0168408P. Giuliano K, Kapur R; WPI; 2002-634730/68. P-PSDB; ABG94459. (GIUL/) GIULIANO K. (KAPU/) KAPUR R. 31-AUG-1999; 17-SEP-1999; 29-OCT-1999; 01-DEC-1999; identifiers

The invention describes methods of automated detection, classification and identification comprising treating cells containing luminescent reporter molecules (i) in array of locations with a test substance, where (i) are detectors, classifiers or identifiers, imaging cells in each location to obtain luminescent signals and converting optical information into odigital data to interpret presence of toxins in the test substance. The method are useful for detection of toxins chosen from proteases, ADP-ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins. Three classes of cell-based luminescent reporter molecules such as reporters of toxic threat agents. The first two levels of characterisation ensure a rapid readout of toxin class without sacrificing the ability to detect many new mutant toxins or dissect several complex mixtures of known toxins. This sequence encodes a protease biosensor recognition site used in the cell-based screening

Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Gaps ; 40.9%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 4.6e+02; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity luv.
9; Conservative

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734 AGAAACAGA 742

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AGAAACAGA 11 ო

ABS71499 standard; DNA; 12 BP. RESULT 399

ABS71499

(first entry) 27-NOV-2002 DNA encoding protease biosensor recognition site #5.

Detection, classification, identification, toxin detection, protease, ADP-ribosylating toxin, cytotoxic phospholipase, exfoliative toxin, toxic threat agent, ds.

Synthetic.

US6416959-B1.

09-JUL-2002

25-FEB-2000; 2000US-00513783

97US-00810983. 98US-00031271. 99US-0122152P. 27-FEB-1997; 27-FEB-1998; 26-FEB-1999;

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Claim 6; Fig 29B; 218pp; English
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98US-0031271.
99US-0122152P.
99US-0123399P.
99US-00352171.
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                                          Guiliano KA, Bright G,
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     (CELL-) CELLOMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identify specific
                                                                             WPI; 2000-365644/31
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les 9; Conserv
                                                                                               P-PSDB; AAY79599
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26-FEB-1999;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 398
The present sequence is that of DNA encoding the substrate recognition sequence (see AAY792) of procaspase-3. The DNA is used in a claimed recombinant nucleic acid encoding a protease biosensor. The nucleic acid (see AAZ7627-43) comprises: (1) a sequence (see AAAZ7661-76) encoding at least 1 detectable signal polypeptide; (2) a sequence (see AAAZ7577-611) that encodes at least 1 protease recognition afte, such as the present sequence, and (3) a sequence (see AAAZ7611-26) that encodes at least 1 reactant target sequence. An expression vector, a genetically engineered host cell and a recombinant protease biosensor are also claimed. A claimed method for identifying compounds that modify protease activity in protease biosensor with a test compound, and determining the procease biosensor distribution in the host cell, where changes in the distribution of the protease biosensor are correlated with modification of protease activity in a host cell include the recombinant nucleic activity by the test compound. Claimed kits for identifying compounds that modify protease activity in a host cell include the recombinant nucleic activity in a host cell in high content screens to detect in vivo activation of anymatic activity, and content screens to detect in vivo activation of a known recognition and identify specific activity based on cleavage of a known recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                  Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protease, biosensor, caspase-8, substrate recognition sequence, cell screening, assay, analysis, drug discovery, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding procaspase-8 substrate recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.9%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 4.6e+02; Live 0; Mismatches 0; Indels
                                                                                           Olson K, Burroughs-Tencza S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                        Claim 6; Fig 29B; 218pp; English.
98US-0106308P.
99US-0136078P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA27588 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0106308P.
99US-0136078P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                           Bright G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               734 AGAAACAGA 742
                                                      (CELL-) CELLOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAACAGA 11
                                                                                                                              2000-365644/31
                                                                                                                          WPI; 2000-365644/
P-PSDB; AAY79592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200026408-A2.
 30-OCT-1998;
                                                                                         Guiliano KA,
                     26-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1998;
26-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-2000
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RESULT 397

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The present sequence is that of DNA encoding the substrate recognition sequence (see AAY79599) of procaspase-8. The DNA is used in a claimed recombinant nucleic acid encoding a procease biosensor. The nucleic acid (recombinant nucleic acid encoding a procease biosensor. The nucleic acid (see AAZ72627-43) comprises: (1) a sequence (see AAA27568-76) encoding at least 1 detectable signal polypebtide; (2) a sequence (see AAA27568-76) encoding at least 1 protease recognition site, such as the present sequence, and (3) a sequence (see AAA27611-26) that encodes at least 1 reactant target sequence. An expression vector, a genetically engineered nost cell and a recombinant protease biosensor are also claimed. A call involves contacting a host cell that possesses the recombinant protease biosensor with a test compound, and determining the protease acil involves contacting a host cell, where changes in the protease biosensor with a test compound, and determining the protease compounds that modify protease activity by the test compound. Claimed kits for identifying compounds that modify protease activity in a host cell include the recombinant nucleic acid, or the recombinant protease biosensor is useful in high contacts are protease biosensor is useful in high and contacting a protease biosensor is useful in high and contacting are protease biosensor or the protease biosensor or the protease biosensor or the protease biosensor of enzymatic activity, and activity has activity has activity by and activity has activity by and activity has activity by activation of enzymatic activity and activity by activation of enzymatic activity and activity by and activity by activation of enzymatic activity and activity by and activity by activation of enzymatic activity and activity by and activity by activation of enzymatic activity and activity by activation of enzymatic activity activation of enzymatic activity and activation of enzymatic activity activation of enzymatic activity activation of enzymatic activity and activity and activ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection, classification, identification, toxin detection, protease, ADP-ribosylating toxin, cytotoxic phospholipase, exfoliative toxin, toxic threat agent; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                      Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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Olson K, Burroughs-Tencza S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding protease biosensor recognition site #12.
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scnutczi-///.rng
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Example 11; Fig 29B; 336pp; English.

cregion of the cell. Once acted on by the protease of interest, the fluorescent protein is cleaved from the localisation sequence, and is free to migrate to other locations within the cell. The presence of a second localisation signal attached to the fluorescent protein enables the fluorescent protein to be directed to a different cellular compartment after cleavage of the protease recognition sequence. The change in distribution of the fluorescent protein can be detected using inaging methods with a high degree of spatial resolution. The methods and biosensors of the invention can be used to investigate a wide range of cellular activities and to screen compounds which modulate these activities. Biosensors containing a recognition site for caspase, for example, may be used for the screening of compounds which modulate compounds which modulates any be used for the extreming of compounds which modulates are compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature extraction, data analysis and automation, resulting in increased quantity and speed of data collection and faster evaluation of drug candidates. Sequences AAA93377-A93411 and AAA93440 represent protease recognition sites biosensor fusion proteins of the invention

Sequence 12 BP; 6 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Gaps ô 40.9%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 4.6e+02; ive 0; Mismatches 0; Indels 0; Indels Query Match
Best Local Similarity 100.
Matches 9, Conservative

734 AGAAACAGA 742

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3 AGAAACAGA 11

AAA93381 standard; DNA; 12 BP. RESULT 395 AAA93381

10-JAN-2001 (first entry) AAA93381;

DNA encoding procaspase-3 substrate recognition sequence, SEQ ID NO:61.

Biodetector protein, fusion protein, recognition site, cellular targetting sequence, cellular localisation, fluorescent protein, protease activity detection; toxin detection, cellular stress detection, drug discovery, cell based screening, protease recognition site, cleavage site; ds.

Unidentified

WO200050872-A2

31-AUG-2000.

25-FEB-2000; 2000WO-US004794

99US-0122152P. 99US-0123399P. 99US-00352171. 08-MAR-1999; 12-JUL-1999;

(CELL-) CELLOMICS INC

Giuliano KA, Kapur R;

WPI; 2000-594086/56. P-PSDB; AAB22890.

Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and analyzing optically.

The invention relates to systems, methods and reagents for cell-based cord screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biodetector concentrations. The methods of the invention utilise fluorescent biodetector molecules which, when acted on by a compound of interest cause an alteration in the cellular distribution of at least the fluorescent concentrations are bloomed and the compound of interest the fluorescent protein (GFP), or derivatives thereof). Such biosensors are located in protein (GFP), or derivatives thereof). Such biosensors are located in the cellular biodetector fusion proteins camped to detect proteins are activity. Such proteins by the proteins a recognition signal which is acted upon by the proteins camped by the proteins and at least one cellular localisation signal. The latter two protease; and at least one cellular localisation signal. The latter two protease; or may be from where rologius sources. Due to the protease, or may be from where localisation signal, the biodetector protein is localised to a particular ceginate to other locations within the cell. The presence of a second localisation signal attached to the fluorescent protein is cleaved from the localisation sequence, and is free compartment after cleavage of the protease recognition of the according methods with a high degree of spatial resolution. The methods and biosensors of the invention of the fluorescent protein and be used to investigate a wide range of calmage in distribution of the fluorescent protein such as antimax activities and to screen compounds which modulate for example, may be used for the detection of proteolytic toxins (such as antimax may be used for the detection of proteolytic toxins (such as antimax and speed of data analysis and automation, resulting any ordinates of compound optimisation by combining many cell accompound optimisation by combining many cell accompound optimisation may be responsed by the many used as compo

Sequence 12 BP; 7 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

. 40.9%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 4.6e+02; iive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100...
Local 9; Conservative

734 AGAAACAGA 742

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RESULT 396

AAA27581 standard; DNA; 12 BP. AAA27581

AAA27581;

29-AUG-2000 (first entry)

DNA encoding procaspase-3 substrate recognition sequence.

Protease; biosensor; caspase-3; substrate recognition sequence; cell screening; assay; analysis; drug discovery; ss.

Unidentified

WO200026408-A2.

11-MAY-2000.

29-OCT-1999; 99WO-US025431

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation cooden, coding reggion, 5' or 3' end ganomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genee encoding a polypeptide associated with lung and/or nasal airway dystunction and a second active agent comprising an entile lammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cust in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of tubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction,
                                                                                                                                                                                                                                                                                                                              ö
                              to ABA89972 represent ESR-alpha gene single nucleotide polymorphism (SNP) containing oligonucleotides, which are used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, antisense, lung dysfunction, nasal airway dysfunction, antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiinflammatory; notiallergic; antisathmatic; hypotensive; immunosuppressive; cytostatic; gene therapy, antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
diseases. The human ESR-alpha gene is located on chromosome 6. ABA89869
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostaglandin D synthase antisense fragment no.1715.
                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                         DB 1; Length 11;
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                                                                                                                                                                                Sequence 11 BP; 7 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                 40.9%; Score 9; DB 1; Let 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Katz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
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                                                                                                                                                                                                                                                     40.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                    Local Similarity 100.
es 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AAACAGAAC 10
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                                                                                                       present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABZ95855
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nyce JW,
                                                                                                                                                                                                                                                                                                                          Matches
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The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biodetector molecules which, when acted on by a compound of interest, cause an alteration in the cellular distribution of at least the fluorescent molecy. In one embodiment, the biosensors comprise heat shock proteins (HSPS) fused to a fluorescent protein (e.g., jellyfish green fluorescent protein (GPP), or derivatives thereof. Such biosensors are located in the cytoplasm, but on stress activation translocate to the nucleus. In the cytoplasm, but on stress activation proteins comprise one or more fluorescent proteins; a recognition signal which is cleaved by the protease; and at least one cellular localisation signal. The latter two components may be components of a single protein which is acted upon by the protease, or may be from heterologous sources. Due to the localisation signal, the biodetector protein is localised to a particular
                                                                                                                                                                          ;
0
lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biodetector protein, fusion protein, recognition site, callular targetting sequence, cellular localisation, fluorescent protein, protease activity detection; toxin detection, cellular stress detection, drug discovery, cell based screening, protease recognition site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding procaspase-8 substrate recognition sequence, SEQ ID NO:75.
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and
                                                                                                                                                                          ;
                                                                                                                                                                        0; Indels
                                                                                                                                   DB 1; Length 11; 4.4e+02;
                                                                                                 Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                   40.9%; Score 9; DB 1
100.0%; Pred. No. 4.4
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 11; Fig 29B; 336pp; English.
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99US-0123399P.
99US-00352171.
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                                                                                                                                   40.9%;
                                                                                                                                                                                                                                                                                                                                                AAA93388 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-2001 (first entry)
                                                                                                                                                      Local Similarity 100.
nes 9; Conservative
                                                                                                                                                                                                              729 CCAGGAGAA 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CELL-) CELLOMICS INC.
                                                                                                                                                                                                                                                 11 CCAGGAGAA 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analyzing optically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB22897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200050872-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cleavage site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
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08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-2000.
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                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                            RESULT 394
                                                                                                                                                                          Matches
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  8X33333
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The present invention describes an isolated peptide (I) consisting of an amino acid sequence selected from: (a) the amino acid sequence of a variant of the oestrogen receptor alpha (ESPA-alpha) protein in AAG68251; or (b) a fragment comprising at least 10 contiguous amino acids of the protein in AAG68251. (I) has cytostatic, osteopathic, cardiant and vasorine cardivities, and can be used in gene therapy and vaccine production. (I) is useful for identifying an agent that binds to (I), by contacting (I) with an agent and assaying the contacted mixture to determine whether a complex is formed with the agent bound to the peptide. A polynuclectide (II), encoding [I), is useful in the development of diagnostics and therapies for diseases and disorders mediated/modulated by an oestrogen receptor (ER). (II) is also useful in gene therapy for treating cancer, osteoporosis and cardiovascular diseases. The human ESR-alpha gene is located on chromosome 6. ABA89869 to ABA89972 represent ESR-alpha gene single nucleotide polymorphism (SNP) Novel variant of estrogen receptor alpha polypeptide useful for determining the biological activity of a protein for high throughput screening and for raising antibodies that elicit an immune response in Human, oestrogen receptor alpha, ESR-alpha, ER; chromosome 6; Syne-2; synaptic nuclei expressed gene 2; haplotype; cytostatic; osteopathic; cardiant; vasotropic; gene therapy; vaccine; cancer; osteoporosis; cardiovascular disease; oestrogen receptor; SNP; single nucleotide polymorphism; ds. /standard_name= "single nucleotide polymorphism" ESR-alpha gene Liverpool clinical tissue sample SNP oligo #29. 0; Indels DB 1; Length 11; BP; 4 A; 4 C; 2 G; 1 T; 0 U; 0 Other; 4.4e+02; Winn-Deen ES; 40.9%; Score 9; DB 1 100.0%; Pred. No. 4.4 cive 0; Mismatches Claim 17; Fig 2a sheet 2; 333pp; English Location/Qualifiers replace(6,G) Hwang SS, BP. 22-FEB-2000; 2000US-0183756P. 20-OCT-2000; 2000US-00692414. 24-JAN-2001; 2001US-00768184. 20-FEB-2001; 2001WO-US005358. ABA89897 standard; DNA; 11 (first entry) Similarity 100 9; Conservative 739 CAGAACACC 747 Cassel MJ, CAGAACACC 11 WPI; 2002-041152/05. (PEKE) PE CORP NY. WO200162969-A2 11-FEB-2002 Homo sapiens Sequence 11 30-AUG-2001 Key variation Kalush F, Query Match Best Local S ABA89897; RESULT 391 ABA89897 XX OS ਨੇ g

The present invention describes an isolated peptide (I) consisting of an amino acid sequence selected from: (a) the amino acid sequence of a variant of the cestrogen receptor alpha (ESR-alpha) protein in AAG68251; or (b) a fragment comprising at least 10 contiguous amino acids of the protein in AAG68251. (I) has eytocatatic, osteopathic, cardiant and vasotropic activities, and can be used in gene therapy and vaccine production. (I) is useful for identifying an agent that binds to (I), by contacting (I) with an agent and assaying the contacted mixture to determine whether a complex is formed with the agent, bound to the development of diagnostics and therapies for diseases and disorders mediated/modulated by an oestrogen receptor (ER). (II) is also useful in gene therapy for treating cancer, osteoporosis and cardiovascular Novel variant of estrogen receptor alpha polypeptide useful for determining the biological activity of a protein for high throughput screening and for raising antibodies that elicit an immune response in host. Human, oestrogen receptor alpha; ESR-alpha; ER; chromosome 6; Syne-2; synaptic nuclei expressed gene 2; haplotype; cytostatic; osteopathic; cardiant; vasotroplic; gene therapy; vaccine; cancer; osteoporosis; cardiovascular disease; oestrogen receptor; SNP; single nucleotide polymorphism; ds. Gaps containing oligonucleotides, which are used in an example from the present invention /*tag= a /standard_name= "single nucleotide polymorphism" ·. 0; Indels Length 11; DB 1; Len 5. 4.4e+02; ESR-alpha gene Coriell Diversity panel oligo #29. Sequence 11 BP; 7 A; 2 C; 2 G; 0 T; 0 U; 0 Other; Hwang SS, Winn-Deen ES 40.9%; Score 9; DB 1 100.0%; Pred. No. 4.4 :ive 0; Mismatches Claim 17; Fig 2b sheet 2; 333pp; English. Location/Qualifiers replace(6,G) ABA89949 standard; DNA; 11 BP. 22-FEB-2000; 2000US-0183756P. 20-OCT-2000; 2000US-00692414. 24-JAN-2001; 2001US-00768184. 20-FEB-2001; 2001WO-US005358. (first entry) 9; Conservative 736 AAACAGAAC 744 Cassel MJ, AAACAGAAC 10 WPI; 2002-041152/05. (PEKE) PE CORP NY. Query Match Best Local Similarity WO200162969-A2 Homo sapiens 11-FEB-2002 30-AUG-2001 Kalush F, variation ABA89949; Best Loca Matches ABA89949 88833 88333 ò .. Gaps ö

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schultz1-727.rng

03-JAN-2001; 2001DE-01000127

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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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           (HENK ) HENKEL KGAA
                                    WPI; 2002-590638/63
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les 9; Conserv
                                                            e.g. skin cancer.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (BAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; soseea, man, malanom, basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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immunosuppressive; antiinflammatory; cytostatic; SAGB; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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40.9%; Score 9; DB 1; Le:
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 0; Mismatches 0;
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100.0%; Pred
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Gaps .; 0

Length 11; 0; Indels The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; sosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

Hofmann K;

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Claim 24; Page 300; 1345pp; German.

e.g. skin cancer.

Disclosure; Page 165; 1345pp; German.

9 AAACAGAAC

662/c ABV65662 standard; cDNA; 11 BP. (first entry) 21-OCT-2002 ABV65662;

Human skin EST 3448

Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

Homo sapiens

WO200253774-A2.

11-JUL-2002.

20-DEC-2001; 2001WO-EP015179

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA

Hofmann K; Σ Petersohn D, Conradt

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

0; Gaps 40.9%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 4.4e+02; tive 0; Mismatches 0; Indels 0; Indels

734 AGAAACAGA 742

g 8

ABV64386
ID ABV64386
XX
AC ABV6438
XX
DT 21-CCTDE Human 8

ABV64386;

Human skin EST 2172.

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens

WO200253774-A2

20-DEC-2001; 2001WO-EP015179

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA.

꿌 Petersohn D, Conradt M,

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 85; 1345pp; German.

The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

Sequence 11 BP; 4 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Gaps . 0 40.9%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 9; Conservative

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729 CCAGGAGAA 737 3 CCAGGAGAA 11 ò

RESULT 388 ABV64098/c

ABV64098 standard; cDNA; 11 BP. ABV64098;

(first entry) 21-OCT-2002

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Human skin EST 1884.

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag; ss.

Homo sapiens.

WO200253774-A2.

11-JUL-2002

20-DEC-2001, 2001WO-EP015179.

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WPI; 2002-590638/63.

e.g. skin cancer.

Disclosure; Page 120; 1345pp; German.

Sequence 11 BP; 0 A; 4 C; 1 G; 6 T; 0 U; 0 Other;

AGAAACAGA 3 11 ABV64386 standard; cDNA; 11

(first entry) 21-OCT-2002 Page 181

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                       e.g. skin cancer.
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                     0; Indels
  DB 1; Length 11; . 4.4e+02;
40.9%; Score 9; DB 1
100.0%; Pred. No. 4.4
tive 0; Mismatches
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CCAGGAGAA 11 m 엄

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ABV62393 standard; cDNA; 11
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RESULT 384
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NAX ABV6239393/
NAX ABV6
NAX ABV6
NAX ABV6
NAY Hums
NAY Hums
NAY Home
NAX Home
NA
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BP.

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens

WO200253774-A2

20-DEC-2001; 2001WO-EP015179.

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA

Conradt M, Hofmann K; WPI; 2002-590638/63 Petersohn D,

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 31; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (\$AGE\$) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin

· 0 disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosace; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (\$AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to be determine skin homeostasis and to test agant (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; subburn; psoriasis; scleroderma; Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss. In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Gaps ; 0 40.9%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels 0; Indels Sequence 11 BP; 0 A; 1 C; 4 G; 6 T; 0 U; 0 Other; Hofmann K; Claim 24; Page 240; 1345pp; German. ABV69814 standard; cDNA; 11 BP. 20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127 (first entry) 9; Conservative Conradt M, of the invention 736 AAACAGAAC 744 Human skin EST 7600 (HENK) HENKEL KGAA WPI; 2002-590638/63 Local Similarity AAACAGAAC e.g. skin cancer. WO200253774-A2 Homo sapiens. Petersohn D, 21-OCT-2002 11-JUL-2002. ABV69814; Query Match RESULT 385 ABV69814/c Matches 88888888 ò

ichthyosis, atopic dermatitis; acne; seborrhea; lugus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of skin. The present sequence is that of a human expressed sequence tag Sequence 11 BP; 0 A; 1 C; 4 G; 6 T; 0 U; 0 Other; the invention oţ

0; Indels Length 11; Score 9; DB 1; Le Pred. No. 4.4e+02; DB 1; 100.0%; Pred. 40.9%; 9; Conservative Ouery Match Best Local Similarity Matches

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Gaps

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736 AAACAGAAC 744

Nyce JW;

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The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                       Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0; Indels
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100.0%; Fre
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                                                                                          20-DEC-2001; 2001WO-EP015178.
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                                                                                                                                                                                                                                                                               WPI; 2002-528865/56.
                                                                                                                                                                                       (HENK ) HENKEL KGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
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WO200253773-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2002.
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                                             11-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                            expression.
                                                                                                                                                                                                                                                                                                                                                           screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV71807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 383
ABV71807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ठ
                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesid, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with committee and cativity of target polypeptides associated with activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide creceptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially bulmonary obstruction and/or treat proteins and malignancy associated proteins and/or surfactant hypoproduction which are associated with a disease or conditions selected from pulmonary vasconstriction, inflammation, allergic susthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CP), allergic rhintis (AR), pulmonary conditions, and processed in the exemplification of read antisense oligonucleotides used in the exemplification of read antisense oligonucleotides used in the exemplification of
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                                                                                                                                                                                                                                                                                    Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.9%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 4.4e+02; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 141; 1592pp; English.
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100.08; Pr.
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                                                                                                                                                                                                                                                                                                                                            and respiratory obstructions.
                              24-MAR-2000; 2000WO-US008020
                                                                             99US-0127958P
                                                                                                                      (UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                 WPI; 2000-679539/66.
                                                                                                                                                                                                                                                                                                                       adenosine receptors
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                                                                                06-APR-1999;
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ABQ86412;

X S X E X E X E X S X X X X S X

RESULT 382

ABQ86412

Query Match

Best Loca Matches

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Gaps

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Nyce JW

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or

WPI; 2000-205971/18.

Disclosure; Page 479; 1343pp; English.

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(UYEC-) UNIV EAST CAROLINA,
   WPI; 1999-229400/19
                                                                                                             WO200009525-A2.
                                                                                                          Homo sapiens
                                                                                                                    03-AUG-1999;
                                                                                                                        03-AUG-1998;
                                                                                                                 24-FEB-2000
                                                                               AAA34039;
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The specification describes antisense oligonucleotides (AAX52869-X55271)
directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, gene initiation
codons, genemic flanking regions, intron-exch borders, the 5-end, the 3'
end and the juxta-section between coding and non-coding regions and all
segments of RNAs encoding proteins associated with one or more diseases,
conditions or mixtures. The antisense oligonucleotides may be derived
from sequences AAX55180-271 can be used for the antisense treatment of
fiseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, respiratory
cute asthma, allergies, asthma, impeded respiration, respiratory
pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
colon cancer, breast cancer, lung cancer, menorestic cancer,
hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastasized
cother lungs, including breast and prostate cancer
New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11 BP; 0 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                    Disclosure, Page 45; 120pp; English.
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Best Local Similarity 100...
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The present invention describes a new composition comprising an antisense oligomucleotide (OM) with low adenosine (Up to 15%), which targets nucleic acids involved in bronchoconstriction, allegies, and/or inflammation. The OM can have antiinflammatory, antiallegies, and/or antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating effects afflict the lungs of a subject. They can be used for treating conficions, pulmonary vasconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including the own procate cancer. The reduction of the adenosine content of the OMs reduces side effects. The A-containing OMs break down with the content content of the mach of the content of the mach of the content of the conten

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nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA33323 to AAA3392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-2001 (first entry)
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Best Local Similarity
Matches 9; Conserv
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ID AAF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, adenosine receptor, low adenosine antisense oligonucleotide, phosphorothioate, impaired respiration; inflammation; allergy, allergic disease, bronchoconstriction; inhibitor; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.9%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 4.4e+02; ttive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA34039 standard; DNA; 11 BP.
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Gaps

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40.9%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 4.4e+02; rative 0; Mismatches 0; Indels

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; aschma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emplyseme; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; Human prostaglandin D synthase polynucleotide fragment #1728. cancer; ss.

WO200062736-A2.

Homo sapiens,

99WO-US017712

Nyce JW;

26-OCT-2000

Koshy

Kazemi A,

Armstrong B,

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The invention relates to haplotyping the protocadherin 2 (PCDH2) gene, comprising determining which of the haplotypes given in the specification defines one or both copies of the individual's pCDH2 gene. The polymorphisms are within a 30244 base pair sequence (ABA05413), fully defined in the specification. The polymorphic variants are useful in studying the expression and function of PCDH2, in expressing PCDH2 or protein for use in screening for candidate drugs to treat diseases such as cancer, related to PCDH2 activity, in studying the effect of the variation on the biological activity of PCDH2 and the binding affinity of candidate drugs targeting PCDH2. The haplotyping methods are useful in validating PCDH2 as a candidate target for treating a specific condition or disease predicted to be associated with PCDH2 activity or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with PCDH2 activity. The present sequence is that of a PCDH2 allele-specific oligonucleotide (ASO) PCR primer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                New protocadherin 2 (PCDH2) polymorphic variants and encoding genes, useful in expressing PCDH2 protein for screening candidate drugs to treat diseases related to PCDH2 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemokine binding protein 2; CCBP2; CCBP2 protein isoform; gene therapy; polymorphic gene variant; single nucleotide polymorphism; human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCBP2 detecting ASO primer SEQ ID No 70.
                                                                                                                                                                                                                                                                                 Claim 18; Page 14; 127pp; English.
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                                                                                                                (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL39543 standard; DNA; 10 BP
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                                              06-JUN-2001; 2001WO-US018321
                                                                                06-JUN-2000; 2000US-0209564P
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                                                                                                                                                                                 WPI; 2002-097928/13.
                                                                                                                                                Koshy B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAACAGAA
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                13-DEC-2001.
                                                                                                                                                Kliem SE,
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The invention relates to an isolated polynucleotide comprising genes and haplotypes of the Chemokine binding protein 2 (CCBP2) gene. Polymorphic variants of the CCBP2 gene are useful in studying the expression and function of CCBP2, and in expressing CCBP2 proteins for use in screening candidate drugs for treating diseases associated with CCBP2 activity. Polynucleotides comprising a polymorphic gene variant or fragment may be used for therapeutic purposes, where a patient could benefit from expression or increased expression of a particular CCBP2 protein isoform, or an expression vector encoding the isoform may be administered to the patient Haplotype information is useful in improving the efficiency and output of several steps in drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. The polynucleotides of the invention can be used to treat disorders related to the CCBP2 gene by gene therapy. This polynucleotide sequence represents a preferred ASO primer for detecting CCBP2 gene polymorphisms relating to the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmorary vasconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary discress syndrome; pain; cystic fibrosis; pulmonary disconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                  New genetic variants having polymorphisms in the chemokine binding protein 2 (CCBP2) gene, useful for studying CCBP2 functions, and for treating disorders affected by expression or function of the CCBP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostaglandin D synthase antisense oligonucleotide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.9%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                       Claim 15; Page 14; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX54592 standard; DNA; 11 BP.
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98US-00093972.
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ses 9; Conservative
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                                   WPI; 2002-435524/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9913886-A1
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Matches
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Human Th1 cell preferentially expressed gene SAGE tag, SEQ ID NO:134

(first entry)

29-NOV-2002

ABV78423;

activated T cell; T lymphocyte; immune response; expression pattern; preferential expression; immune disorder; ss.

SAGE tag; serial analysis of gene expression; human; Th1 cell;

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Human, v-fos FBJ murine osteosarcoma viral oncogene homologue; FOS; PCR; cyrostatic; gene therapy; single nucleotide polymorphism; haplotyping; haplotype pair; developmental bone disorder; cancer; tumour; ss; primer; chromosome 14q1-q11.
                                                                                                                                                                                                                                                                                         Novel genetic variants of V-Fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS) isogenes, useful for improving efficiency and reliability in drug development for treating developmental bone disorders.
                                                          Human FOS gene allele-specific oligonucleotide PCR primer #19.
                                                                                                                                                                                                                                                     Anastasio AE, Kliem SE, Koshy B,
                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 15; 73pp; English
 ABK81376 standard; DNA; 10 BP
                                                                                                                                                                                                                                (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                            19-OCT-2000; 2000US-0241620P.
                                                                                                                                                                                          19-OCT-2001; 2001WO-US046142.
                                                                                                                                                                                                                                                                        WPI; 2002-435529/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                  WO200232931-AZ.
                                                                                                                               Homo sapiens
                                       13-AUG-2002
                                                                                                                                                                      25-APR-2002
                   ABK81376;
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Lee HH;

Human activated Th1 and Th2 cell expression gene group, useful for the diagnosis and treatment of Th1 and Th2-related diseases.

Claim 19; Page 10; 60pp; Japanese.

KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN

WPI; 2002-594261/64.

19-DEC-2000; 2000JP-00385816. 19-DEC-2000; 2000JP-00385816.

JP2002186482-A.

02-JUL-2002.

Homo sapiens.

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Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;
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The invention relates to single nucleotide polymorphisms in the gene encoding the human v-fos FbJ murine osteosarcoma viral oncogene homologue (FOS) polyreptide. A method for haplotyping the FOS gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the FOS haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pair. This method is useful in genotyping, whereby all possible haplotype pair. This method is useful in genotyping, whereby all possible haplotype pair in the anglotype or haplotype or haplotype or haplotype pair in a reference population, where a higher the haplotype frequency in the trait population indicates the trait is associated with the haplotype or haplotype pair. FOS and its corresponding DNA are used for studying the expression and function of FOS, for use in screening for candidate drugs to treat diseases related to FOS, for use in screening for candidate drugs to treat diseases related to FOS, for use also useful for studying the effect of variation on the biological activity of FOS as well as on the binding affinity of candidate drugs targeting FOS. Sequences ABR81377 represent alleles appearing objecting FOS. Sequences ABR81377 represent
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The invention relates to SAGE (serial analysis of gene expression) tags and/or Th2 cells. The SAGE tags of this invention consist of a sequence of 10 mucleotides located donstream of the 5.-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in Th1 and/or Th2 cells, antibodies against these proteins, and inhibitors of the expression of groups of genes that are expressed in his and/or Th2 cell types. Groups of genes expressed in than and/or the two cell types may be used for the diagnosis and treatment of Th1 and Th2-related disorders. Sequences ABVR3850 are SAGE tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP; single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31; allele-specific oligonucleotide; ASO; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PCDH2 ASO PCR primer SEQ ID NO 109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABI99152 standard; DNA; 10 BP.
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nes 9; Conserv
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Gaps . 0

Indels

40.9%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 4.38+02; artive 0; Mismatches 0; Indels

Conservative

6

Best Loc Matches

732 GGAGAAACA 740

GGAGAAACA

a

WO200194361-A2

ABV78423 standard; cDNA; 10 BP.

ABV78423/c ID ABV784 XX

RESULT 376

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Human, lipase, hormone sensitive, LIPE; isogene, obesity, male sterility;

polymorphism; primer; ss.

WO200240502-A2 Homo sapiens.

23-MAY-2002

16-NOV-2001; 2001WO-US043518. 16-NOV-2000; 2000US-0249302P.

Human LIPE gene polymorphism detection oligonucleotide primer #7.

(first entry)

24-SEP-2002

ABK96032;

BP.

ABK96032 standard; DNA; 10

RESULT 374

ABK96032

739 CAGAACACC 747

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9 CAGAACACC 1

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CSFIR isogenes in vivo, for in vivo screening and testing of drugs targeted against CSFIR protein, and for testing the efficacy of therapputic agents and compounds. Allele specific oligomucleotides (ASO) are useful as probes and primers, and for assaying a polymorphism in the target region. Without requiring any a priori knowledge of the phenotypic effect of any particular CSFIR or haplotype the invention provides a method for identifying lad compounds that are more likely to show efficacy in clinical trials. This sequence is a primer used to detect CSFIR gene polymorphisms by primer extension, described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids involved in neuronal regeneration, useful in screening for modulators of regeneration or synaptic efficiency, and potential therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to nucleic acids (ABL98957-ABL99004) involved in regenerative neuronal processes and encoded proteins (ABB79405-ABB79409) used to screen for compounds and potential therapeutic agents that modulate nerve cell regeneration and/or synaptic efficiency. They may also be used for treatment or diagnosis of defective or pathological memory and learning conditions. The present sequence is that of an isolated from serial analysis of gene expression (SAGE) experiments organizated from serial analysis of gene expression (SAGE) experiments versus a wildtype control. The resultant EST were used to isolate the nucleic acids of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse, neuronal, regeneration, nerve cell, synaptic efficiency, memory, learning disorder, serial analysis of gene expression, SAGE, gene expression, hippocampus, expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                              DB 1; Length 10;
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                                                                                                                                                                                                            Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse neuronal regeneration related SAGE EST 35.
                                                                                                                                                                                                                                                40.9%; Score 9; DB 1
100.0%; Pred. No. 4.3
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL99040 standard; cDNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32-OCT-2000; 2000DE-01048893.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                       731 AGGAGAAAC 739
                                                                                                                                                                                                                                                                                                                                                             AGGAGAAAC 10
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Best Local Similarity
-hes 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-341428/38.
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                                                                                                                                                                          the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp.
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The present invention relates to a new polynucleotide comprising a nucleotide sequence which comprises lipase, hormone sensitive (LIPB) isogenes. The invention is useful in screening for drugs targeting LIPE isogenes that are useful for treating obseity and male sterility. The methods of the invention are useful for improving the efficiency and reliability of several steps in the discovery and development of drugs or is useful in studying the expression and function of LIPE, and in expressing LIPE protein for use in screening for candidate drugs to treat discusses related to LIPE activity. It is also useful in studying the effect of the variation on the biological activity of LIPE as well as on the binding affinity of candidate drugs to great the binding affinity of candidate drugs targeting LIPE for the treatment of obseity and male sterility. The invention is useful for studying the expression of LIPE isogenes in vivo, for in vivo screening and testing of drugs targetical against LIPE protein, and for testing the efficacy of therapeutic agents and compounds for treating obseity and male sterility in a biological system. The present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents and control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence represents one control of the present nucleic acid sequence active the presents one control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel genetic variants of Lipase, Hormone-Sensitive isogenes, useful for improving efficiency and reliability in drug development for treating diseases associated with LIPE activity, e.g. obesity and male sterility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in the invention to detect polymorphisms in the human LIPE gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.9%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chew A, Koshy B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nilarity 100.0%; Pred. No. 4.3
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 16; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anastasio AE, Bentivegna SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENA-) GENAISSANCE PHARM INC.
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ABK81376
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Matches
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Gaps ò

Query Match 40.9%; Score 9; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 4.38+02; Matches 9; Conservative 0; Mismatches 0; Indels

schultz1-727.rng

antifungal drugs comprising (a) contacting a test substance with a yeast call; and (b) monitoring expression of a NORF gene whose expression of varies as in Mi, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose contoring expression in the yeast cell of at least 1 NORF gene whose to study, monitor and affect phases of the call cycle, the differentially expressed genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF31268 to AAF41064 represent SAGE tags used in the exemplification of the present invention. S phase and G2/M; (2) a method (M2) for screening candidate method, in the exemplification of the present invention $\mathcal{G}_{\mathcal{G}} \mathcal{G}_{\mathcal{G}} \mathcal{G}$

Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Gaps .. 0 0; Indels 40.9%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 4.3e+02; cive 0; Mismatches 0; Indels 9; Conservative Local Similarity Query Match Matches

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RESULT 371

AAS19577 standard; DNA; 10 BP. AAS19577;

(first entry) 26-MAR-2002 Primer-extension oligonucleotide #8 to detect human MPL polymorphisms

Human, single nucleotide polymorphism, SNP, MPL, chromosome 1p34; myeloproliferative leukaemia virus oncogene; haplotyping; genotyping; congenital amegakaryocytic thrombocytopaenia; CAMT; primer; ss.

Homo sapiens

WO200179232-A2

16-APR-2001; 2001WO-US012301.

14-APR-2000; 2000US-0197839P

(GENA-) GENAISSANCE PHARM INC

Koshy B, Stephens JC; Choi JY, Chew A,

WPI; 2002-055251/07.

Nucleotide polymorphisms in the human myeloproliferative leukemia virus oncogene (MPL) gene, useful for studying the function of and expressing MPL protein for use in screening drugs for treating diseases related to MPL activity.

Claim 17; Page 16; 85pp; English.

The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human myeloproliferative leukaemia virus oncogene (MPL) gene located on chromosome 1934, and methods for haplotyping and/or genotyping the MPL gene. The methods of the invention make use of allele-

The invention describes a novel isolated polynucleotide (I) comprising a sequence which is a polymorphic variant (PV) of a reference sequence for colony stimulating factor I receptor (CSPIR) gene, found on The colony stimulating factor I receptor (CSPIR) gene, found on The dolypeptide are useful for improving the discovery and development of malignant histocytosis, myeloid mainganencies, and inflammantory discorders and the haplotypes can be used to validate CSFIR activity, e.g. and the haplotypes can be used to validate CSFIR as a candidate target for treating a specific condition or disease predicted to be associated with CSFIR gene of an individual can also be used in developing disgnostic tests and therapeutic treatments. (I) is useful in studying the expression and function of CSFIR, and in creating the expression and function of CSFIR, and in creating the effect of treat diseases related to CSFIR and in studying the effect of the variation on the biological activity and in studying the effect of binding affinity of candidate drugs targeting CSFIR. Antibodies are useful in a variety of disanostic and prognostic formats and therapeutic methods. A transgenic animal is useful in studying expression of the ö perferning oligonaclectides for detecting MPL gene polymorphisms. The polymucleotides and screened compounds are useful for the treatment of diseases associated with MPL activity, such as congenital amegakaryocytic thrombocytopaenia (CAMT). AAS15570-AAS15607 represent primer-extension oligonucleotides for detecting human MPL gene polymorphisms Novel polymorphic variants of colony stimulating factor 1 receptor useful in studying expression and function of the protein, useful for screening candidate drugs to treat diseases e.g. inflammatory disorders. Colony stimulating factor 1 receptor; CSFIR; polymorphic variant; cytostatic; gene therapy; malignant histocytosis; isogene; myeloid malignancy; inflammarcry disorder; transgenic animal; haplotype; genotype; human; allele specific oligonucleotide; ASO; primer; specific oligonucleotides (ASOs) as probes and primers and/or primer-Gaps Colony stimulating factor 1 receptor (CSFIR) oligonucleotide #176. .. 0; Indels Score 9; DB 1; Length 10; Pred. No. 4.3e+02; Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other; 100.0%; Pred. ... 40.9%; Score 9; Claim 17; Page 17; 164pp; English (GENA-) GENAISSANCE PHARM INC. AAS98810 standard; DNA; 10 BP. 12-APR-2001; 2001WO-US012044. 12-APR-2000; 2000US-0196411P. Koshy B; (first entry) Best Local Similarity 100. Matches 9; Conservative 732 GGAGAAACA 740 10 primer extension; ss. WPI; 2002-075058/10 2 GGAGAAACA Choi JY, WO200179225-A2 Homo sapiens 25-OCT-2001. 26-MAR-2002 AAS98810; Chew A, RESULT 372 AAS98810 8888888888 ઠ

(transient receptor potential) family protein; (ii) is connected with etiology of BMS (Beckwith-Wiedemann syndrome) and/or (iii) is connected with tumors involving 11p15.5 abnormalities. The products of the match tumors involving 11p15.5 abnormalities. The products of the connected invention have anticaner and developmental activity. MRTI is involved in regulation of intracellular calcium in levels, which are essential for cequilation of intracellular calcium in longwith factors; also in apoptosis and cell growth, death and differentiation, and in urogenital diseases. Concluding polycystic kidney disease. (I) and related ribozymes, antisense RNA, proteins and antibodies (Ab) are used to treat or prevent diseases associated with altered expression of the MRTI gene or activity of its protein, or with calculum infilux into cells, e.g. BMS, Wilms tumor, rhabdoid tumors and thabdomyosarcoma. Probes from (I), or Ab, are also used for diagnosis of such diseases. (I) can also be used for recombinant thereby, as tissue or chromosomal markers, for identifying genetic diseases and related sequences, as primers for genetic fingerprinting, as competitive assays for (II), are used to raise Ab, as reagents in competitive assays for (II), as tissue markers; for identifying crothing and in screening for (ant) agonists. This sequence represents human MTRI gene intron9/exonl0 junction region described in the method of the invention

Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

DB 1; Length 10; 5. 4.3e+02; cches 0; Indels 40.9%; Score 9; DB 1 100.0%; Pred. No. 4.3 tive 0; Mismatches Local Similarity 100 nes 9; Conservative Query Match

729 CCAGGAGAA 737

CCAGGAGAA 10 ठ 음

AAF70411 standard; DNA; 10 AAF70411; RESULT 369

BP

(first entry) 20-APR-2001

Human DRD2 polymorphism detection oligonucleotide primer SEQ ID NO:154.

Human, dopamine receptor D2, DRD2, polymorphism; allele specific, drug target isogene, detection, single nucleotide polymorphism; SNP; genotype; schizophrenia, Parkinson's disease; myoclonus dystonia; MD; genotype; schizophren: probe; PCR primer; ss

Homo sapiens

WO200105832-A1.

25-JAN-2001

19-JUL-2000; 2000WO-US019644.

99US-0144493P. 19-JUL-1999; (GENA-) GENAISSANCE PHARM INC

Stephens JC; Duda A, Nandabalan K, Denton RR, Chew A,

WPI; 2001-091967/10.

Polynucleotides comprising single nucleotide polymorphisms in the hum dopamine receptor D2, useful for detecting mutations associated with, e.g. schizophrenia, Parkinson's and myoclonus dystonia.

Disclosure, Page 24; 135pp; English.

(DRD2). The present invention describes polynucleotides comprising single nucleotide polymorphisms (SNPs) in the human dopamine receptor D2

The polynucleotides may be used in assays to detect and characterise polymorphisms in DRD2 that affect its expression and activity and are involved in disorders such as schizophrenia, Parkinson's and myoclonus dystonia (MD). This information would be useful for studying the biological function of DRD2 as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function. Polymorphisms in the DRD2 gene affect the expression of active and functional polypeptides. Therefore it is advantageous to detect polymorphisms in the DRD2 gene and how those polymorphisms are combined in different copies of the gene. AAF7026 to AAF70308 represent human DRD2 allele specific oligonucleotide probes, and AAF70309 to AAF70304 represent human DRD2 allele specific oligonucleotide probes, to AAF70309 to AAF70405 allele specific oligonucleotide primers which are used in the detection of DRD2 polymorphisms. AAF70405 to AAF70453 to AAF7045 888888888888888888888888

Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;

ö Gaps .; 0 0; Indels 40.9%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 4.3e+02; Live 0; Mismatches 0; Indels 9; Conservative Query Match Best Local Similarity Matches 9; Conserv

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AAF42486

AAF42486 standard; DNA; 10

BP.

AAF42486;

(first entry) 23-MAR-2001 Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10625.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000

14-JUN-2000; 2000WO-US016223.

16-JUN-1999; 99US-00335032

(UYJO) UNIV JOHNS HOPKINS

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SACE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example, Page 329, 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log

schultz1-727.rng

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expressed genes, or of their encoded proteins, can be used to identify calls as belonging to the monocyte lineage. Cells containing these genes can be used in active immunocherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing APC-associated costimulatory Co-administration of tumour antigens and presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell growth factors and secretion of co-stimulatory signals, migration to T cell rich sites, secretion of I meune effector cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, metastatic breast tumour tissue; breast cancer; tag; primer;
non-metastatic breast tumour tissue, gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metastatic breast tumour cell downregulated transcript tag #5890.
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                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                        Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                        DB 1; Len
                                                                                                                                                                                                                        40.9%; Score 9; DB 1
100.0%; Pred. No. 4.3
ative 0; Mismatches
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98US-0089997P.
98US-0090039P.
98US-0090040P.
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                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.'
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                           734 AGAAACAGA 742
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-106079/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9965928-A2
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Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, Polypeptides encoded by the transcripts are also useful in vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter immunotherapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor; transient receptor potential family; BRS; Beckwith-Wiedemann syndrome; 11p15.5 abnormality; Ohromosome 11; anticancer; developmental activity; intracellular calcium ion regulation; hormone; growth factor; apoptosis; cell growth, cell death; cell differentiation; urogenital disease; polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor; rhabdomyosarcoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann syndrome and tumors, also related proteins and antibodies.
                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                   Sequence 10 BP; 5 A; 3 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MTR1 intron9/exon10 junction.
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/*tag= b
/number= 10
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/*tag= a
/number= 9
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                                                                                                                                                                                                                                                                                                                                         738 ACAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                           ACAGAACAC 10
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Homo sapiens.

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expression) tags used to identify mRNA transcripts encoding immunostiminatory cofactor proteins which are preferentially or immunostiminatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell complex) and subsequent recognition by T-cell receptors is alone activation of the cytotoxic immune response, particularly against tumour cells, immunostimulatory cofactors also being required for the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses.

They may be used in vaccines to induce an immune response, particularly against a tumour antigen, to modulate the genotype of an APC; to screen for against that modulate expression of differential cell differentially expressed genes. Detection of diseases related to abnormal expression of these dendritic cell differentially expressed genes, or of their encoded proteins, can be used in active immunotherapy (or to stimulate production of a containing them are used in active immunotherapy (or to stimulate production of a containing them are used in active immunotherapy (or to stimulate production of a containing them are used in active immunotherapy (or to stimulate antigen presentation of containing them are used in active immunotherapy (or to stimulate antigen presentation of containing containing them are used in active immunotherapy (or to stimulate antigen presentation of containing expectation of conta
                                                                                                                                                                                                                                   Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
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                                                                                                                                                                                                                                                                                                                      Claim 1; Page 119; 130pp; English.
                                                                                                                                          Roberts BL, Shankara S;
                                     GENZYME CORP.
ROBERTS B L.
SHANKARA S.
                                                                                                                                                                                             WPI; 2000-106077/09.
                                          (GENZ ) (ROBE/) 1
                                                                                          SHAN/)
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0; Indels Length 10; 40.9%; Score 9; DB 1; Len 100.0%; Pred. No. 4.3e+02; tive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 9; Conservative 738 ACAGAACAC 746 9 ACAGAACAC 1 g

AAZ79359 standard; DNA; 10 BP. RESULT 366

AAZ79359;

Human dendritic cell SAGE tag, SEQ ID NO:1787.

10-APR-2000 (first entry)

SAGE tag, serial analysis of gene expression, antigen-presenting cell, APC; moncoyte-derived denditic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte, tumour antigen; immunotherapy; anticancer; ss.

98US-0089844P 98US-0089853P 98US-0089992P 98US-0089992P 98US-0089997P 98US-0089997P 98US-0089997P 98US-0089997P 98US-0089997P 98US-0090035P 98US-0090043P 98US-0090041P 98US-0090041P 98US-0090041P 98US-0090044P 98US-0090044P 98US-0090044P 98US-0090044P 98US-0090044P 98US-0090044P 98US-0090044P 98US-0090044P 98US-0090044P 99WO-US013800 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; W09965924-A2 18-JUN-1999; 23-DEC-1999, 19-01-NUL-01 19-JUN-1998

(GENZ) GENZYME CORP. (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.

Roberts BL, Shankara S;

WPI; 2000-106077/09.

Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.

Claim 1; Page 116; 130pp; English.

expression) tags used to identify mRNA transcripts encoding captession) tags used to identify mRNA transcripts encoding captession) tags used to identify mRNA transcripts encoding cifferentially expressed in monocyte-derived dendritic cells compared differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs correspond to differentially expressed in dendritic cells, while preferentially or differentially expressed in dendritic cells, while cother transcripts correspond to novel genes. Antigen-presenting cell cother transcripts correspond to novel genes. Antigen-presenting cell cother transcripts correspond to novel genes. Antigen-presenting cell cother transcripts or expressed costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells, immunostimulatory cofactors also being required for the tumour cells, immunostimulatory cofactors also being required for the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid against a tumour antigen; to modulate the genotype of an APC; to screen for against a tumour antigen; to modulate the genotype of an APC; to screen correspondent modulate expression of differentially expressed genes in an APC; and as hybridisation probes (amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially

for enhancing the prophylactic or therapeutic respiratory effect of an autinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPPO at ftp.wipo.int/pub/published_pct_sequences 82333333333333333

Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

41.8%; Score 9.2; DB 1; Length 14; 78.6%; Pred; No. 4.5e+02; ative 0; Mismatches 3; Indels 732 GGAGAAACAGAACA 745 14 GCAGAAAGAGGACA 1 Conservative Local Similarity 11; Query Match Best Loca Matches d à

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Gaps

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ABZ96451 standard; DNA; 14 BP ABZ96451;

17-OCT-2003 (first entry)

Human nucleic acid sequence.

Human, antisense, lung dysfunction, nasal airway dysfunction, antinflammatory, antiallergic, antinflammatory, antiallergic, antiasthmatic; hypotensive; immunosuppressive, cytostatic; gene therapy, antisense gene therapy, respiratory; lung, adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

sapiens. HOMO WO200285308-A2.

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar D; Katz E, Sandrasagra A, Ka , Shahabuddin S; Li Y, Sa Tang L, Nyce JW, I Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired ö respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid

Disclosure; SEQ ID NO 11693; 872pp; English.

ubiquinone

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention immunosuppressive, and cytostatic activity. The composition app have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also AB2296451 ID AB232 ARX AB23 XX AB23 XX AB23 XX AB23 XX AB23 XW AB101 XW AB101 XW AB101 XW AB20 YW AB

19-JUN-1998

for enhancing the prophylactic or therapeutic respiratory effect of an antinflammatory steroid in a subject, for reducing or depleting levels of the reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences ö SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss. Gaps .; 0 41.8%; Score 9.2; DB 1; Length 14; 78.6%; Pred. No. 4.5e+02; tive 0; Mismatches 3; Indels Seguence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other; Human dendritic cell SAGE tag, SEQ ID NO:1921. ; AAZ79493 standard; DNA; 10 BP 98US-0089993P. 98US-0089994P. 98US-0089994P. 98US-0089999P. 98US-0090000P. 9805-00900369-9805-00900369-9805-00900410-9805-00900418-9805-00900447P-9805-0090045P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090078P-9805-0090009P-9805-009009P-9805-00 98US-0089853P. 98US-0089878P. 98US-0089991P. 99WO-US013800 745 10-APR-2000 (first entry) 14 GCAGAAAGAGACA 1 Conservative 732 GGAGAAACAGAACA Local Similarity Homo sapiens WO9965924-A2 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 18-JUN-1999; 23-DEC-1999. 11; 19-000-01 19-7UV-1998; 19-JUN-1998 .9-TUN-1998 19-JUN-1998 19-JUN-1998 9-JUN-1998 19-JUN-1998 .9-JUN-1998 19-JUN-1998 19-JUN-1998 19-JUN-1998 AAZ79493; Query Match Best Loca Matches SAGE AAZ79493, RESULT 88888888888888

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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense cligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activity of target polypeptides associated with lung/respiratory disorders and transmitters, transcription factors, immunoglobulins and antibodies, and transmitters, cytokines and chemokine receptors, adenosine receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system petide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The creeptors, binding proteins and malignancy associated proteins. The antipulatory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human, airway disorder; bronchoconstriction; lung inflammation; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory, bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human multiple target antisense (MTA) oligonucleotide #3027.
   Length 14;
Score 9.2; DB 1; Length 14
Pred. No. 4.5e+02;
0; Mismatches 3; Indels
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   41.8%;
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(NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                  AAF21460 standard; DNA; 14
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                                                                                                                                                                                                                GCAGAAAGAGGACA 1
   Query Match
Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                   732 GGAGAAACAGAACA
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                                                                                                                                                                                                                                                                                                                                  RESULT 362
                                                                                                                                                                                                                                                                                                                                                        AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF21460/AAF
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                                                                                                                                                                                                                                                                                                                                                                                                                 Human, antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; forminosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allegies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allegic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF10434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                          Gaps
                                                                                                                                                                                         0
                                                                                                                                                              Length 14;
                                                                                                                                                              Score 9.2; DB 1; Length 14 Pred. No. 4.5e+02; 0; Mismatches 3; Indels
                                                                                                                                     Seguence 14 BP; 0 A; 5 C; 2 G; .7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                ABZ97154 standard; DNA; 14 BP.
                                                                                                                                                               41.8%;
78.6%;
                                                                                                                                                                                                                    732 GGAGAAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               Human MTA oligonucleotide.
                                                                                                                                                                                                                                             14 GCAGAAAGAGGACA 1
                                                                                                                                                                                          11; Conservative
                                                                                                               the present invention
                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                    17-0CT-2003
                                                                                                                                                                                                                                                                                                                                           ABZ97154;
                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                        RESULT 363
                                                                                                                                                                                                                                                                                                     ABZ97154/c
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                           826666666666888
                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                             셤
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Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ä Pabalan J, Aguilar œ, Katz Nyce Jw, Li Y, Sandrasagra A, K. Miller S, Tang L, Shahabuddin S; WPI; 2003-229219/22 ubiquinone

23-APR-2002; 2002WO-US013135. 24-APR-2001; 2001US-0286137P. (EPIG-) EPIGENESIS PHARM INC.

WO200285308-A2.

31-OCT-2002.

Disclosure; SEQ ID NO 12396; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5 or 3 end genemic flanking regions, 5 and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nastal alraway dysfunction and a second active agent comprising an antiinflammatory steroid and ubsquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, and immunosuppressive, and extocratic activity. The composition may have a use in antisense gene thrappy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also

Human, adenosine receptor; low adenosine antisense oligonucleotide; phosphorothicate; impaired respiration; inflammation; allergy; allergy; disease; bronchoconstriction; inhibitor; antinflammatory; antiallergic antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss. 99WO-US017712. 98US-0095212P, (UYEC-) UNIV EAST CAROLINA WPI; 2000-205971/18. WO200009525-A2 Homo sapiens. 03-AUG-1999; 03-AUG-1998; 24-FEB-2000. Nyce JW;

The present invention describes a new composition comprising an antisense oligomucleotide (ON) with low adenosine (up to 15%), which targets cutcled acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergid, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, cuseful for the treatment of diseases and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating c.g. impaired airways, including lung diseases ond diseases whose secondary impeded respiration, respiratory distress syndrome, pain, cystic impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the consension of the adenosine state of deoxyadenosine which activates adenosine receptors causing concluded esquences given in the sequence listing from the present cinvention, which correspond to SEQ ID NO:1 to 1815, but the sequences differ cinvention, which correspond to SEQ ID NO:1 to 1815, but the sequences of from the previously named sequences. SEQ ID NO:1 to 1816, AAA3333 to AAA33922 are specifically claimed ONs from the present invention. N B. Sequences given in the disclosure of the present invention. N B. including the present invention of the present invention. The sequence of the present invention. New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or Disclosure; Page 556; 1343pp; English

Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Gaps ; 0 41.8%; Score 9.2; DB 1; Length 14; 78.6%; Pred. No. 4.5e+02; tive 0; Mismatches 3; Indels Query Match
Best Local Similarity 78.6
Matches 11; Conservative

745

732 GGAGAAACAGAACA

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AAF20757 standard; DNA; 14 BP. GCAGAAAGAGGACA 1 14 RESULT 361 AAF20757/ ID AAF2

AAF20757;

(first entry) 14-MAR-2001

Human multiple target antisense (MTA) oligonucleotide #2324.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasconstriction, asthma; RBS; respiratory distress syndrome; pann; cystic fibrosis; allergic rhinitis; pulmonary hypotrension; emplyeema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss

Homo sapiens.

WO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US008020.

99US-0127958P. 06-APR-1999;

(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Claim 14; Page 623; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (C) can have respiratory, bronchoditator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. (The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with cativity of target polypeptides associated with cativiting peptide factors and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, indiving proteins, adenosine receptors, brinding proteins, adenosine receptors, brinding proteins and malignancy associated proteins. The receptors, canding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including proteins and malignancy associated proteins. The and/or bronchoconstriction and/or lung inflammation, allergy olices and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstratorion, inflammation, allergic fibrosis (CF), allergic rhinitis (AR), pulmonary transplantation rejection, pulmonary disease (CPD), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary transplantation rejection, pulmonary under and/or ancer. AAR/18434 to AAR/21543 represent human polymucleotide invention of the exemplification of the exemplification of the exemplification of the proper of the exemplification of the exemplification of the exempletices. the present invention

Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

MOD CCT IS 14:40:01 2004

myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss. 99WO-US006507. Homo sapiens WO9950403-A2 07-0CT-1999

98US-0079678P 27-MAR-1998; (RIBO-) RIBOZYME PHARM INC.

Jarvis T,

Roberts E,

Pavco PA,

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors. WPI; 1999-591315/50.

Coeshott C, Mcswiggen JA;

Claim 56; Page 136; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl bydrocarbon nuclear transporter (ARNY) gene, an integrin subunit bete 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA1762 to AAA19154 represent their recresponding target sequences; and AAA19155 to AAA19152 represent their corresponding target sequences; and AAA19155 to AAA1922 represent their corresponding target sequences; AAA19223 to AAA1922 represent their corresponding target sequences; AAA21689 to AAA21689 represent their corresponding target sequences; AAA21689 to AAA21689 represent their corresponding target sequences; AAA21689 to AAA21687 and AAA21635 to AAA21635 to AAA21633 represent their corresponding target sequences; AAA21689 to AAA21687 and AAA22476 to AAA23262, AAA23343 to Cfor integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to the invention are used for modulating the sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit belas, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARND), inflammation, and arthritis, as well as macular degeneration (ARND), inflammation, and arthritis, as well as macular degeneration (ARND), inflammation, soler-Weber-Rendu syndrome, syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, cynthem syndrome, whymit alpha-6, or recent the levels of AAA214 the l integrin subunit alpha-6, or integrin subunit beta-3

Seguence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;

0; Gaps 41.8%; Score 9.2; DB 1; Length 14; 78.6%; Pred. No. 4.5e+02; ive 0; Mismatches 3; Indels Query Match
Best Local Similarity 78.6'

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731 AGGAGAAACAGAAC 744

ò g

14 AGAAGGAACAGCAC 1

AAX55188 standard; DNA; 14 BP. RESULT 359 ZXEXHXEXB ZXEXHXXXX

(first entry) 05-JUL-1999 Multiple antisense oligonucleotide 9.

Antisense oligonucleotide; multiple target; antisense treatment;

impaired respiration; inflammation; lung disease;
pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
respiratory distress syndrome; pain; cystic fibrosis;
pulmonary hypertension; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; pancreatic cancer;
hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
prostate cancer; ss.

Synthetic.

WO9913886-A1.

25-MAR-1999.

98WO-US019419. 17-SEP-1998;

97US-0059160P L7-SEP-1997;

UYEC-) UNIV EAST CAROLINA. 09-JUN-1998;

98US-00093972.

Nyce JW;

WPI; 1999-229400/19.

New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction.

Disclosure; Page 73; 120pp; English.

The specification describes antisense oligomucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
con-coding regions of RNAs corresponding to target genes, coding and
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
codons, genomic flanking regions associated with one or more diseases,
conditions or mixtures. The artisense oligomucleotides may be derived
cronditions or mixtures. The artisense oligomucleotides may be derived
from sequences AAX55272-74. These multiple target oligomucleotides
conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, allergic rhinitis,
diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
acute asthma, allergies, asthma, impeded respiration, respiratory
disease (COPD), and cancers such as leukemias, lymphomasy carcinomas e.g.
colon cancer, breast cancer, lung cancer, pancreatic cancer,
colon cancer, breast cancer, lung cancer, pancreatic cancer,
chepatocellular carcinoma, kidney cancer, melanoma, hepatic metastasized
colon cancer, breast cancer, under cancer, melanoma, hepatic metastasized
colon cancer, breast cancer, melanoma, hepatic metastasized
colon cancer, breast and prostate cancer

Sequence 14 BP; 0 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Gaps .. Query Match 41.8%; Score 9.2; DB 1; Length 14; Best Local Similarity 78.6%; Pred. No. 4.5e+02; Matches 11; Conservative 0; Mismatches 3; Indels

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732 GGAGAAACAGAACA 745 GCAGAAAGAGGACA 1 셤

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14

RESULT 360 AAA34635/c

AAA34635 standard; DNA; 14 AAA34635; EXEXEXE

BP.

28-JUL-2000 (first entry)

Human adenosine receptor related polynucleotide SEQ ID NO:2324.

schultz1-727.rng

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Composition with a modified oligonucleotide useful for treating a patient with a pathological disorder such as abnormal appetite, hypertension, eczema, anxiety, stress, and cancer.
inflammation; heart burn; infection; colon cancer; malignant melanoma; skin disorder; antisense oligonucleotide; ss.
                                                                                                                                                                        Claim 17; Page 6; 173pp; English.
                                                                                                                Thompson T;
                                                                     10-JUL-2002; 2002WO-US021664.
                                                                                    10-JUL-2001; 2001US-0303820P
                                                                                                  (OLIG-) OLIGOS ETC INC
                                                                                                                Dale RMK, Arrow A,
                                                                                                                              WPI; 2003-221709/21
                                          WO2003006478-A1
                     Homo sapiens.
                                                        23-JAN-2003
                             Synthetic.
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The present invention describes a composition (I) suitable for administration in a mammal, which comprises a modified oligonucleotide (II) of 7-7s nucleotides contraining 7 or more contiguous ribose groups linked by achiral 5-3' internucleoside phosphate linkages, where the modified oligonucleotide is complementary to a region of a gene associated with a pathological disorder. Also described: (I) a nutritional supplement comprising (II); and (2) a cosmetic composition comprising (II), where the modified oligonucleotide is complementary to a region of a gene associated with a skin disorder. (I) and (II) can have comprising (II), where the modified oligonucleotide is complementary to a region of a gene associated with a skin disorder. (I) and (II) can have tranquilliser, antilinflammatory, antiuncer, laxative, antimigraine, conversing tranquilliser, antilinflammatory, antiuncer, laxative, antimigraine, conversing a patient with a conversion of a gene associated with a stone store for treating a patient with a pathological disorder selected from abnormal appetite, hypertension, on pathological disorder selected from abnormal appetite, hypertension, anxiety, stress, inflammatory bowel syndrome, ulcerative collisis, crohn's disease, and proposite stores, and stones, gall stones, constipation, colds, chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome, convenient fatigue syndrome, rosacea, arthritis, poriasis, prostatis, prostatis, chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome, chronic fatigue syndrome, rosacea, arthritis, positis, prostatis, constitient of supplementing the diet of an individual supplementing the diet of an individual with a skin disorder. ACF63279 to ACF63410 represent invention controlectide sequence given in the exemplification of the present invention Seguence 14 BP; 4 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

ö Gaps .. 0 42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; ive 0; Mismatches 1; Indels Conservative Local Similarity 10; Query Match Matches

AAQ78386 standard; DNA; 14 BP. 3 TGTCAGGAGAA 13 RESULT 357
AAQ78386
ID AAQ7838
XX
AC AAQ7838
XX
DT 25-MAR

(revised)

25-MAR-2003

AAQ78386;

727 TGCCAGGAGAA 737

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The antisense oligonucleotides are useful in the treatment of tumours in which expression of TGF-beta is of relevance for pathogenicity and/or inhibition of pathological angiogenesis. They are used especially for the treatment of the immunosuppressive effect of TGF-beta, augmentation of the proliferation of cytocixic lymphocytes, treatment of endogenous hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas and malignant gliomas, including glioblastomas, treatment and prophylaxis of skin cardinogenesis, and treatment of oscophageal and gastrio. AAQ78352-Q78488 The sequences given in GENEEEO files AAQ78352-Q78488 are antisense oligodeoxymucleotides of TGF-beta 1. The sequences given in GENEEEO files oligodeoxymucleotides of TGF-oligodeoxymucleotides of TGF-beta 2 in the form of physhorothioate analogues. (Updated on 25-MAR-2003 to correct PV field.) tumour; New transforming growth factor beta anti:sense oligo:nucleotide(s) - for Schlingensiepen R; Transforming growth factor beta; TGF-beta; antisense; treatment; anglogenesis; breast tumour; neurofibroma; glioma; glioblastoma; carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut; immunosuppression; oligonucleotide; ss. 41.8%; Score 9.2; DB 1; Length 14; 78.6%; Pred. No. 4.5e+02; rative 0; Mismatches 3; Indels Antisense oligonucleotide hybridising to TGF-beta gene. Schlingensiepen K, Sequence 14 BP; 6 A; 2 C; 5 G; 1 T; 0 U; 0 Other; (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK. treating immunosuppression, tumours, etc. Claim 6; Page 34; 74pp; English. Schlingensiepen G, Brysch W, Bogdahn U; 94WO-EP001362. 93EP-00107089. (first entry) WPI; 1994-358266/44. 27-JUN-1995 409425588-A2 29-APR-1994; 30-APR-1993; 13-MAY-1993; .0-NOV-1994. Synthetic. Query Match

Human, aryl hydrocarbon nuclear transport, ARNT; TIE-2; angiogenesis, integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme, angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; Human TIE-2 target site SEQ ID NO:2381. AAA19155 standard; RNA; 14 BP. 19-JUN-2000 (first entry) AAA19155; AAA19155,

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Gaps

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730 CAGGAGAAACAGAA 743

11; Conservative

Matches

Best Local Similarity

1 CATGAGAAGCAGGA 14

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MOD CGC TO T4:40:07
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an centinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in activity to adenosity if or reducing or depleting levels of for entitialmantatory steroid in a subject, for reducing or depleting levels of, or receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, at issue, or treating bronchoconscription, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed or the specification, but was obtained in electronic format directly from WIPO at the subject of the parents. Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone. Disclosure; SEQ ID NO 11128; 872pp; English. ftp.wipo.int/pub/published_pct_sequences Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; 23-APR-2002; 2002WO-US013135. 24-APR-2001; 2001US-0286137P (EPIG-) EPIGENESIS PHARM INC WPI; 2003-229219/22. Miller S, Nyce JW,

Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;

Gaps ô 42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; tive 0; Mismatches 1; Indels 10; Conservative Local Similarity Query Match Matches

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ABZ95313; RESULT 355

(first entry) 17-0CT-2003

Human IL-6 receptor fragment no.1177.

Human, antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cyrostartic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

WO200285308-A2

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar D; Katz B, Li Y, Sandrasagra A, K Tang L, Shahabuddin S; Nyce JW, I Miller S,

WPI; 2003-229219/22.

Katz E, Pabalan J, Aguilar D;

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

Disclosure; SEQ ID NO 10555; 872pp; English.

X#X#X#X#H#X#X#######X#X#X######

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligomucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' or segions within 2-10 mucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antilinflammatory steroid and ubiquinone. A composition of the invention has attiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory defect of an antifich ammatory steroid in a subject, for reducing or depleting levels of or reducing sensitivity to adenosine, reducing levels of adenosine creeptor, producing bronchodilation, increasing levels of budguinone or lung inflammation, lung allergies, or a respiratory disease or condition.

Conspecification, but was obtained in electronic format directly from WIPO care for the interpersoner. at ftp.wipo.int/pub/published_pct_sequences

Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Gaps ö 42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; ive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.9
Matches 10, Conservative

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728 GCCAGGAGAA 738 12 GCCAGGGAAA 2 ö 염

ACF63279 standard; DNA; 14 BP. ACF63279 KARAKA KARAKA KARA BALA KA

(first entry) 09-OCT-2003

ACF63279;

Human phosphodiesterase 4 antisense oligonucleotide SEQ ID NO:1.

Human, pharmacological; hypotensive; antilipaemic; vasotropic; laxative; dermatological, antidepressant; tranquilliser; antilnflammatory; eczema; antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic; gnaecological; virucide; vulnerary; antiarthritic; antipsoriatic; cold; antimicrobial; oytostatic; luholytic; pathological disorder; depression; abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia; erctile dysfunction; anxiety; stress; inflammatory bowel syndrome; ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine; constipation; headache; seizure; multiple sclerosis; polymyostis; fibromyalgia; parkinson's disease; amyotrophic lateral sclerosis; trauma; chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome; chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatis;

> à d

ABZ95313 standard; DNA; 14 BP ABZ95313/C
XX
AAC
ABZ95
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AUM91
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Recombinant influenza virus for transfer and expression of foreign genes and RNA molecules into cells and for preventing, treating influenza, has biscistronic viral RNAs coding for two genes in tandem arrangement.
                                                                                                                                              Disclosure; Page 15; 39pp; English.
                                                                               Menke A, Meyer-Rogge
                               20-JUL-2000; 2000EP-00115626
                                               20-JUL-2000; 2000EP-00115626
                                                                                                                                                                                                                                                                                                             the method of the invention
                                                              (ARTE-) ARTEMIS PHARM GMBH.
                                                                                              WPI; 2002-156694/21
EP1174514-A1
               23-JAN-2002,
                                                                               Hobom G,
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. 0 Sequence 14 BP; 1 A; 6 C; 1 G; 0 T; 6 U; 0 Other;

731 AGGAGAAACAG 741 AGTAGAAACAG 4 14 δ

ABZ95299; RESULT 353
ABZ95299/c
XX
AC ABZ952
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AC ABZ952
DT 17-OCT
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AX
BW Human;
KW Human;
KW antiin
KW ANTIIO
KW ANTIIO
KW ANTIIO
KW ANTIIO

Homo sapiens

WO200285308-A2 31-OCT-2002.

The invention describes a recombinant influenza virus (I), stable in the absence of any helper virus, that has a viral RNA segment being a biscistronic RNA molecule coding for two genes in tandem arrangement (tandem RNA segment, TRS). (I) is useful for expression of incorporated foreign gene(s) and RNA molecules in cells. (I), preferably a recombinant influenza A virus is useful for: preventing and/or treating influenza, and for preparing a medicament for vaccination purposes; somatic gene therapy, and as immunogen for inducing antibodies; as an expression vector for producing proteins or glycoproteins; preparing agents for somatic gene therapy; immunotherapy, preferably autologous immunotherapy; transfer and expression of foreign genes and RNA molecules into cells infected by such viruses, where the RNA molecules to be expressed include antisense or double-stranded sequences relative to the target cell cellular mRNA molecules, and/or the agent is suitable for sequence sequence represents a 3 conserved region mutant of influenza C virus the mathy of the mathy influenza C construct, described in

Gaps 42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; ive 0; Mismatches 1; Indels Query Match Best Local Similarity 90.9 Matches 10, Conservative

ABZ95299 standard; DNA; 14 BP. 17-OCT-2003 (first entry)

Human; antisense; lung dysfunction, nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human IL-6 receptor fragment no.1163.

24-APR-2001; 2001US-0286137P.

23-APR-2002; 2002WO-US013135.

(EPIG-) EPIGENESIS PHARM INC

Aquilar D; Pabalan J, Katz E, ŝ Li Y, Sandrasagra A, Tang L, Shahabuddin Nyce JW, I Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

Disclosure; SEQ ID NO 10541; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligomucleotide antisense to the instraction codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubjunione. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an preventing sensitivity to adenosine reducing levels of denosine receptor, producing sensitivity to adenosine, reducing levels of adenosine receptor, producing sensitivity to adenosine, reducing levels of ubjuinnon or ung inflammation, lung allergies, or a respiratory disease or condition, ung inflammation, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences

Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Gaps .. 42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; ative 0; Mismatches 1; Indels Local Similarity 90.9 Query Match tches

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ABZ95886 standard; DNA; 14 BP. ABZ95886;

RESULT 354

17-OCT-2003 (first entry)

Human monocyte activating factor antisense fragment no.1746.

Human, antisense, lung dysfunction, nasal airway dysfunction, antinflammatory steroid, ubiquinone, antinflammatory; antiallergic, antiasthmatic; hypotensive, immunosuppressive, cytostatic; gene therapy, antisense gene therapy; respiratory; lung, adenosine sensitivity; adenosine receptor, bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. ABZ95886/A XX ABZ95 AC ABZ95 AC ABZ95 XX ABZ95 AC A

WO200285308-A2.

31-OCT-2002.

WPI; 2002-657594/70

Hobom G,

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                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for the expression of tumour associated antigens (TAA) or virus-associated antigens (VAA) by dendritic cells comprising: preparing a recombinant influenza virus containing a nucleotide sequence coding for the TAA or VAA; and infecting dendritic cells with the recombinant virus. The method is used for expressing TAA or VAA in dendritic cells. The cells are used for preparing a medicament for treating tumours or viral infections. A vaccine can be created by using dendritic cells presenting tumour antigens to induce an immune response. This polynucleotide sequence represents an RNA region of a modified influenza C virus of the invention
                                                                                                                                                                                                                                                                                                            Expressing tumor or viral associated antigens by dendritic cells, used for treating tumors or viral infections, comprises using recombinant influenza virus containing nucleic acid encoding the antigens.
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virus-associated antigen; VAA; recombinant influenza virus; vaccine; viral infection; immune; influenza C virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenza C virus general structure oligonucleotide SEQ ID NO:19.
                                                                                                                                                                                                                                               Grassmann R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                               Strobel I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14 BP; 1 A; 6 C; 1 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                 Steinkasserer A,
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 16; 33pp; English
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                                                                                                                                                30-OCT-2000; 2000EP-00123687.
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                                                                                                                                                                                   30-OCT-2000; 2000EP-00123687.
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14 AGTAGAAACAG 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                     Influenza virus
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                                                                                      BP1201760-A1
                                                                                                                     02-MAY-2002.
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The present invention describes a human influenza virus (I) comprising an CRNA-sequence encoding a modified RNN-polymerase that differs from the wild-type RNA-polymerase of the human influenza virus in that at least 1 of the human influenza virus from FVV Bratislava RNA-polymerase of the human influenza virus from FVV Bratislava RNA-polymerase of the human influenza virus from FVV Bratislava RNA-polymerase of the human influenza virus from FVV Bratislava RNA-polymerase of the budden with the corresponding amino acid residue(s) as present in FVV Bratislava RNA-polymerase. (I) has virucide, cytostatic, anti-HIV, competenced in gene therapy and vaccines. The influenza virus is useful for used in gene therapy and vaccines. The influenza virus is useful for preparing agents for: (a) gene transfer into cells, preferably into commanalian cells, particularly into human cells, by viral infection; (b) gene transfer into antigen-presenting cells, and the use of the obtained commanalian cells, ravivo mammalian cells, and the use of the obtained contained in memune response, including the induction of a T-cell contained in immunotherapy, in vivo somatic on infections disease; (c) transfer and expression of foreign genes into cells infected by such viruses; or contained preferably for autologous immunotherapy; (f) transfer and expression of RNA molecules into cells infected by such viruses, preferably the RNA molecules to the target cellular mRNA molecules, and complease, and of the agent is suitable for sequence specific gene collections, and vor the agent is suitable for sequence specific gene collections, and vor the agent is suitable for sequence specific gene collections, and vor the agent is suitable for sequence specific gene collections, and vor the agent is suitable for sequence specific gene collections, and vor the agent is suitable for sequence specific gene collections agained HIV, hepatists of viruses can be influenza virus general structure related oligonuclectide, given in the completion of the present invent
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                                                                                                      New human influenza virus comprising an RNA-sequence encoding a modified RNA-polymerase, useful for preparing agents for therapeutic and prophylactic vaccination, or treating a growing tumor or a chronic
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"Specifically claimed in claim 11"
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                                                                                                                                                                                                                           Disclosure, Page 16; 172pp; English.
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2. .14
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/note= '
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                                                                                                                                                            prophylactic vaccir
infectious disease
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The present sequence is an oligonucleotide which was used to demonstrate the invention. The invention concerns end-blocked acid resistant oligonucleotides which are also resistant to nuclease degradation and are capable of binding specifically in an antisense manner. This means that they are useful in the treatment and prevention of infections, inflammatory diseases and cancer, as well as having non-therapoutic applications in cosmetics, for example in skin tanning products. In addition, they can be used in antibacterial applications such as sterilisation of surgical instruments, and in antibacterial lotions and soaps. A number of different versions of this sequence were produced, including an unblocked 2'-O-methyl RNA, a 2'-O-methyl RNA with 3' and 5' buttanol blocked ends, a 3'-O-methyl phosphodiseter; a 2'-O-propargyl and a 2'-O-methyl phosphodiseter. These were all used to show that the modified sequence is less susceptible to degradation than the natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified nucleic acid polymer used for treating inflammation, cancer, bacterial, viral and fungal infections and in disinfectants has a blocking chemical modification at the end of the polymer.
                                                                                                                     End-blocked acid-resistant oligonucleotide; infection; inflammatory disease; cancer; antibacterial application; phosphorothicate linkage; primer; ss.
                                                                                   Modified end-blocked acid-resistant oligonucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14 BP; 4 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 32; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dale RMK, Gatton SL, Arrow A;
                                                  19-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OLIG-) OLIGOS ETC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-465945/40.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     WO200040592-A1
                                                                                                                                                                                                                               Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-1999;
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19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                      13-JUL-2000.
                                                                                                                                                                                             Synthetic
                  AAA65226;
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/mod_base= OTHER /note= "optional phosphorothioate backbone"

99WO-US030266. 98US-00223498.

Location/Qualifiers

1. .14 /*tag= a

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The present sequence represents an antisense oligonuclectide, directed against the phosphodiesterase 4D (PDE4D) gene. The oligonuclectide is used to construct the polymer of the invention. The specification describes an acid resistant polymer which is complementary to PDE4, and comprises a nucleic acid with a backbone structure that is modified from that of a naturally occurring nuclectide polymer and a blocking chemical modification at or near one end of the nucleic acid. The acid resistant polymer is characterized by a pH stability of an hour at pH 0.01 to 10 and a nuclease resistance of twice that of naturally occurring nucleic acids which have the same number of nucleotides. The polymers are used to inhibit the expression of genes encoding PDE4. They are useful as analytical tools in the study of individual PDE isoforms and can treat analytical tools in the study of individual PDE isoforms and can treat expression, thrombosis, cystic fibrosis, gastric lesions, pulmonary hypertension, glaucoma, multiple solerosis, atopic dermatitis, asthma, and other allegic disorders. Other illnesses in which as increase of the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cyclic AMP or decrease in phosphodiesterase levels is useful, can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New acid resistant polymer complementary to phosphodiesterase 4 for treating depression, thrombosis, cystic fibrosis, gastric lesions, pulmonary hypertension, glaucoma, multiple sclerosis, atopic dermatitis
                                                                                                                                                                        Antisense oligonucleotide; phosphodiesterase 4; PDE4; cystic fibrosis, acid resistant polymer; nuclease resistance; depression; thrombosis; pulmonary hypertension; glaucoma; multiple sclerosis; gastric lesion; atopic dermatitis; asthma; allergy; ss.
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                                                                                        Antisense oligonucleotide for the human PDE4D gene.
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99US-00364626.
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(first entry)
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OLIG-) OLIGOS ETC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-465980/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200040714-A2
20-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1998;
29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL37793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL37793/
EXECUTED A SECULAR AND A SECURAR AND A SECULAR AND A SECURAR AND A SECULAR AND A SECULAR AND A SECULAR AND A SECURAR AND A SECULAR AND A SECULAR AND A SECURAR AND A SECUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2X2X2X2X
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Gaps ô

Score 9.4; DB 1; Length 14; Pred. No. 4.2e+02; 0; Mismatches 1; Indels

42.7%; 90.9%;

Conservative 727 TGCCAGGAGAA 737

10;

Matches

à g

TGTCAGGAGAA 13

AAA57799 standard; DNA; 14 BP.

RESULT 349

AAA57799

AAAS7799 ID AAAS XX AC AAAS

Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell;

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The present invention describes low adenosine (A) content antisense coligonucleotides and compositions (1) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (C. (I) can have respiratory, pronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.

C. immunosupressive, antiasthmatic, hypotensive and cytostatic activities.

C. immunosupressive, antiasthmatic, hypotensive and cytostatic activities.

C. immunosional controlled and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with a crimunosiobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, chemokines, endogenously produced specific and non-specific enzymes, chemokine receptors, adenosine receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central creceptors, binding proteins and molecules and non-nervous system peptide creceptors, binding proteins, agrewth factors, vasocative peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy (les) and/or constriction and and a disease or consistion and and a disease or consistion and and a disease or consistion and an antise of the minimum and an and a disease or consistion and an and a disease or consistion and and an antise and and an antise and and an antise and and an antise and and an an
                                                                                                                                                                                                                                                                                                                                         Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; Page 209; 1592pp; English.
24-MAR-2000; 2000WO-US008020.
                                                          99US-0127958P
                                                                                                                           (UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention
                                                                                                                                                                                                                                                                                         WPI; 2000-679539/66.
                                                          06-APR-1999;
                                                                                                                                                                                                                           Nyce JW;
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Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

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.
42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; ive 0; Mismatches 1; Indels
  Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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728 GCCAGGAGAAA 738

8

AAF19605 standard; DNA; 14 BP. 12 GCCAGGGGAAA 2 RESULT 347 AAF19605/c &&&&&&&&

Human IL6 receptor polynucleotide fragment #1172.

(first entry)

14-MAR-2001 AAF19605;

Low adenosine antisense oligonucleotide, phosphorothioate, allergy, human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive, antisethmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration;

surfactant hypoproduction, pulmonary vasoconstriction, asthma; RDS, respiratory distress syndrome; pain; oystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

WO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US008020.

06-APR-1999; 99US-0127958P.

(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Claim 14; Page 209; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the cytostesion and or activity of target polypeptides associated with lung/respiratory disorders and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, committers, anderson molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, brinding proteins adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system petities and peripheral nervous and non-nervous system cerptors, defensins, growth factors, vasocative peptides and circlestors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders conditions selected from pulmonary obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(iss) and/or surfact ant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergy (RDS), pain, cystic fibrosis (CF), allergic whinding respiratory disease (CDP), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or enacer. APF18434 to AAF21543 represent human polynucleotide fra present invention the present

Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Gaps . 0 Length 14; 1; Indels 42.7%; Score 9.4; DB 1; 90.9%; Pred. No. 4.2e+02; tive 0; Mismatches 1; Local Similarity 90.9 Query Match Best Loca Matches

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RESULT 348 **AAA**65226

ç., }

AAA65226 standard; DNA; 14 BP.

Mon Oct 18 14:40:07 2004

42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; ative 0; Mismatches 1; Indels Query Match Best Local Similarity 90.9 Matches 10; Conservative 728 GCCAGGAGAAA 738

Sequence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

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Gaps

. 0

12 GCCAGGGAAA 2 RESULT 345

AAF20192 standard; DNA; 14 BP. 14-MAR-2001 (first entry) AAF20192;

cancer; ss.

26-OCT-2000

Low adenosine (A) content antisense oligonucleotides which do not trigger Low adenosine antisense oligonuclectide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antihinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emplyeema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; Human endothelial monocyte activating factor DNA fragment #1759. 99US-0127958P. 24-MAR-2000; 2000WO-US008020 (UYEC-) UNIV BAST CAROLINA. (NYCE/) NYCE J W. WPI; 2000-679539/66. WO200062736-A2. Homo sapiens. 06-APR-1999; Nyce JW; AAF20192/C
ID AAF2011
XX
XX
XX
DE Human 14-MAR
XX
KW Low add
KW Surfac
KW respir.
KW respir.
KW respir.
KW cancer
XX
CANCOL
XX
HOMON
KW CANCOL
XX

The present invention describes low adenosine (A) content antisense oligonuclectides and compositions (I) comprising them. In the antisense cligonuclectides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiathmatic, hypotensive and cytostatic activities. The antisense oligonuclectides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with ung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoslobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, chemokines, endogenously produced specific and non-specific enzymes, chemokines endogenously produced specific and non-specific enzymes, chemokine receptors, adenosine receptors, brinding proteins, adenosine receptors, practice and non-nervous system (CNS) and peripheral nervous and non-nervous system petide actors and malignancy associated proteins. The creeptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, and/or lung inflammation, altergas syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary disease (CDD), when any transplantation respiration, respiratory disease (CDD), when any analyty and any promobilis, and any promobilis, and any promobilis, and any promobilis, and any promobilis. adenosine receptors during metabolism, useful e.g. for treating cancers and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other; Claim 14; Page 207; 1592pp; English respiratory obstructions. the present invention

Gaps . Match 42.7%; Score 9.4; DB 1; Length 14; Local Similarity 90.9%; Pred. No. 4.2e+02; les 10; Conservative 0; Mismatches 1; Indels Query Match Matches

· 0

731 AGGAGAAACAG 741 11 AGGAGGAACAG 1 à . q

MAF19619 standard; DNA; 14 BP. AAF19619; RESULT 346 AAF19619

Human IL6 receptor polynucleotide fragment #1186.

14-MAR-2001 (first entry)

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammation; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypotension; emplysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

Homo sapiens.

WO200062736-A2.

26-0CT-2000

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release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the uncleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1860 (AAA32323 to AAA33923) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             listing
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Seguence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

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Gaps
                        .
0
    42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; ive 0; Mismatches 1; Indels
728 GCCAGGAGAA 738
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AAA34070 standard; DNA; 14 BP RESULT 343

AAA34070;

Human adenosine receptor related polynucleotide SEQ ID NO:1759. 28-JUL-2000 (first entry)

Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergy; disease; bronchoconstriction; inhibitor; antinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain, cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000.

99WO-US017712 03-AUG-1999; 98US-0095212P, 03-AUG-1998;

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.

Disclosure; Page 483; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects affilict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, AAA34070/0/
XXX
XXX
AAA3.
AAAA3.
AAA3.
AAA3.
AAAA3.
AAAA3.
AAAA3.
AAAA3.
AAAA3.
AAAA3.
AAAA3.
AAAA3.
AAA

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impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the constructions side effects. The A-containing ONB break down with the relass of decoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the incledition sequences given in the sequence listening from the present in the sequences are also called SEQ ID No.11 to 2815, and then the last sequences are also called SEQ ID No.1 to 185, but the sequences differ from the previously named sequences. SEQ ID No.11 to 1680 (AAA32323 to AAA3392) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention. N.B. Sequences given in the disclosure of the present invention do not match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   listing
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Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;

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Gaps
                                    ö
42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; ive 0; Mismatches 1; Indels
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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Š 셤 RESULT 344 AAA33497/C

AAA33497 standard; DNA; 14 BP.

AAA33497;

28-JUL-2000 (first entry)

Low adenosine antisense oligonucleotide SEQ ID NO:1186.

Human, adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergy; allergy; allergy; antiantion; antiantiantializament.

antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cytic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000.

99WO-US017712. 03-AUG-1999;

03-AUG-1998;

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonuclectides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.

Claim 18; Page 413; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or

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Gaps

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well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer
                                                                                                                                                                                                                                                                                                       impaired respiration; inflammation; lung disease;
pulmonary vasconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
respiratory distress syndrome; pain; cystic fibrosis;
pulmonary hypertension; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; pancreatic cancer;
hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                 Antisense oligonucleotide; multiple target; antisense treatment;
                                                                                                                                                                                                                                                                        Endothelial moocyte activating factor antisense oligonucleotide
                                                           Score 9.4; DB 1; Length 14;
Pred. No. 4.2e+02;
0; Mismatches 1; Indels
                                        Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 47; 120pp; English.
                                                                                                                                                                                                 BP.
                                                             42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0059160P.
98US-00093972.
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                                                                                                                                                                                                AAX54623 standard; DNA; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                 05-JUL-1999 (first entry)
                                                                                       Conservative
                                                                                                              728 GCCAGGAGAAA 738
                                                                                                                                      4
well as all types of
                                                                                                                                    14 GCCAGGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                            prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-229400/19.
                                                                        Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vasoconstriction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9913886-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                        AAX54623;
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nyce JW
                                                                                     Matches
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The specification describes antisense oligonucleotides (AAX52869-X55271)
directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, gene initiation
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
end and the juxae-section between coding and non-coding regions and all
segments of RNAs encoding proteins associated with one or more diseases,
conditions or mixtures. The antisense oligonucleotides may be derived
from sequences AAX55272-74. These multiple target oligonucleotides
(specifically AAX55180-271) can be used for the antisense treatment of
diseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, respiratory
cutte asthma, allergies, asthma, impeded respiration, respiratory
distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
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The present invention describes a new composition comprising an antisense oligonuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiniflammatory, antialergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treament of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating effects afflict the lungs of a subject. They can be used for treating effects afflict the lungs of a subject. They can be used for treating impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphonas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONS reduces side effects. The A-containing ONS break down with the

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or

99WO-US017712. 98US-0095212P

03-AUG-1999; 03-AUG-1998;

24-FEB-2000.

WO200009525-A2

Homo sapiens.

(UYEC-) UNIV EAST CAROLINA

WPI; 2000-205971/18

Nyce JW;

Claim 18; Page 411; 1343pp; English

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               as
colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocoallular carcinoma, kidney cancer, melanoma, hepatic metastasses, a well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer
                                                                                                                                                                                                                                                                                                                  Human, adenosine receptor; low adenosine antisense oligonucleotide; phosphorothicate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain, cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                              Gaps
                                                                                                            ..
                                                                                     Length 14;
                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                              Low adenosine antisense oligonucleotide SEQ ID NO:1172.
                                                            Sequence 14 BP; 0 A; 5 C; 1 G; 8 T; 0 U; 0 Other;
                                                                                    Score 9.4; DB 1;
Pred. No. 4.2e+02;
                                                                                                            0; Mismatches
                                                                                                                                                                                                                      AAA33483 standard; DNA; 14 BP.
                                                                                    42.7%;
                                                                                                                                                                                                                                                                      (first entry)
                                                                                Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                  731 AGGAGAAACAG 741
                                                                                                                                                          11 AGGAGGAACAG 1
                                                                                                                                                                                                                                                                      28-JUL-2000
                                                                                                                                                                                                                                              AAA33483;
                                                                                                                                                                                               RESULT 342
                                                                                                                                                                                                            AAA33483,
 8838888
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Seguence 14 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

X S

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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
coding regions of RNAs corresponding to target genes, gene initiation
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
conditions or mixtures. The antisense oligonucleotides may be derived
from sequences AAX5572-74. These multiple target oligonucleotides
conditions or mixtures. The antisense oligonucleotides may be derived
from sequences AAX5572-74. These multiple target oligonucleotides
conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
alters syndrome, pain, cystic fibrosis, pulmonary hypertension,
disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
colon cancer, brast cancer, lung cancer, melanoma, hepatic metastasized
to the lungs, including breast and prostate cancer
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                                                                                                                                                                                                                                                                                                                                             Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmorary vasconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vascoonstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction.
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0
Score 9.4; DB 1; Length 14; Pred. No. 4.2e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                            Human IL-6 receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 50; 120pp; English.
                                                                                                                                                                                                      AAX54053 standard; DNA; 14 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0059160P.
98US-00093972.
42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                             (first entry)
   Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                           728 GCCAGGAGAA 738
                                                                                                    GCCAGGAGACA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-229400/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1997;
09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1998;
                                                                                                                                                                                                                                                                             05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9913886-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                             14
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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, coding and
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
end and the juxta-section between coding and non-coding regions and all
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
conditions or mixtures. The antisense oligonucleotides may be derived
conditions or mixtures. The antisense treatment of diseases and conditions are those
conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, respiratory
distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
cute asthma, allergies, asthma, impeded respiration, respiratory
distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
pulmonary vasoconstriction, emphysema, directive pulmonary
disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
colon cancer, breast cancer, lung cancer, melanoma, hepatic metastases, as
                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                       Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasconstriction; inflammation; altergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasconstriction; emphysema; chronic obstructive pulmonary vasconstriction; emphysema; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                         ;
0
42.7%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 4.2e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                      Human IL-6 receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 50; 120pp; English.
                                                                                                                                                                                                                                   AAX54039 standard; DNA; 14 BP.
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98US-00093972.
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                                                                                                                                                                                                                                                                                                                 (first entry)
                          Best Local Similarity 90.9
Matches 10; Conservative
                                                                                     728 GCCAGGAGAAA 738
                                                                                                                          12 GCCAGGGGAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-229400/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9913886-A1,
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                                                                                                                                                                                                                                                                                                                   05-JUL-1999
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                                                                                                                                                                                                                                                                            AAX54039;
        Query Match
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The present invention describes a recombinant adeno-associated virus (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, compression of polypeptide, or peptide selected from the group of rod opsin, iNOS.

RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha 1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha 1, integrin alpha 2, integrin alpha 1, integrin alpha 1, integrin alpha 2, integrin alpha 1, integrin and 1, integrin alpha 1, integrin and 1, integrin alpha 1, integrin and 1, integrin and 1, integrin alpha 1, integrin and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asthma; airway epithelium; adenosine free; cystic fibrosis;
chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 9.4; DB 1; Length 13;
Pred. No. 4.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13 BP; 1 A; 3 C; 2 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human IL6 receptor antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT76263 standard, DNA, 14 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 90.5
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 AGGAGAAACAG 741
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                                                                                                       A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human IIG receptor. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human li6 receptor. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchits and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asthma; airway epithelium; adenosine free; cystic fibrosis;
chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
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Example 5; Page 32; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          728 GCCAGGAGAA 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 338
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Gaps

Sequence 14 BP; 0 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 175624; 29pp + Sequence Listing; German.
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42.7%; Score 9.4; DB 1; Length 13;

Best Local Similarity 76.9%; Pred. No. 4.1e+02;

Matches 10; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13 BP, 9 A, 3 C, 0 G, 0 T, 0 U; 1 Other;
                                                                                                                                                                                     Berlin K;
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                                                                                                                                                                                     Olek A, Piepenbrock C,
                                                                                                                                                            (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                               WPI; 2001-657177/75
    central nervous
                                                       WO200177384-A2
                             Homo sapiens.
                                                                                 18-OCT-2001
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target; ophthalmological; gene therapy; eye; retinal dysfunction; AAV; diabetic retinopathy; macular degeneration; autosomal dominant retinitis; blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A recombinant adeno-associated virus-vectored ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rod opsin hammerhead ribozyme target oligonucleotide SEQ ID NO:59.
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                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                         Claim 1; SEQ ID NO 156507; 29pp + Sequence Listing; German
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Best Local Similarity 76.9%; Pred. No. 4.18+02;
Matches 10; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13 BP; 0 A; 1 C; 6 G; 5 T; 0 U; 1 Other;
Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 72; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ72819 standard; RNA; 13 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2002; 2002WO-US013679.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYFL ) UNIV FLORIDA.
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                                                                                                         designed to detect methylation status.
                                          WPI; 2001-657177/75
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Query Match

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Matches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82071 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences
                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                            Oligonucleotide SEQ ID NO 248814 for detecting SNP TSC0060796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin K;
                                                                      ABH48837 standard; DNA; 13 BP.
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                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AAACACAACAC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methylation status.
                                                                                                                                                                                                                                                                                                                                                                                               WO200177384-A2,
                                                                                                                                                                  22-FEB-2002
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                             RESULT 333
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                                                   ABH48837
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                                                                                                          Score 9.4; DB 1; Length 13;
Pred. No. 4.1e+02;
0; Mismatches 1; Indels
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                                                                 Sequence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                             42.7%;
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                                                                                                                                     Local Similarity 90.9
nes 10; Conservative
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18-OCT-2001

ABF50801;

RESULT 332

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; Oligonucleotide SEQ ID NO 175624 for detecting SNP TSC0043631.

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Query Match

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                 Claim 1; SEQ ID NO 82745; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
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                                                                                           Berlin K;
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06-APR-2001; 2001WO-IB000713
                             07-APR-2000; 2000DE-01019173
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Best Local Similarity 90.9'
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                                                                                         Piepenbrock C,
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                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC099889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invantion. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at fitted specification, but fit.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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             Claim 1; SEQ ID NO 130256; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                 42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                           Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABH19619 standard; DNA; 13 BP.
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Best Local Similarity 90.9
Matches 10; Conservative
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2 AAACAAAACAC 12
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form mat for the printed specification, but the wipo int/pub/published_pct_sequences
                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                Oligonucleotide SEQ ID NO 50439 for detecting SNP TSC0014176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; Live 0; Mismatches 1; Indels
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                                                                                                               ABC50422 standard; DNA; 13 BP.
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ID ABCS6820 standard; DNA; 13 BP.
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                 Piepenbrock C,
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 GAGAAACAGAACA
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                     Homo sapiens,
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733
                                                                                                                                               ABC50422;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                Oligonucleotide SEQ ID NO 56837 for detecting SNP TSC0015389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; ative 0; Mismatches 1; Indels
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG
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                                                                                                                       Homo sapiens
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21-FEB-2002 (first entry)

ABC56820;

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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                               Claim 1; SEQ ID NO 250884; 29pp + Sequence Listing; German.
WPI; 2001-657177/75
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Gaps ; 42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; tive 0; Mismatches 1; Indels Sequence 13 BP; 7 A; 4 C; 1 G; 1 T; 0 U; 0 Other; 10; Conservative Query Match Best Local Similarity

736 AAACAGAACAC 746

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ABC71283 standard; DNA; 13 21-FEB-2002 ABC71283 RESULT 325

BP

Oligonucleotide SEQ ID NO 71300 for detecting SNP TSC0018470. (first entry)

SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 71300; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF92073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                       Sequence 13 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 1 Other;
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ö Gaps . 0 Score 9.4; DB 1; Length 13; Pred. No. 4.1e+02; 1; Mismatches 2; Indels 42.7%; 76.9%; Ouery Match
Best Local Similarity 76...
Local 10; Conservative

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ABC72903 standard; DNA; 13 RESULT 32 ABC72903

BP.

(first entry) 21-FEB-2002 Oligonucleotide SEQ ID NO 72920 for detecting SNP TSC0018823.

SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2

18-0CT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 72920; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99389, ABC0010-ABC99389, ABC0010-ABC99389, ABC0010-ABC99389, ABC0010-AB

Sequence 13 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 1 Other;

Gaps ö Query Match
42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels

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06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2

18-OCT-2001.

(EPIG-) EPIGENOMICS AG

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine
                                                           Oligonucleotide SEQ ID NO 156383 for detecting SNP TSC0039445.
                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 156383; 29pp + Sequence Listing; German.
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                                                                                                                                                                               06-APR-2001; 2001WO-IB000713.
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                                        (first entry)
                                                                                                                                                                                                                                         Piepenbrock C,
                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                         designed to detect a
 ABF56386 standard;
                                                                                                                                         WO200177384-A2
                                        21-FEB-2002
                                                                                                                      Homo sapiens
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                     ABF56386
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cointral nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 tapesent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from wIPO at . 0 Sequence 13 BP; 10 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Gaps ; 0 42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; tive 0; Mismatches 1; Indels Best Local Similarity 90.8 Matches 10, Conservative Query Match

GAGAAAAAGAA 12 a RESULT 323 ABF87396/ 원

733 GAGAAACAGAA 743

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide SEQ ID NO 187393 for detecting SNP TSC0046193. BP. ABF87396 standard; DNA; 13 22-FEB-2002 (first entry) ABF87396;

Homo sapiens

Berlin K; 06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173 (EPIG-) EPIGENOMICS AG 18-OCT-2001 Olek A,

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABI82073 targressent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but thouson int/pub/published_pct_sequences ·. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, a designed to detect single-nucleotide polymorphisms and cytosine . 0 Claim 1; SEQ ID NO 187393; 29pp + Sequence Listing; German. 42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.16+02; ative 0; Mismatches 1; Indels Sequence 13 BP; 2 A; 1 C; 4 G; 6 T; 0 U; 0 Other Ä, Berlin Local Similarity 90.9 es 10; Conservative 736 AAACAGAACAC 746 Piepenbrock C, 11 AAACCGAACAC 1 WPI; 2001-657177/75 methylation status. Query Match Olek A, Matches g

Oligonucleotide SEQ ID NO 250884 for detecting SNP TSC0061240. ABH50907 standard; DNA; 13 BP. 22-FEB-2002 (first entry) ABH50907;

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2. Homo sapiens

Piepenbrock C,

Sequence 13 BP; 0 A; 0 C; 5 G; 8 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999 and ABI00010-ABF92073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.7%; Score 9.4; DB 1; Length 13; 76.9%; Pred. No. 4.1e+02; ive 1; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABE99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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Score 9.4; DB 1; Length 13; Pred. No. 4.1e+02;
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Best Local Similarity 90.9
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Query Match
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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             This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 targresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE82073 data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine

Berlin

Piepenbrock C,

olek A,

WPI; 2001-657177/75

methylation status.

(EPIG-) EPIGENOMICS AG.

Claim 1; SEQ ID NO 72288; 29pp + Sequence Listing; German

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Gaps

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Score 9.4; DB 1; Length 13; Pred. No. 4.1e+02; 0; Mismatches 1; Indels

Sequence 13 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 1 Other;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                 Oligonucleotide SEQ ID NO 72919 for detecting SNP TSC0018823.
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                                                                             ABC72902 standard; DNA; 13 BP.
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736 AAACAGAACAC 746
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Claim 1; SEQ ID NO 72919; 29pp + Sequence Listing; German.

BP

(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                  ABH14816 standard; DNA; 13
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABC0010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formmat from WIPO at this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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claim 1; SEQ ID NO 214793; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 BP; 1 A; 1 C; 5 G; 6 T; 0 U; 0 Other;
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Best Local Similarity 90.9
Matches 10; Conservative
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Gaps

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731 AGGAGAAACAG 741

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABH54888 standard; DNA; 13 BP
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 capeseen the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
      designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                               Claim 1; SEQ ID NO 254865; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                          Sequence 13 BP; 0 A; 1 C; 4 G; 8 T; 0 U; 0 Other;
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      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00101800018 ABC0010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                              ligonucleotides, useful for diagnosis and cell typing, to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 187394; 29pp + Sequence Listing; German.
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                                                                                                                                                                 Berlin K;
                                       06-APR-2001; 2001WO-IB000713.
                                                                            07-APR-2000; 2000DE-01019173
                                                                                                                                                                                                                                              of oligonucleotides,
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                                                                                                                      (EPIG-) EPIGENOMICS AG
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18-OCT-2001.
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42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; Live 0; Mismatches 1; Indels

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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073
                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                             Oligonucleotide SEQ ID NO 27538 for detecting SNP TSC0007662.
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(first entry)
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20-FEB-2002
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Set of oligonuclectides, useful for diagnosis and cell typing, i designed to detect single-nuclectide polymorphisms and cytosine methylation status.
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                                                       Oligonucleotide SEQ ID NO 219595 for detecting SNP TSC0053410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 219595; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 4.1e+02;
0; Mismatches 1; Indels
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90.98;
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  Best Local Similarity 90.5
Matches 10; Conservative
                                                                735 GAAACAGAACA 745
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Best Local Simil
Matches 10; C
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ABH19618/C
ID ABH196
XX
AC ABH196
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Gaps

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WO200177384-A2

Homo sapiens

)618/c ABH19618 standard; DNA; 13 BP.

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ABH19618;

Gaps

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Score 9.4; DB 1; Length 13; Pred. No. 4.1e+02; 1; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The colonners are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire printed specification, but ftp.wipo.int/pub/published_pcr_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
      oligonucleotides are used for diagnosis and/or prognosis of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide SEQ ID NO 67314 for detecting SNP TSC0017613.
                                                                                                                                                                                                             Sequence 13 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 1 Other;
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                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                    typing, i
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                                                                                                                                                                 Claim 1; SEQ ID NO 180898; 29pp + Sequence Listing; German.
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                                                                                 of oligonucleotides, useful for diagnosis and cell igned to detect single-nucleotide polymorphisms and
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Berlin K;
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Piepenbrock C,
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Olek A,
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence and fate for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 67314; 29pp + Sequence Listing; German.
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Berlin K;

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42.7%; Score 9.4; DB 1; Length 13;

Berlin K;

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06-APR-2001; 2001WO-IB000713.
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                                                                                                                                                                             Oligonucleotide SEQ ID NO 66060 for detecting SNP TSC0017378.
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                                                  ABC66043 standard; DNA; 13 BP.
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                                                                                                                                                                                                        Claim 1; SEQ ID NO 130258; 29pp + Sequence Listing; German.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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   SEQ ID NO 57798; 29pp + Sequence Listing; German.
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99899 and ABI00010-ABI82073 the present the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                                                                    Score 9.4; DB 1; Length 13;
Pred. No. 4.1e+02;
1; Mismatches 2; Indels
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                                         Sequence 13 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 1 Other;
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76.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                               SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 166265 for detecting SNP TSC0041660.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 166265; 29pp + Sequence Listing; German.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABC0010-ABE9989, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at this published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 4.1e+02;
0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                         42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.18+02; Ative 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                    Oligonucleotide SEQ ID NO 166156 for detecting SNP TSC0041649.
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735 GAAACAGAACACC
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Query Match 42.7%; Score 9.4; DB 1; Length 13; Best Local Similarity 76.9%; Pred. No. 4.1e+02; Matches 10; Conservative 1; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC009989, ABC0010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                   Claim 1; SEQ ID NO 125404; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                      42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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     Length 13;
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 Score 9.4; DB 1; Length 13
Pred. No. 4.1e+02;
1; Mismatches 2; Indels
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   42.78;
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                                    10; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF32073 tepseson the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                   Oligonucleotide SEQ ID NO 83644 for detecting SNP TSC0021064.
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                  ABC83627;
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RESULT 294 ABC83627 ID ABC83627 standard; DNA; 13 BP.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, certical nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF00010-ABH99989 and ABI00010-ABI82073 febresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; Live 0; Mismatches 1; Indels 0; Gaps
                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                          Berlin K;
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                                        Olek A, Piepenbrock C,
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and extensine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABE09989, ABF00010-ABE09989, ABF00010-ABE9989, ABF00010-ABE9989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methylation status.
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                                                                           Homo sapiens
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                                                                                                                                                                                                                             Oligonucleotide SEQ ID NO 10572 for detecting SNP TSC0002662
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42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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                                                                                     ABC10581 standard; DNA; 13 BP
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                    Claim 1; SEQ ID NO 196833; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABR00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNE) and cytosine meethylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. . 0 Oligonucleotide SEQ ID NO 180897 for detecting SNP TSC0044758. Claim 1; SEQ ID NO 180897; 29pp + Sequence Listing; German. 42.7%; Score 9.4; DB 1; Length 13; 76.9%; Pred. No. 4.1e+02; tive 1; Mismatches 2; Indels Claim 1; SEQ ID NO 124392; 29pp + Sequence Listing; German Sequence 13 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 1 Other; Berlin K; BP. 06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173. ABF80900 standard; DNA; 13 733 GAGAAACAGAACA 745 (first entry) RAAAAACATAACA 13 10; Conservative Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG Query Match Best Local Similarity WPI; 2001-657177/75 methylation status. WO200177384-A2. Homo sapiens 22-FEB-2002 18-OCT-2001 ABF80900;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC0010-ABC99989, ABR0010-ABF99899, ABH0010-ABF99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at from MIPO at
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                       42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; cive 0; Mismatches 1; Indels
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                                                                        Sequence 13 BP; 1 A; 1 C; 3 G; 7 T; 0 U; 1 Other;
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Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 90.9'
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(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
              Oligonucleotide SEQ ID NO 77843 for detecting SNP TSC0019825.
                                                                                                        06-APR-2001; 2001WO-IB000713.
                                                                                                                       07-APR-2000; 2000DE-01019173,
                                                                                                                                     (EPIG-) EPIGENOMICS AG
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                                                            Homo sapiens
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Berlin K;

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The coligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010 ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF99989, ABF00010-ABF99999, ABF00010-ABF999999, ABF00010-ABF99999, ABF00010-ABF999999, ABF00010-ABF999999, ABF00010-ABF99999, ABF00

Sequence 13 BP; 0 A; 1 C; 4 G; 8 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide bolymorphisms (SNP)

Claim 1; SEQ ID NO 124373; 29pp + Sequence Listing; German.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

36-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for dececting cell type differentiation. ABC00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                          Claim 1; SEQ ID NO 77843; 29pp + Sequence Listing; German.
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42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; ive 0; Mismatches 1; Indels
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine

WO200177384-A2

18-OCT-2001

Homo sapiens

Gaps

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Indels

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Mismatches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC099389, ABC0010-ABE99989, ABC0010-ABE99899 and ABI00010-ABE3073 and act for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09988, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nuclectide polymorphisms and cytosine
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76.9%;
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                                                                                                                                                                                                                                                  10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    designed to detect methylation status.
                                                                                                                                                                                                          Query Match
Best Local Similarity
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42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02;

Query Match Best Local Similarity

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, axidovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABF99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                Oligonucleotide SEQ ID NO 50440 for detecting SNP TSC0014176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 50440; 29pp + Sequence Listing; German.
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                                                                                                                  BP.
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                                                                                                                   ABC50423 standard; DNA; 13
                                                                                                                                                                                    (first entry)
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Best Local Similarity 90.9
Matches 10; Conservative
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735 GAAACAGAACA 745
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                     GAAACACAACA 2
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ABC77826/c
                                                                                   RESULT 282
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Homo sapiens

WPI; 2001-657177/75.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABH99889 and ABI00010-ABH82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fup.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                    of oligonucleotides, useful for diagnosis and cell typing, igned to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 215089; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                   Berlin K;
                                                                                                          06-APR-2001; 2001WO-IB000713.
                                                                                                                                          07-APR-2000; 2000DE-01019173
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42.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
Sequence 13 BP; 0 A; 0 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                              736 AAACAGAACAC 746
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m AAACACAACAC 13 d

BP.

Oligonucleotide SEQ ID NO 166154 for detecting SNP TSC0041649. ABF66157 standard; DNA; 13 22-FEB-2002 (first entry) ABF66157; RESULT 279 ABP66157

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DD D11;

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PR 06
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PR 07
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YX XX CEP

YX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. sapiens Homo

WO200177384-A2.

18-OCT-2001

36-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine

WPI; 2001-657177/75.

methylation status

Claim 1; SEQ ID NO 166266; 29pp + Sequence Listing; German.

Olek A, Piepenbrock C,

Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                            Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                            Claim 1; SEQ ID NO 166154; 29pp + Sequence Listing; German.
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Matches 10, Conservative
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(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                          Oligonucleotide SEQ ID NO 156384 for detecting SNP TSC0039445.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2001; 2001WO-IB000713.
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                    ABF56387 standard; DNA; 13
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                                                                      ABF56387;
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ABH15112/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                      Score 9.4; DB 1; Length 13; Pred. No. 4.1e+02; 1; Mismatches 2; Indels
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                            Sequence 13 BP; 6 A; 4 C; 1 G; 1 T; 0 U; 1 Other;
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                                                                      Best_Local Similarity 76.9%;
Matches 10; Conservative 1
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AC ABE756
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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735 GAAACAGAACACC 747

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RESULT 277

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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07-APR-2000; 2000DE-01019173,
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                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                              3 AGGAGAAAGAG 13
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                 (EPIG-) EPIGENOMICS AG
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                                                    WPI; 2001-657177/75
                                                                              designed to detect methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tapeses the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13 BP; 8 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
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Best Local Similarity 90.9
Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABF9989, ABR00010-ABF9989, ABR00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 11971; 29pp + Sequence Listing; German.
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Gaps

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Score 9.4; DB 1; Length 13; Pred. No. 4.1e+02; 0; Mismatches 1; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC99989, ABF00010 -ABF99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide SEQ ID NO 174446 for detecting SNP TSC0043390.
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RESULT 27
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ID ABF7
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ABF7
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Claim 1; SEQ ID NO 124374; 29pp + Sequence Listing; German.

Berlin K;

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                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; se; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SMP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCO0010
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-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the Oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the print pub/published_pct_sequences
                                                                                                                                                                  Sequence 13 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 1 Other;
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                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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cytosine
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designed to detect single-nucleotide polymorphisms and methylation status.
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Score 9.4; DB 1; Length 13; Pred. No. 4.1e+02; 0; Mismatches 1; Indels

42.7%; 90.9%;

BP.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                          Oligonucleotide SEQ ID NO 51785 for detecting SNP TSC0014434.
                                                                                                                                                                                                     06-APR-2001; 2001WO-IB000713.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                         ABC72270 standard; DNA; 13
                                                                                                                                                                                        (first entry)
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Berlin K;

Piepenbrock C,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                             Claim 1; SEQ ID NO 51785; 29pp + Sequence Listing; German.
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                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nuclectide polymorphisms and cytosine
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                                                           Oligonucleotide SEQ ID NO 37765 for detecting SNP TSC0011740.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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06-APR-2001; 2001WO-IB000713.
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo int/pub/published_pct_sequences
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 Score 9.4; DB 1; Length 13;
Pred. No. 4.1e+02;
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Berlin K;

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                           Claim 1; SEQ ID NO 37766; 29pp + Sequence Listing; German.
            Olek A, Piepenbrock C,
                                       WPI; 2001-657177/75.
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 central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                  methylation status.
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ABC37749
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 76.9
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RESULT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNB; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                   ch 42.7%; Score 9.4; DB 1; Length 13; 1 Similarity 90.9%; Pred. No. 4.1e+02; 10; Conservative 0; Mismatches 1; Indels
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                                                 Sequence 13 BP; 0 A; 1 C; 4 G; 8 T; 0 U; 0 Other;
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invantion. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                              Oligonucleotide SEQ ID NO 196834 for detecting SNP TSC0048453.
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                   ABF96837 standard; DNA; 13
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989 ABH00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                      Claim 1; SEQ ID NO 77844; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 73176; 29pp + Sequence Listing; German.
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Best Local S:
Matches 10
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens,

Oligonucleotide SEQ ID NO 248813 for detecting SNP TSC0060796.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 tepsesmt the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                   Oligonucleotide SEQ ID NO 215090 for detecting SNP TSC0052336
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                                                                                                                 ABH15113 standard; DNA; 13
735 GAAACAGAACACC 747
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Best Local Similarity 90.9
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
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ABH48836 standard; DNA; 13 BP

736 AAACAGAACAC 746

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.22-FEB-2002 (first entry)

ABH48836;

RESULT 255
ABH48836/c
ID ABH48
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AC ABH48
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Berlin K;
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                                                                                                10; Conservative
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WPI; 2001-657177/75.
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                                                                                                                                          This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                  Set of oligonuclectides, useful for diagnosis and cell typing, i designed to detect single-nuclectide polymorphisms and cytosine methylation status.
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                                                                                                                German.
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                                                                                                            Claim 1; SEQ ID NO 174290; 29pp + Sequence Listing;
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at this pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 76.9%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 2; Indels
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Best Local Similarity 90.9
Matches 10; Conservative
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ABC83624 standard; DNA;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                          Oligonucleotide SEQ ID NO 83641 for detecting SNP TSC0021064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide SEQ ID NO 10571 for detecting SNP TSC0002662,
                                                                                                                                                                                                                                         Berlin K;
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ses 10; Conserv
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                                                                                                                     Homo sapiens,
                                       21-FEB-2002
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pot_sequences

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine

Berlin

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

methylation status.

06-APR-2001; 2001WO-IB000713.

WO200177384-A2

18-OCT-2001,

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Claim 1; SEQ ID NO 10571; 29pp + Sequence Listing; German.

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Gaps

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Sequence 13 BP; 9 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

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Score 9.4; DB 1; Length 13;
Pred. No. 4.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                     ABF74293 standard; DNA; 13 BP.
 42.78;
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 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                        733 GAGAAACAGAA 743
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                Oligonucleotide SEQ ID NO 174290 for detecting SNP TSC0043357.
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42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; tive 0; Mismatches 1; Indels

Local Similarity 90.9 les 10; Conservative 736 AAACAGAACAC 746

Matches

Query Match

Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABI82073 tepses the oligomers described in the invention, NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                          Oligonucleotide SEQ ID NO 254866 for detecting SNP TSC0062123.
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Best Local Similarity 90.9%; Pred. No. 4.18+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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                                                                                        ABH54889 standard; DNA; 13 BP.
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13 AAACAAAACAC 3
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RESULT 249 ABC83624/c

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Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
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Matches 10; Conservative
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                                                                                              Piepenbrock C,
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diseases and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABF09989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF99989, represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WFPO at
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                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide SEQ ID NO 82746 for detecting SNP TSC0020863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 27537; 29pp + Sequence Listing; German.
```

Gaps

60

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

WPI; 2001-657177/75.

Claim 1; SEQ ID NO 125403; 29pp + Sequence Listing; German.

```
This invention describes a novel method for identifying major histocompatibility complex (MHC)-restricted antigens. A gene or CDNA bank is constructed from the cells or organism under test, then incorporated into a retroviral genome or, as additional RNA, into a modified influenzation to a retroviral genome or, as additional RNA, into a modified influenzative to the wild type, so as to produce viral particles (VP). The case to infect immortalized autologous cells that expression the gene bank inserts are expressed and their cleavage products exposed the gene bank inserts are expressed and their cleavage products exposed to the cells that express antigens cells are co-cultured with T cells which are stimulated if the autologus cells express a T cell-restricted antigen. Contens that express antigens are isolated and the antigens sequenced. The probable use in antitumor vaccines, but may also identify autoantigens or microbial antigens. The method does not require knowledge of the content of the invention cells in the method does not require knowledge of the content of the invention cells in the subject cells in antigens. The level expression of the invention of the invention cells in the content of the invented gene, providing high contents and contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying major histocompatibility complex-restricted antigens, useful potentially in antitumor vaccines, by forming DNA bank in virus and testing for I cell stimulation.
                                                    Major histocompatibility complex restricted antigen; antitumor vaccine; MHC-restricted antigen; T cell-restricted antigen; antigen identification; promoter; ss.
                    Wildtype influenza virus C promoter-UP variant 1104 RNA fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide SEQ ID NO 27537 for detecting SNP TSC0007662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.7%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 4.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13 BP; 1 A; 5 C; 1 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                      (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
(ARTE-) ARTEMIS PHARM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nimmerjahn F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sensitivity and simple detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 5; 10pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                        99DE-01062508,
                                                                                                                                                                                                                                                                                                                                                  99DE-01045171.
99DE-01051543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 244
ABC27520/c
ID ABC27520 standard; DNA; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mautner J, Bornkamm GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 731 AGGAGAAACAG 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 AGTAGAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-246290/26.
                                                                                                                                                              Influenza virus
                                                                                                                                                                                                             DE19962508-A1
                                                                                                                                                                                                                                                                                                     23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                     21-SEP-1999;
26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2002
                                                                                                                                                                                                                                                        29-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABC27520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a bridged oligonucleotide derivative. The invention relates to C-5 thiol-substituted nucleoside derivatives which can be incorporated into an RNA or DNA strand during synthesis of oligonucleotides. These compounds can be in the form of cross-linked linear, cross-linked hairpin or bridged circular oligonucleotides. The oligonucleotides may be used for detection and isolation of target mucleic acids, or for targeting drugs to specific cell types (e.g. treatment of Alzheimer's disease, beta-thalassemia, osteogenesis treatment of Alzheimer's disease, beta-thalassemia, infections). The presence of the nucleoside derivatives in a linear oligonucleotide allows the formation of covalent crosslinks between non-complementary DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New C-5 thiol-substituted nucleoside derivatives - whose presence in oligo:nucleotide(s) allows formation of covalent cross-links between non-complementary DNA domains.
                                                                                               /*tag= a //ote= "Thiol-substituted nucleoside derivative, 5-(3-thiopropyn-1-y1)-2'-deoxyurine, optionally disulphide bonded to the nucleoside derivative at position 5 of another strand of the same sequence"
                                                                                                                                                                                                                                      /*tag= b //note= "Thiol-substituted nucleoside derivative, 5-(3-fnote= "Thiol-substituted nucleoside derivative at position 6 of another strand of the same sequence"
                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
//note= "Thiol-substituted nucleoside derivative, 5-(3-
thiopropyn-1-y1)-2'-deoxyurine, optionally disulphide
bonded to the nucleoside derivative at position 7 of
another stand of the same sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.7%; Score 9.4; DB 1; Length 13; Best Local Similarity 83.3%; Pred. No. 4.1e+02; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; Page 101; 122pp; English.
                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF61477/C
ID AAF61477 standard; RNA; 13 BE
XX
AC AAF61477;
XX
DT 18-JUN-2001 (first entw.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0004778P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGAANAGAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-245044/22.
                                                                                                                                                                                                                                                                                                                                                               modified_base
                                                                        modified base
                                                                                                                                                                                                                  modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9714708-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-1995;
       Synthetic.
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Kool ET;

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Gaps

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domains

RESULT 243

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17

/*tag= a
/note= "thiopropynyldeoxyuridine or unmodified thymidine"

Location/Qualifiers

Key misc_difference

Synthetic.

(RESE) RESEARCH CORP TECHNOLOGIES INC.

Kool ET;

96WO-US004525.

29-MAR-1996;

24-APR-1997.

04-OCT-1995;

WO9714708-A1

Oligonucleotide containing a thiol-substituted nucleoside derivative.

(first entry)

02-JUN-1998

Thiol-substituted oligonucleotide; covalent cross-link; disulphide; circular; bridged; hairpin; detection; ss.

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Cell based toxin characterization method for e.g. in drug discovery paradigm, involves treating cells possessing luminescent reporter molecules with fluorescence based molecules reagents to detect presence
                                                                                                                                                                                           Example 10; SEQ ID NO 73; 98pp; English.
                                  98US-00031271.
99US-0122152P.
99US-0123399P.
                                                      99US-00352171.
99US-0151797P.
99US-00398965.
99US-00430656.
                                                                                   99US-0168408P.
              19-MAR-2002; 2002US-00100957
                            97US-00810983
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 90.9
Matches 10, Conservative
                                                                                                        (CELL-) CELLOMICS INC.
                                                                                                                      Giuliano K, Kapur R;
                                                                                                                                    WPI; 2003-786988/74.
P-PSDB; ADC18386.
                                                                                          25-FEB-2000;
                                                       12-JUL-1999;
31-AUG-1999;
                                                                      17-SEP-1999;
                                                                            29-OCT-1999
22-MAY-2003
                                                 08-MAR-1999
                                                                                                                                                                              of toxins
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Best Loc
Matches
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The invention relates to characterising cell based toxins, where the cell possessing luminescent reporter molecules (biosensors) are provided on a microchip, and are treated with fluorescence based molecular reagents. The cells are photographed with fluorescence optics, and the optical information is converted into digital data. The presence of the toxin in care reagent, is detected using the digital data, based on changes in the closalisation, distribution structure of identifier, detector and closalisation, distribution structure of identifier, detector and closalisation storing a cell based toxin characterisation program, and a kit for cell based toxin detection. The method is used for characterising or detecting a biological cell based toxin that affect particular biological cell based toxin that affect particular biological discovery paradigm. It is also used in automated DNA sequencing, pCR application, positional cloning, hybridisation arrays for new drug discovery paradigm. It is also used in automated DNA sequencing, pCR application, positional cloning, hybridisation marys and bioinformatics cusing cell based scanning and screening system. The method improves the target validation and candidate optimisation by combining many cell craspet with fluorescence based molecular reagents, thereby cresulting in increased quantity and speed of data collection, shortened cycle times and faster evaluation of promising drug candidates. The method also provides increased throughput while decreasing the volumes of cycle times and faster evaluation of promising drug candidates. The cathering it to microtubules) or detectable signal (epitope or affinity tettering it to microtubules) or detectable signal (epitope or affinity tettering it to microtubules) or detectable signal (epitope or affinity compartment). The present sequence encodes a protease recognition site (e.g. for a caspase protein) and a target domain (localising the biosensor to a particular compartment) and a protease recognition or processed a protease re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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AAV06771 standard; DNA; 13 BP.

RESULT 241
AAV06771/c
ID AAV067
XX
AC AAV067

AAV06771;

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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an oligonucleotide containing a thiol-substituted nucleoside derivative or an unmodified oligonucleotide. The invention relates to a C-5 thiol-substituted nucleoside derivatives which can be incorporated into an RNA or DNA strand during synthesis of oligonucleotides. These compounds can be in the form of cross-linked linear, cross-linked hairpin or bridged circular oligonucleotides. The oligonucleotides may be used for detection and isolation of target nucleic acids, or for targeting drugs to specific cell types (e.g. for treatment of Allzheimer's disease, beta-thalassemia, osteogenesis imperfecta, archritis, sickle cell anaemia or viral infections). The presence of the nucleoside derivatives in a linear oligonucleotide allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                New C-5 thiol-substituted nucleoside derivatives - whose presence in oligo:nucleotide(s) allows formation of covalent cross-links between non-complementary DNA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thiol-substituted oligonucleotide; covalent cross-link; disulphide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 formation of covalent crosslinks between non-complementary DNA
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.7%; Score 9.4; DB 1; Length 13; 83.3%; Pred. No. 4.1e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        circular; bridged; hairpin; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bridged oligonucleotide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 82; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV06762 standard; DNA; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GAAGAAANAGAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-245044/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV06762;
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UXAXEXEXEX
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Modified influenza virus A 3' conserved region SEQ ID NO:6.
                                                                                                                                                                                                                         Sequence 12 BP; 1 A; 4 C; 1 G; 0 T; 6 U; 0 Other;
                                            Claim 10; Page 50; 172pp; English.
                                                                                                                                                                                                                                                                                                   ABQ75464 standard; RNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2002; 2002WO-EP001257.
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                              the present invention
                                                                                                                                                                                                                                                           731 AGGAGAAACAG 741
                                                                                                                                                                                                                                                                      12 AGTAGAAACAG 2
    WPI; 2002-657594/70.
                                 infectious disease.
                                                                                                                                                                                                                                                                                                                                                                      Influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                       WO200264757-A2
                                                                                                                                                                                                                                                                                                                         07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                              ABQ75464;
                                                                                                                                                                                                                                                                                        RESULT 239
ABQ75464/0
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The present invention describes a human influenza virus (I) comprising an CC RNA-sequence encoding a modified RNA-polymerase that differs from the wild-type RNA-polymerase of the human influenza virus in that at least 1 of the human influenza virus influenza virus at least 1 of the human influenza virus from FPV Bratislava RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of 1) has viruside, cytostatic, anti-HIV, bepartoropic, antiinflammatory and immunomodulator activities and can be used in gene therapy and vaccines. The influenza virus is useful for cy preparing agents for: (a) gene transfer into cells, preferably into mammalian cells, particularly into human cells, by viral infection; (b) conduct for ex vivo immunotherapy; in vivo somatic gene therapy and vaccination, including therapeutic and prophylactic vaccination; (c) vaccination, including therapeutic and prophylactic vaccination; (d) treating a growing the induction of a T-cell cresponse; (d) treating a growing the induction of a T-cell cresponse; (d) treating a growing the induction of a T-cell cresponse; (d) treating a growing the induction of a T-cell cresponse; (d) treating a growing the induction of a real content of a chronic infected by such viruses; preferably the RNA molecules into cells infected by such viruses; or collening, preferably by antisense RNA or RNA interference mechanisms condecules, and/or the agent is suitable for sequence-specific gene can be at indozyme classage and content sequence repension of transfer and expression of transfer expense. The present sequence represents a modified viruses or papilloma viruses. The present sequence represents a modified coff the present invention influence in vaccines against HVA, hepatitis B or C virus, herpes viruses or papilloma viruses. The present sequence represents invention and viruse or papilloma viruses. The present sequence are mediation.
                                                                                                                                                                                                                                              New human influenza virus comprising an RNA-sequence encoding a modified RNA-polymerase, useful for preparing agents for therapeutic and prophylactic vaccination, or treating a growing tumor or a chronic infectious disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.7%; Score 9.4; DB 1; Length 12; 90.9%; Pred. No. 4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 16; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC18385 standard; DNA; 12 BP
09-FEB-2001; 2001EP-00103060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                  (ARTE-) ARTEMIS PHARM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
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                                                                                                                                                                                             WPI; 2002-657594/70.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                 Menke A;
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                                                                                                                                     Hobom G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 240
ADC18385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                    The present invention describes a human influenza virus (I) comprising an RNA-sequence encoding a modified RNA-polymerase that differs from the vild-type RNA-polymerase of the human influenza virus in that at least 1 of the amino acid residues distinguishing the wild-type RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of the particular activities and can be consed in gene therapy and vaccines. The influenza virus is useful for preparing agents for: (a) gene transfer into ells, preferably into mammalian cells, particularly into human cells, by viral infection; (b) gene transfer into antigen-presenting cells, and the use of the obtained product for a vivo immunotherapy; in vivo somatic gene therapy in vivo vaccination, including theresenting cells, and the use of the obtained product for a vivo immunotherapy; in vivo somatic gene therapy; (c) transfer and expression of RNA molecules infected by such viruses; or and expression of RNA molecules into cells infected by such viruses; or (g) transfer and expression of RNA molecules into cells infected by such viruses; or sequences or double-strand sequences relative to the target cellular mRNA molecules, and/or the agent is suitable for sequence-specific gene solutions, preferably by antisense RNA or RNA interference mechanisms contains a ribozyme clavages of target RNAs. The recombinant viruses can be made for use in vaccines against HIV, hepatitis B or C virus, herpes contains and viruses. The present sequence represents a modified contains in the expresents a modified contains in the expresents and expresents and influenza virus, given in the expresents
                                                                                              New human influenza virus comprising an RNA-sequence encoding a modified RNA-polymerase, useful for preparing agents for therapeutic and prophylactic vaccination, or treating a growing tumor or a chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza virus, transcription, replication; RNA polymerase; vaccine; gene therapy, cytostatic; anti-HIV, hepatotropic; antiinflammatory; immunomodulator; virucide; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Gaps

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US2003096322-A1 Unidentified.

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The invention relates to a method for the expression of tumour associated antigens (TAA) or virus-associated antigens (VAA) by dendritic cells comprising; preparing a recombinant influence virus containing a nucleotide sequence coding for the TAA or VAA, and infecting dendritic cells with the recombinant virus. The method is used for expressing TAA or VAA in dendritic cells. The cells are used for preparing a medicament for treating tumours or viral infections. A vaccine can be created by using dendritic cells presenting tumour antigens to induce an immune response. This polynucleotide sequence represents a preferred 3 conserved RNA influenca virus region of the invention
                                                                                                                                                                                                                       Expressing tumor or viral associated antigens by dendritic cells, used for treating tumors or viral infections, comprises using recombinant influenza virus containing nucleic acid encoding the antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection; classification; identification; toxin detection; protease; ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
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0
                                                                                                                                                                 Grassmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.7%; Score 9.4; DB 1; Length 12; 90.9%; Pred. No. 4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding protease biosensor recognition site #11.
                                                                                                                                                                Strobel I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 BP; 1 A; 4 C; 1 G; 0 T; 6 U; 0 Other;
                                                                                                                                                              Steinkasserer A,
                                                                                                                                                                                                                                                                                  Claim 7; Page 19; 33pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00810983.
98US-01031271.
99US-0123122P.
99US-0123399.
99US-00352171.
99US-00398965.
99US-004306965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS71505 standard; DNA; 12 BP.
                                                                       30-OCT-2000; 2000EP-00123687.
                                                                                                     30-OCT-2000; 2000EP-00123687.
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                                                                                                                                  (ARTE-) ARTEMIS PHARM GMBH
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Matches 10; Conservative
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                                                                                                                                                              Hobom G,
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                                                                                                                                                                                         WPI; 2002-418777/45.
            EP1201760-A1
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17-SEP-1999;
29-OCT-1999;
                                          02-MAY-2002.
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08-MAR-1999;
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                                                                                                                                                              Schuler G,
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Gaps

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The invention describes methods of automated detection, classification and identification comprising treating cells containing luminescent responsive molecules (I) in array of locations with a test substance, where (I) are detectors, classifiers or identifiers, imaging cells in each location to obtain luminescent signals and converting optical information into odigital data to interpret presence of toxins in the test substance. The method are useful for detection of toxins in the test substance. The method are useful for detection of toxins chosen from proteases, ADP-ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins. Three classes of cell-based luminescent reporter molecules such as reporters of toxic threat agents. The first two levels of characterisation ensure a rapid readout of toxins class without secreticing the ability to detect many new mutant toxins or dissect several complex mixtures of known toxins. This sequence encodes a protease biosensor recognition site used in the cell-based screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza virus, transcription, replication, RNA polymerase, vaccine, gene therapy, cytostatic, anti-HIV, hepatotropic, antiinflammatory, immunomodulator, virucide, infectious disease, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                              or
                                                                                                                                                               Automated cell-based toxin detection, classification, and/or identification by treating cells involves use of three classes luminescent reporter molecules such as detectors, classifiers o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified influenza virus A 3' conserved region SEQ ID NO:5.
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Pred. No. 4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                    Example 10; Fig 29B; 214pp; English.
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01-DEC-1999; 99US-0168408P.
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                               Giuliano K, Kapur R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 732 GGAGAAACAGA
                                                                                                               WPI; 2002-634730/68.
P-PSDB; ABG94458.
                            (GIUL/) GIULIANO K.
(KAPU/) KAPUR R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza virus.
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                                                                                                                                                                                                                       identifiers
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ABQ75463/
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(ARTE-) ARTEMIS PHARM GMBH.

Menke A;

Hobom G,

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The invention relates to a method for the expression of tumour associated antigens (TAA) or virus-associated antigens (VAA) by dendritic cells comprising: preparing a recombinant influenza virus containing a nucleotide sequence coding for the TAA or VAA; and infecting dendritic cells with the recombinant virus. The method is used for expressing TAA or VAA in dendritic cells. The cells are used for preparing a medicament for treating tumours or viral infections. A vaccine can be created by using dendritic cells presenting tumour antigens to induce an immune response. This polynucleotide sequence represents a preferred 3'-terminal RNA region of an influenza virus mutant G3C, USC, C8G of the invention
                                                                                                                   /*tag= b
/note= "The wild-type nucleotide U has been replaced with
C"
                                                                   a
"The wild-type nucleotide G has been replaced with
                                                                                                                                                                                                     /*tag= c
/noce= "The wild-type nucleotide C has been replaced with
G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressing tumor or viral associated antigens by dendritic cells, used for treating tumors or viral infections, comprises using recombinant influenza virus containing nucleic acid encoding the antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic, antiviral, tumour associated antigen, TAA, dendritic cell, virus-associated antigen, VAA, recombinant influenza virus, vaccine, viral infection, immune, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Steinkasserer A, Strobel I, Grassmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.7%; Score 9.4; DB 1; Length 12; 90.9%; Pred. No. 4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preferred 3' conserved RNA influenza virus region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 6; 33pp; English.
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                                                                                                                                                                                                                                                                                                                                                                              30-OCT-2000; 2000EP-00123687.
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                                                                                                                                                                                                                                                                                                                                                                                                               (ARTE-) ARTEMIS PHARM GMBH.
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                    note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schuler G, Hobom G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-418777/45.
Influenza virus.
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                                  Key
mutation
                                                                                                                     mutation
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, artdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH0010-ABH99999 and ABI00010-ABI22073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell; virus-associated antigen; VAA; recombinant influenza virus; vaccine; viral infection; immune; mutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                       Oligonucleotide primer SEQ ID NO 351860 for detecting SNP TSC0047526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, :
designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 351860; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.7%; Score 9.4; DB 1; Length 12; 90.9%; Pred. No. 4e+02; ive 0; Mismatches 1; Indels

    terminal RNA influenza virus mutant G3C, U5C, C8G.

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                                                                                                                                                                                                                                                                                                                                                                                                                                       쏬
                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin
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                                                                                                                                                                                                                                                                                                                                                                   07-APR-2000; 2000DE-01019173.
                     ABI51887 standard; DNA; 12
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                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Local 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-657177/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           designed to detect methylation status.
                                                                                                                                                                                                                                                              WO200177384-A2
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                                                                                                                                                                                                                               Homo sapiens
                                                                                      22-FEB-2002
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RESULT 234 ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).

and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99889 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 323286 for detecting SNP TSC0031304. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. .. 0 Claim 1; SEQ ID NO 323286; 29pp + Sequence Listing; German. Score 9.4; DB 1; Length 12; Pred. No. 4e+02; 0; Mismatches 1; Indels Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other; Berlin K; 42.7%; 06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173 ABI23313 standard; DNA; 12 (first entry) Query Match Best Local Similarity 90.9 Matches 10; Conservative 737 AACAGAACACC 747 1 AACATAACACC 11 Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WO200177384-A2. Homo sapiens. 22-FEB-2002 18-OCT-2001 ABI23313 olek A,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pot_sequences
                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                      Claim 1; SEQ ID NO 313539; 29pp + Sequence Listing; German.
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07-APR-2000; 2000DE-01019173
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             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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42.7%; Score 9.4; DB 1; Length 12; 90.9%; Pred. No. 40+02; Live 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, artdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 tepseson the oligomers described in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                              Oligonucleotide primer SEQ ID NO 299593 for detecting SNP TSC0018645.
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                                                                                                           22-FEB-2002
                                                                                                                                                                                                                                                              Homo sapiens
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                                                                        ABH99600;
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RESULT 228
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                     ABH9960
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ABH75111 standard; DNA; 12 BP.

RESULT 229 ABH75111 ABH75111;

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Gaps

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42.7%; Score 9.4; DB 1; Length 12; ilarity 90.9%; Pred. No. 4e+02; Conservative 0; Mismatches 1; Indels

Query Match Best Local Similarity Matches 10; Conserv

1 AGGAGAAAGAG 11

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736 AAACAGAACAC 746

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                             Berlin K;
                                                       06-APR-2001; 2001WO-IB000713
                                                                                              07-APR-2000; 2000DE-01019173
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                                                                                                                                    (EPIG-) EPIGENOMICS AG
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                   18-OCT-2001
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 328511; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disponsis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
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                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 368871 for detecting SNP TSC0057287.
                                    Gaps
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Query Match
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                     ABI68898 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                     (first entry)
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                                                                                                  1 GGAGAAAAAGA 11
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Berlin

Olek A, Piepenbrock C,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS AG

07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713

WO200177384-A2 Homo sapiens

18-OCT-2001

Oligonucleotide primer SEQ ID NO 328511 for detecting SNP TSC0034363.

(first entry)

22-FEB-2002

AB128538;

ABI28538 standard; DNA; 12 BP.

RESULT 225 ABI28538 ID ABI2853

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 324195 for detecting SNP TSC0031857.
                                                                                   Gaps
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       Score 9.4; DB 1; Length 12; Pred. No. 4e+02;
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                                                                           1; Indels
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                                    4e+02;
                                                                           0; Mismatches
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42.7%;
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                                                                    10; Conservative
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                                       Local Similarity
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Best Local Similarity
Matches 10; Conserv
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       Query Match
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but the obtained in electronic format from WIPO at
                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                Oligonucleotide primer SEQ ID NO 303092 for detecting SNP TSC0020318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 277756 for detecting SNP TSC0004835.
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                                  (first entry)
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Best Local Similarity 90.9°
Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                WO200177384-A2.
                                 22-FEB-2002
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 ABI03119;
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WO200177384-A2.

Homo sapiens

ABI03119 standard; DNA; 12 BP.

RESULT 223 ABIO3119 ID ABIC XX

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733 GAGAAACAGAA 743 GAGAAAAAGAA 12

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ABI66282 standard; DNA; 12 BP.
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   Piepenbrock C,
                                                                                                                                 11 AAACCGAACAC 1
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Best Local Similarity
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           WPI; 2001-657177/75
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                                                                                                                   Matches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form are from WIPO at
and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardicovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 309289; 29pp + Sequence Listing; German.
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                           olek A,
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Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic
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06-APR-2001; 2001WO-IB000713.
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                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, azdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fur wipo.int/pub/published_pct_sequences
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                 Claim 1; SEQ ID NO 363398; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosie; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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06-APR-2001; 2001WO-IB000713.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                Oligonucleotide primer SEQ ID NO 309520 for detecting SNP TSC0023558.
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                                                                                                                                                                                                                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                           Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-657177/75.
                                                                                                                                                                                                                                                                                                                                                                                                             designed to detect methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ABH70673 standard; DNA; 12

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             oligomers are also used for detecting cell type differentiation. ABC00010 ABC99889, ABF0010-ABF99889, ABF00010-ABF99889 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the obtained in electronic format from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovaecular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 294114 for detecting SNP TSC0015962.
     cardiovascular and metabolic disorders. The
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     nervous system,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a cange of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                               Oligonucleotide primer SEQ ID NO 270650 for detecting SNP TSC0002216.
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                                                                                                                                                                                                                                                                                                                                                                                     Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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               ABH70673;
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42.7%; Score 9.4; DB 1; Length 12; 90.9%; Pred. No. 4e+02; 1; Indels rative 0; Mismatches 1; Indels

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Query Match Best Local Similarity Matches 10; Conserv

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABC0010-ABE99999, ABM0010-ABH99999 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 297817 for detecting SNP TSC0017786.
                                                                                                                                                                                                                                    ligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 288468; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 42.7%; Score 9.4; DB 1; Length 12; Local Similarity 90.9%; Pred. No. 4e+02; les 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
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ID ABH97824 standard; DNA; 12 BP.
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                                                                           06-APR-2001; 2001WO-IB000713
                                                                                                            07-APR-2000; 2000DE-01019173
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                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                       WPI; 2001-657177/75
                                                                                                                                                                                                                                                          designed to detect amethylation status.
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             WO200177384-A2
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 300956 for detecting SNP TSC0019274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                               Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                          Claim 1; SEQ ID NO 297817; 29pp + Sequence Listing; German
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hes 10; Conservative
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WPI; 2001-657177/75
                                                         designed to detect methylation status.
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Berlin K;

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(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                         Oligonuclectide primer SEQ ID NO 275374 for detecting SNP TSC0003875.
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        ABH75383 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene for hypocretin (orexin) receptor 2 (HCRTR2) which is associated with narcolepsy, useful in methods of diagnosis of narcolepsy and pharmaceutical compositions for therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HCRTR2) splice acceptor site SEQ ID NO:36.
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; narcolepsy; hypocretin receptor 2; orexin receptor 2; HCRTR2;
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                                                Score 9.4; DB 1; Length 12;
Pred. No. 4e+02;
0; Mismatches 1; Indels
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Pred. No. 4e+02;
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  G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                 BP.
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  Sequence 12 BP; 5 A; 1 C; 6
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                                                                      Local Similarity
                                                                                                                                                 731 AGGAGAAACAG 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; PCR
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                     Claim 1; SEQ ID NO 275374; 29pp + Sequence Listing;
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     Berlin K;
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  Piepenbrock C,
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Gaps

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Local Similarity 90.9

727 TGCCAGGAGAA 737

TGCCAGGAAAA 11

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RESULT 206 ABH75383

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the fluorescent protein to be directed to a different cellular comparation to be directed to a different cellular comparation after cleavage of the protein cellular change in distribution of the fluorescent protein can be detected using imaging methods with a high degree of spatial resolution. The methods and biosensors of the invention can be used to investigate a wide range of cellular activities and to screen compounds which modulate these activities. Biosensors containing a recognition site for caspase, for example, may be used for the screening of compounds which modulate apoptosis, while biosensors containing of their protease recognition site apoptosis, while biosensors containing of compounds which modulate and be detection of proteolytic toxins (such as anthrax length of the detection of proteolytic toxins (such as anthrax candidate compound optimisation by combining many cell screening formats with fluorescence-based molecular reagents and computer-based feature in the compound optimisation and computer-based feature.
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                                                                                                                                                                                                                                                 extraction, data analysis and automation, resulting in increased quantity and speed of data collection and faster evaluation of drug cardidates. Sequences AAA93177-A93411 and AA93340 represent protease recognition sites (AAB22886-B22220, AAB22988) which may used as components of biosensor fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Score 9.4; DB 1; Length 12; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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99US-0136078P.
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Best Local Similarity 90.9%;
Matches 10; Conservative
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The present sequence is that of DNA encoding the substrate recognition sequence (see AAY79598) of caspase-8. The DNA is used in a claimed recombinant nucleic acid encoding a protease biosensor. The nucleic acid (see AA277627-43) comprises: (1) a sequence (see AAA27568-76) encoding at least 1 detectable signal polypeptide; (2) a sequence (see AAA275-611)

Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences.

WPI; 2000-365644/31. P-PSDB; AAY79598. Claim 6; Fig 29B; 218pp; English.

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that encodes at least 1 protease recognition site, such as the present sequence; and (3) a sequence (see AAA27611-26) that encodes at least 1 reactant target sequence. An expression vector, a genetically engineered host cell and a recombinant protease biosensor are also claimed. A claimed method for identifying compounds that modify protease activity in a cell involves contacting a host cell that possesses the recombinant. CC protease biosensor with a test compound, and determining the protease consons with a test compound, and determining the protease consons of alstribution in the host cell, where changes in the correlation of the protease biosensor are correlated with modification of distribution of the protease activity by the test compound. Claimed kits for identifying compounds that modify protease activity in a host cell include the recombinant nucleic acid, or the recombinant protease biosensor, or the content screens to detect in vivo activation of enzymatic activity, and cotific activity based on cleavage of a known recognition contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a method for amplifying a DNA fragment. The method comprises successive repetitions of heat-denaturing, annealing of a primer and an extending step using a DNA polymerase. The method makes uses of a cDNA pool in which the primer is one primer or a pair of primer sets and has an amplification probability which allows it to amplify a DNA fragment from a limited number of the cDNAs among the DNA pool (where the limited number of the cDNAs among the DNA pool (where the limited number is in the range of 1 to 25). Also included in the invention are apparatus used for carrying out the method, a primer and a DNA polymerase and a kit used for carrying out the method, a primer and a be used to amplify a limited number of cDNAs from a pool in which a wide variety of cDNAs are present. Oligonucleotides AAC37775 - AAC97990 represent primers used in an example illustrating the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to illustrate DNA amplification method SEQ ID 162.
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amplification of a DNA fragment and its apparatus.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 12 BP; 6 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAOL ) SANYO ELECTRIC CO LTD.
(NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer, amplification; selective; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 11; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC97936 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 732 GGAGAAACAGA 742
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1 GTAGAAACAGA 11
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Matches
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Gaps

Score 9.4; DB 1; Length 12; Pred. No. 4e+02; 0; Mismatches 1; Indels

Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative

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Sequence 12 BP; 5 A; 1 C; 6 G; 0 T; 0 U; 0 Other;

organic waste

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The specification describes a method for the determination of the nucleotide sequence of a polynucleotide. The method comprises providing a set of primers in which each primer has an extension region containing a terminal nucleotide, a template arranging segment and at least one complexity-decreasing nucleotide, forming a template containing primer-combining sites and the polynucleotide in which the primer-combining an amplicon from the template by amplifying a double-stranded DNA formed selectively by extending the primer from the set in which the extending region forms a double-strand completely matched to primer-combining sites of the terminal nucleotide of the extending region of the primer by an identification of the amplicon, shifting the region of the primer by an identification of the amplicon, shifting the primer-combining sites of the terminal mucleotide of extending the primer-combining sites of the template, and repeating this until the nucleotide sequence of the polynucleotide is determined. The method can be used for DNA sequencing. The present sequence represents a primer contains an expension by a primer combining sites of the polynucleotide is determined. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microbe detection in organic waste arbitrarily primed PCR primer #162
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amplification of a DNA fragment - in order to establish the state of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbe, detection, organic waste, arbitrarily primer PCR, random amplified polymorphic DNA, amplification, PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                               Score 9.4; DB 1; Length 12;
Pred. No. 4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 1 A; 5 C; 2 G; 0 T; 4 U; 0 Other;
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(NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
                                                                                                                                                                                                                                                                                                                                primer used to demonstrate the invention
                  Disclosure; Page 26; 32pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ41585 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                    42.7%;
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Best Local Similarity 90.99,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      728 GCCAGGAGAA 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       existence of a microbe.
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AAZ41585
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The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biological functions. The methods of the invention of all last to didetector molecules which, when acted on by a compound of interest, cause an alteration in the cellular distribution of at least the fluorescent moiety. In one embodiment, the biosensors comprise heat shock proteins (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent protein (GFP), or derivatives thereof). Such biosensors are located in the cytoplasm, but on stress activation translocate to the nucleus In another embodiment biodetector proteins can be used to detect protease critical activation signal, which is cleaved by the protease; and at least one cellular localisation signal. The latter two components may be components of a single protein which is acted upon by the protease, or may be from heterologous sources. Due to the localisation signal, the biodetector protein is localised to a particular fluorescent protein is cleaved from the localisation sequence, and is fluorescent protein is cleaved from the localisation sequence, and is free to migrate to other locations within the cell. The presence of a
                                                                                                                                                                                                  Biodetector protein, fusion protein, recognition site;
cellular targetting sequence; cellular localisation; fluorescent protein,
protease activity detection; toxin detection; cellular stress detection;
drug discovery; cell based screening; protease recognition site;
                                                                                                                                                               DNA encoding caspase-8 substrate recognition sequence, SEQ ID NO:73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; Fig 29B; 336pp; English.
                                     AAA93387 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0122152F.
99US-0123399P.
99US-00352171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2000; 2000WO-US004794
                                                                                                                    10-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giuliano KA, Kapur R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CELL-) CELLOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-594086/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing optically.
                                                                                                                                                                                                                                                                                      cleavage site; ds.
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12-JUL-1999;
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                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                            AAA93387;
RESULT 202
                   AAA93387
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A method has been developed for the amplification of a DNA fragment in which amplification is carried out on the DNA fragments of a number of different DNAs. The method comprises a PCR reaction repeatedly carrying out a heat-denaturing step, a primer annealing step and a polymerase extending step, to amplify the DNA fragments of a plural of different DNAs. The method can detect the existence of a microbe in organic waste. AAZ41424 to AAZ41639 represent PCR primers used in random amplified polymorphic DNA arbitrarily primed PCR, for the detection of microbes in

Example; Page 9; 40pp; Japanese.

RESULT 198

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This invention describes a novel method for the amplification of DNA comprising (i) preparing many primers (P) with different probabilities of amplification and (ii) simultaneous polymerase chain reaction (PCR) of different DNA using these primers. The method is used (i) to differentiate between different microorganisms in a mixed population and (ii) to determine presence/absence of an impurity (pollutant), or its concentration, in e.g. soil, foods, compost etc., typically metals, agricultural chemicals, polymers, organochlorine compounds etc. A particular use is monitoring composting of organic material.

Amplification with many primers produces a lot of information, so reliability of the test is improved, and many samples may be tested quickly. AAZ1640-Z41855 represent the primers described in the method of the invention. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extension of DNA using rolling primer - useful as DNA sequencing method
                                                                                                                                                                                                                                                                                                Novel polymerase chain reaction method, for differentiating between microorganisms and for detecting contaminants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extension region; terminal nucleotide; template arranging segment; complexity decreasing nucleotide; DNA sequencing; primer; ss.
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Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Released tag used in a novel method of DNA sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12 BP; 5 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
                                                                                                                                                          (SAOL ) SANYO ELECTRIC CO LTD.
(NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
                                                                                                                                                                                                                                                                                                                                                                  78pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LYNX-) LYNX THERAPEUTICS INC.
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99JP-00069694
                                                       99DE-01014461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1999 (first entry)
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                                                                                                                                                                                                                                                               WPI; 1999-592157/51.
                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 21;
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                                                       30-MAR-1999;
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16-MAR-1999;
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                 21-OCT-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is homologous to that upstream of the interleukin-2 gene, in the enhancer region. DNA sequence analysis of the promoter/ enhancer regions of several genes that respond to T-cell activation signals has identified putative NF-AT protein binding sites. The oligonucleotide, and ones homologous to it, may be used in methods for screening immunosuppressive agents. See also AAQ37029-35. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunomodulatory agents screening compsn. for immunosuppressant tests -comprises isolated transcription factor binding nucleic acid sequence of 20 base pairs and polypeptide activating NF AT dependent transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amplification; polymerase chain reaction; PCR; microorganism; compost; detection; pollutant; soil; food; agricultural chemical; polymer; organochlorine; primer; ss.
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                                                                                                                                                                                                                         NF-AT transcription factor; immunomodulatory agent; screening; immunosuppressive; interleukin 2 enhancer; promoter; ss.
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42.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                  WF-AT complex binding oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 50; 72pp; English
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                                         AAQ37032 standard; DNA; 12 BP.
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(first entry)
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(first entry)
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21-JAN-2000
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01-JUL-1993
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RESULT 199 AAZ41801

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Score 9.4; DB 1; Length 11; Pred. No. 3.9e+02; 0; Mismatches 1; Indels

Sequence 11 BP; 1 A; 2 C; 2 G; 6 T; 0 U; 0 Other;

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42.7%;

Query Match
Best Local Similarity 90.9
Matches 10; Conservative

734 AGAAACAGAAC 744

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11 AGAAACAGATC 1

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ö The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from synession. (A) comprises protein or mRNAs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmettic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ87680) of the invention The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (GAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin discorders, specifically neurodermatitis; sunburn; psoriacis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the (ESI) of the invention In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer. Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss. Gaps . 0 42.7%; Score 9.4; DB 1; Length 11; 90.9%; Pred. No. 3.9e+02; Live 0; Mismatches 1; Indels Sequence 11 BP; 1 A; 2 C; 2 G; 6 T; 0 U; 0 Other; Disclosure; Page 154; 1345pp; German. Hofmann BP 20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127 ABV66898 standard; cDNA; 11 (first entry) Petersohn D, Conradt M, 10; Conservative 734 AGAAACAGAAC 744 11 AGAAACAGATC 1 Human skin EST 4684 (HENK) HENKEL KGAA WPI; 2002-590638/63 Local Similarity WO200253774-A2. Homo sapiens. 21-OCT-2002 11-JUL-2002 Query Match ABV66898; Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of an antisense oligonucleotide which can be used an antisense sequence of a herpesvirus site, pref. in a gene that is essential for synthesising nucleic acids e.g. the immediate early genes or Wmw65. It can be prepd by solid phase triester or phosphor-amdite chemistry or by recombinant DNA techniques. It can be used for treating infection by herpesviruses, e.g. herpes simplex type I (HSV-1) and type (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus (CNV), human herpesvirus growth or replication may indirectly forestail the progression of events from HIV exposure to the clinical manifestation of AIDS: It may also be useful in the detection, diagnosis and manipulation of herpes virus. See also AAQ23764-Q22788 and AAQ24014- (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New anti:sense oligo:nucleotide(s) for inhibiting HSV - also used for diagnosis and for inhibiting HIV activation by herpes virus.
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                                                                                                                                                                              HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster; Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.
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                                                                                                                                             Herpesvirus inhibiting antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 BP; 0 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                            (UYMA-) UNIV MARYLAND BALTIMORE. (UYJO ) UNIV JOHNS HOPKINS.
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                               AAQ24029 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                              90US-00586185
                                                                                              (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                               18-SEP-1991;
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                                                                                              25-MAR-2003
21-SEP-1992
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                                                                                                                                                                                                                               Synthetic.
                                                              AAQ24029;
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RESULT 19
AAQ24029/
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oligonuclectides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonuclectides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for traplication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The pathogen which is not found in the genome of pathogen's host. The suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triplendelices with such sequences in cancervus cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mycobacterium tuberculosis complex; precursor rRNA; rDNA; 5S rRNA; ss; mycobacterium other than tuberculosis; 235-mediated macrolide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; 23S rRNA; 16SrRNA; tuberculosis; MTC; MOTT; peptide nucleic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mod_base= OTHER
/note= "G is covalently linked to Lys(Rho) where Rho=
Rhodamine, optional"
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                                                                                                                                                                                                                                                                                                    Score 9.8; DB 1; Length 15;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                     Seguence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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/note= "C is amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                       methods of the present invention
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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MOLLERUP T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium avium.
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ABX76569/c
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The invention relates to a peptide nucleic acid capable of hybridising to a target sequence of Mycobacterial rDNA, precursor rRNA or rRNA (5S, 16S or 23S) forming detectable hybrids. Also included are detecting a target sequence of mycobacteria in a sample comprising contacting at arget sequence of mycobacteria in a sample comprising contacting at rarget or the probability of probes (hybridisation takes place between the probe and the rRNA or rDNA, observation or measurement to formed detectable hybrids are rDNA, observation or measurement to the presence of a target sequence of mycobacteria in the sample, and a kit for detecting a target sequence of mycobacteria in particular a target sequence of mycobacteria in particular a target sequence of mycobacteria in particular a target sequence of mycobacteria of MTC (and distinguishing them from mycobacterium other than tuberculosis. MOTT) present in a sample, e.g. sputum, laryngeal swabs, gastric lavage, bronchial washings, biopsies, aspirates, expectorates, body fluids, curne, tissue sections as well as food samples, soil, air and water samples and their cultures. The probe is able to penetrate the cell wall of the mycobacteria. It is able to hybridise to Mycobacterial precursor rRNA and rRNA without harsh treatment of the mycobacterial precursor therefore avoiding a risk of interfering with the morphology of the cells. The present sequence is an N. avium mutated probe for 235 RNA around positions 2568-2569, associated with 235-mediated macrolide
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screening for cosmetic or therapeutic agents, based on differential gene
Mycobacteria in samples, e.g., sputum, which are capable of hybridizing to a target sequence of mycobacterial rDNA, precursor rRNA or rRNA forming detectable hybrids.
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                                                                                         Claim 22; Page 40; 74pp; English.
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Matches
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Claim 8; Page 87; 325pp; German.

Claim 14; Page 14; 84pp; English

activity of CYP7A1, and the binding affinity of candidate drugs targeting dry7A1 for the treatment of disorders such as cholesterol and bile disorders. Haplotyping methods are useful in validating CYP7A1 as a candidate target for treating a specific condition or disease predicted to be associated with CYP7A1 activity, or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with CYP7A1 activity, such as cirrhosis, familial hypertally veridated activity, such as cirrhosis, familial hypertally veridated activity, such as cirrhosis, familial hypertally veridated and hypercholesterolaemia. Transgenic animals are also useful for studying expression of the CYP7A1 isogenes in vivo, for in vivo screening and testing of drugs targeted against CYP7A1 protein, and for testing the efficacy of therapeutic agents and compounds related to cholesterol and bile acid metabolism. The present sequence represents and compared condition to an allele-specific oligomorelectide (ASO) probe, used in the invention to

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The invention relates to a novel polymorphic variant of a sequence of CYPA1 protein or its fragment. The polymorphic has hepatotropic and antilipaemic activity. The polymorphic variants are useful in studying the expression and function of CYPA1, in expressing CYPA1 protein for use in screening candidate drugs to treat diseases related to CYPA1 activity, in studying the effect of the variation on the biological
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ABW991137/c
ID ABW991137/c
XX ABW991137/c
XX ABW99117
XX ABW99117
XX Human,
XW Human,
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\overset{\mathsf{M}}{\mathsf{X}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset{\mathsf{M}}{\mathsf{Q}}\overset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The invention relates to an isolated polynuclectide comprising genes and haplotypes of the Chemokine binding protein 2 (CCBP2) gene. Polymorphic variants of the CCBP2 gene are useful in studying the expression and function of CCBP2, and in expressing CCBP2 proteins for use in screening candidate drugs for treating diseases associated with CCBP2 activity. Polynucleotides comprising a polymorphic gene variant or fragment may be used for therapeutic purposes, where a particular CCBP2 protein isoform, expression or increased expression of a particular CCBP2 protein isoform, or an expression vector encoding the isoform may be administered to the patient. Haplotype information is useful in improving the efficiency and output of several steps in drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. The polynucleotides of the invention can be used to treat disorders related to the CCBP2 gene by gene therapy. This . 0 Human, CYP7A1; hepatctropic, antilipaemic; cholesterol disorder; cirrhosis; bile disorder; hypertriglyceridaemia; hypercholesterolaemia; cytochrome P450, subfamily VIIA, polypeptide 1; probe; ss. New cytochrome P450 subfamily VIIA (cholesterol 7 alphamonooxygenase) polypeptide 1 gene variants, useful for studying the expression and activity of CYP7Al and screening drugs for treating disorders of cholesterol and bile metabolism. Gaps ; 44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 3.8e+02; 2; Indels Human CYP7A1 allele-specific oligonucleotide probe #7. the invention Sequence 15 BP; 6 A; 2 C; 5 G; 1 T; 0 U; 1 Other; Stephens JC; 0; Mismatches CCBP2 gene polymorphisms relating to Nandabalan K, BP. (GENA-) GENAISSANCE PHARM INC. 31-JAN-2001; 2001WO-US003164. 31-JAN-2001; 2001WO-US003164 ABV99157 standard; DNA; 15 727 TGCCAGGAGAAC 739 (first entry) 1 TGGAAGGAGAAAC 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; cancer; concogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA troontrol gene expression.
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                 Query Match
44.5%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 3.8e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triple helix forming associated oligonucleotide #30.
                                                                                                                                                                                                                                        Sequence 15 BP; 1 A; 3 C; 2 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 4B; 108pp; English.
                                                                                                                                                                                                           detect CYP7Al gene polymorphisms
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                                                                                                                                                                                                                                                                                                                                   731 AGGAGAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                         14 AAGACAAACAGAA 2
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ABK98147/c
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Macejack D;

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The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV tribozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or replication of hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon. The present sequence represents a substrate for a HCV hammerhead (HH) inbozyme. Note: Some of the sequence data for this patent did not form part of the princed specification. The complete sequence data for this patent was constant of the at the constant of the unit of the constant of the unit of the at the constant of the unit of the at the constant of the unit of the at the constant of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemokine binding protein 2; CCBP2; CCBP2 protein isoform; gene therapy; polymorphic gene variant; single nucleotide polymorphism; human; primer; PCR; ss.
                                                                             New ribozymes targeting RNA derived from hepatitis C virus inhibit vireplication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New genetic variants having polymorphisms in the chemokine binding protein 2 (CCBP2) gene, useful for studying CCBP2 functions, and for treating disorders affected by expression or function of the CCBP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 3.8e+02; ative 0; Mismatches 2; Indels
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Pavco PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seqdata.uspto.gov/psipsDIDEntry.html
Roberts B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   щ
                                                                                                                                                             Claim 1; Page 40; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000; 2000US-0239638P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             732 GGAGAACAGAAC 744
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Best Local Similarity 84.6
Matches 11, Conservative
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  Mcswiggen JA,
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                                        WPI; 2002-617759/66
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    Blatt L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection; HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide; liver failure; hepatocellular carcinoma; HCV infection; drug therapy; type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon; hepatotropic; antiinflammatory; substrate; hammerhead ribozyme; HH ribozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               purified human nucleic acid (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus substrate #654 for HCV hammerhead ribozyme #654.
                                                                                                                                                                                                                                                                                                                            New human nucleic acid containing specific SAGE tags, useful as diagnostic markers for cancer, also derived probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 3.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 BP; 1 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                               Zhou W;
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated,
                                                                                                                                                                                                                                               Zhang L,
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 53; 161pp; English.
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                                                                                                                                                               98US-00081646.
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                                                                                                                                                                                                                                               Vogelstein B, Kinzler KW,
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                                                                                                                                                                                                      SNINGO UNIV (OLYU)
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                                                                                                                                                                                                                                                                                      WPI; 2002-153821/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 11; Conserv
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    Homo sapiens
                                        US6333152-B1
                                                                                                                        20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33-MAR-1999;
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                                                                                 25-DEC-2001
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Gaps

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/mod_base= OTHER //mod_base= OTHER //mode= "This sequence is a peptide nucleic acid i.e it /motes = N-acetyl (2-aminoethyl) glycine backbone instead of a deoxyribose-phosphate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                              Killing or inhibiting growth of bacteria using peptide nucleic acid complementary to a region of the bacterial ribosomal RNA is useful treat a bacterial infection in a mammal and as a disinfectant.
         Bacterial growth inhibitor; bacterial infection; disinfectant; PNA; antibacterial; peptide nucleic acid; ribosomal RNA; ss.
                                                                                                                                                                                  /*tag= b
/mod_base= OTHER
/note= "N-acetyl (2-aminoethyl)-C-lysine- glycine
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                     97US-00932140.
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                                                                                                                                                                                                                           backbone"
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/*tag=
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Best Local Similarity
                                               Escherichia coli
                                                                                      Key
modified base
                                                                                                                                                                         modified base
                                                                                                                                                                                                                                                                                                     16-SEP-1997;
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                                                            Synthetic.
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ABK32359/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein, gene and cDNA sequences of human P650 (dytochrome) oxidoreductase POR, and single nucleotide polymorphisms (SNPs) identified therein. The sequences can be used to haplotype the POR gene of an individual, and to establish whether POR is a sultable target for drugs to treat cancer and disorders associated with impaired protein synthesis in cells. The present sequence is an allele specific primer for the coding sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genetic variants comprising haplotypes of the P450 (cytochrome) oxidoreductase (POR) isogene, useful in improving the efficiency of drug screening protocols for compounds targeting POR.
                                                                                                                                                                                                                                                   Human, P450(cytochrome) oxidoreductase, POR, cancer, haplotype, SNP, single nucleotide polymorphism; flavoprotein, enzyme; PCR, primer; ss
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                           Human P450(cytochrome) oxidoreductase allele specific PCR primer #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duplex forming PNA #1 targetted to Escherichia coli ribosomal RNA.
                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
      Score 9.8; DB 1; Length 15;
Pred. No. 3.8e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 3.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 BP; 1 A; 3 C; 5 G; 5 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Messer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 14; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Lanz EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                    (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2001; 2001WO-US030877.
          44.5%;
                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-2000; 2000US-0236449P
                                                            727 TGCCAGGAGAACAG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD24257 standard; DNA; 15
                                                                                                                                                  ABN80567 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   728 GCCAGGAGAAACA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-2002 (first entry)
          Query Match
Best Local Similarity 73.3
Matches 11; Conservative
                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCTGCAGAACA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            Kliem SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-394236/42.
                                                                                                                                                                                                                                                                                                                  WO200226768-A2.
                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                  19-JUL-2002
                                                                                                                                                                                                                                                                                                                                          04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kazemi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD24257;
                                                                                                                                                                          ABN80567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 188
AAD24257/C
ID AAD242:
XX
AC AAD242:
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DT 07-MAR
XX
DE DUD1ex
                                                                                                                         RESULT 187
ABN80567/c
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                                                          The patent discloses methods and compositions for killing or inhibiting growth of bacteria comprising contacting the bacteria with a peptide nucleic acid (PNA) complementary to a region of the bacterial ribosomal RNA. The method is used to treat a bacterial infection in a mammal and as a disinfectant. The present sequence is a duplex forming peptide nucleic acid (PNA) which is targetted to Escherichia coli ribosomal RNA. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag; serial analysis of gene expression; diagnostic; prognostic; probe; cancer marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                              44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 3.8e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                Seguence 15 BP; 2 A; 6 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer SAGE tag #460.
Example 5; Col 12; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK32359 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 731 AGGAGAAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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bacteria

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neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining bacterial target gene function, involves preparing peptide nucleic acid (PNA) compounds complementary to bacterial nucleotide sequence, determining activity of PNA, contacting active PNA compounds and determining the effect.
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-[acetyl(2-aminoethyl)]-C-lysine-glycine
backbone"
                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "N-acetyl(2-aminoethyl)glycine backbone"
                                                                                                                                          44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 3.8e+02; rative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of a control peptide nucleic acid.
                                                                                                         Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide nucleic acid; PNA; antibacterial; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Col 13; 34pp; English.
                                                                         vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                    AAF79911 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00932140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00049190
                                                                                                                                                                                                              734 AGAAACAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                               AGCAACAGAGCAC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= b
                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NIEL/) NIELSEN P E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-256212/26.
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6190866-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-2001
                                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nielsen PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                         AAF79911;
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this invention describes a novel isolated genes and haplotypes of the human aldehyde dehydrogenase 5 (ALDH5) gene containing polymorphic sites. The polymorphic ALDH5 variant is useful in studying the effect of the variation on the biological activity of ALDH5 and on the binding affinity of candidate drugs targeting ALDH5 for the treatment of alcoholism and alcohol-induced disorders. Polymucleotides comprising a polymorphic gene variant or fragment may be used for the treatment of alcoholism and isoforms may be used in assays to measure the binding affinities of one correction to the same that a protein a protein such a section of a section of the same and a polymorphic gene variant or fragment and a polymorphic gene variant or disease predicted to be used by scientists to validate ALDH5 as a candidate target for treating a specific condition or disease predicted to be associated with ALDH5 activity, and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with applied for studying the biological function of ALDH5 as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function. The products of the invention have antialcoholic activity. This sequence represents a human and a plant of the disclosure of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genetic variants with polymorphisms in the aldehyde dehydrogenase 5 (ALDHS) gene, useful for studying the function of ALDHS, and for expressing ALDHS protein which is useful in screening drugs for treating ALDHS-related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ALDH5; human; gene; polymorphism; haplotype; aldehyde dehydrogenase 5; binding affinity; drug targeting; alcoholism; alcohol-induced disorder;
                                                                              Gaps
                                                                              ö
                                  Match 44.5%; Score 9.8; DB 1; Length 15; Local Similarity 84.6%; Pred. No. 3.8e+02; les 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Human ALDH5 allele-specific oligonucleotide SEQ ID No 12.
Sequence 15 BP; 2 A; 6 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kazemi A, Messer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 76; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2001; 2001WO-US017253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000; 2000US-0207508P.
                                                                                                                                                                                                                                                  292/c
ABA99292 standard; DNA; 15
                                                                                                                      731 AGGAGAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                    13-MAY-2002 (first entry)
                                                                                                                                                             15 AGGAGAAAGAGTA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-122054/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Finkel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antialcoholic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200192279-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                           ABA99292;
                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duda A,
                                                                                                                                                                                                                            RESULT 186
                                                               Best Loc
Matches
                                                                                                                                                                                                                                                  ABA99292
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Sequence 15 BP; 3 A; 6 C; 3 G; 2 T; 0 U; 1 Other;

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receptor, IGF binding protein [TGFB9]. Which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligomucleotide which can be used to design the antisense oligomucleotide which can be used to design the antisense oligomucleotides of the present invention (see AAF45151 and AF45153 - P45161). The method is useful for ameliotrating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
                                                                                                                                                                                                                                                                                                                                                                                                   vessels or any other hyperplasia
888888888888888888888888
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Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

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Score 9.8; DB 1; Length 15; Pred. No. 3.8e+02;
                          2; Indels
                          0; Mismatches
 44.5%;
                                                   732 GGAGAAACAGAAC 744
                                                                             3 GGAGAAGCTGAAC 15
                           11; Conservative
             Local Similarity
  Query Match
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Gaps

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AAF50112 standard; DNA; 15 30-MAR-2001 (first entry) AAF50112;

IGF-I oligonucleotide #1072

ВР

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding proctein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatosis; neophasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasis, kidney disease; neobascular condition; hyperplasis, kidney disease;

Homo sapiens.

WO200078341-A1

21-JUN-2000; 2000WO-AU000693.

99US-0140345P 21-JUN-1999; (MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR; Wraight CJ, Werther GA,

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 67; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antiense oligomucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell profiferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligomic estimates the present invention (see ARP45151 and AAP45153-6150.). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,

Example 8; Page 89; 201pp; English.

inflammation.

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oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliotrating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serbornhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperpoliferation of the inside of blood vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                   44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 3.8e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                      Sequence 15 BP; 1 A; 4 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                               Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGF-I oligonucleotide #4414.
                                                                                                                                                                                                                                                                                                                                                                                        AAF53454 standard; DNA; 15
                                                                                                                                                                                                                                                                     CAGGAGAAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wraight CJ, Werther GA,
                                                                                                                                                                                                                                                                                                    CAGAAGTAACAGA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-041421/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-1999;
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                                                                                                                                                                                                                                                                      730
                                                                                                                                                                                                                                                                                                                                                                                                                        AAF53454;
                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                        RESULT 184
                                                                                                                                                                                                                                                                                                                                                                           AAF53454
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kin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFB]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, inchthyosis, pityriasis, ruba, pilaris, serborrhoea, concers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; Keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplama; kidney disease; neoblation of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                        present invention relates to a method for ameliorating the effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9.8; DB 1; Length 15;
Pred. No. 3.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                  Example 8; Page 93; 201pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                 vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAFS0109/c
ID AAFS0109 standard; DNA; 15 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGF-I oligonucleotide #1069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             732 GGAGAAACAGAAC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGAGAAGCTGAAC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-041421/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200078341-A1.
                                             inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF50109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 181
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                                                   skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-Ike Growth Factors [IGFP]-1 receptor, IGF binding protein [IGFPB]-2 or IGFBB3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF45151 and AAA45153-845161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pllaris, serborthoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense therapy, antiproliferative, antinflammatory; antipsoriatic; cytostatic; dermataclogical, catdiant; vitudide; ophthalmological, kaloid; skin disorder; Insulin-11ke Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthytosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an
                                    The present invention relates to a method for ameliorating the effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                    44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 3.8e+02; Astive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 2 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Edmondson SR
Example 8; Page 67; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 93; 201pp; English
                                                                                                                                                                                                                                                                                                                             ressels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGF-I oligonucleotide #4971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF54011 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      731 AGGAGAAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AGAAGTAACAGAA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Werther GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-041421/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF54011;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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WO200078341-A1
               inflammation.
                                                                                            Home sapiens.
                                                                                                        21-JUN-1999;
                                                                                                  28-DEC-2000.
                                                                     AAF54012;
                                                 Query Match
                                                               RESULT 179
                                                    Matches
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antiscence oligomucleotide, (for Insulin-like Growth Factor [IGF]. receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligomucleotide which can be used to design the antisense oligomucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, tuda, plaris, serborrhoea, keloids, keratosis, ineoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or Antisense therapy, antiproliferative, antiinflammatory, antipsoriatic, cytostatic, dermatological, cardiant; virucide, ophthalmological, keloid, skin disorder, insulin-like Growth Factor I receptor; IGFF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keardosis; neoplasia; sclaroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; byperplasis; kidney disease; neovascular condition of the retina; ss. Ameliorating the effects of a disorder, e.g. psoriasis, by administering Score 9.8; DB 1; Length 15; Pred. No. 3.8e+02; 0; Mismatches 2; Indels Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other; SR; Edmondson (MURD-) MURDOCH CHILDRENS RES INST. Example 8; Page 93; 201pp; English. vessels or any other hyperplasia BP. 44.5%; 21-JUN-2000; 2000WO-AU000693 99US-0140345P IGF-I oligonucleotide #4973. AAF54013 standard; DNA; 15 744 (first entry) GGAGAAGCTGAAC 14 11; Conservative Wraight CJ, Werther GA, 732 GGAGAAACAGAAC WPI; 2001-041421/05 Query Match Best Local Similarity VPI; 2001-041421/05 WO200078341-A1. inflammation. Homo sapiens. 21-JUN-1999; 30-MAR-2001 28-DEC-2000. Best Loc Matches **AAF54**01 ò g YAC X ö The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBB]-2 or IGFBB3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF4151 and AFF45153-F45161). The method is useful for ameliotating the effects of psoriasis, ichthyosis, pityriasis, ruba, plants, serborrhoea, keloids, keratosis, ineoplasis, soleroderma, warts, benign growths, cancers of the skin, a hypermeovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic condition in the inside of blood Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF1: pitryliasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; necovascular condition; hyperplasia; kidney disease; Gaps ; 0 Score 9.8; DB 1; Length 15; Pred. No. 3.8e+02; 0; Mismatches 2; Indels Sequence 15 BP; 7 A; 4 C; 3 G; 1 T; 0 U; 0 Other; Edmondson SR; Edmondson SR; (MURD-) MURDOCH CHILDRENS RES INST. (MURD-) MURDOCH CHILDRENS RES INST. Example 8; Page 89; 201pp; English vessels or any other hyperplasia 44.5%; 84.6%; 99US-0140345P. 21-JJN-2000; 2000WO-AU000693 IGF-I oligonucleotide #4972. AAF54012 standard; DNA; 15 734 AGAAACAGAACAC 746 30-MAR-2001 (first entry) 3 AGCAACAGAGCAC 15 Wraight CJ, Werther GA, 11; Conservative Wraight CJ, Werther GA, WPI; 2001-041421/05 Local Similarity

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Gaps

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This invention relates to hybridisation probes which target a specific sequence within a large double-helical nucleic acid. The probe is complementary to the target sequence and contains at least one nucleotide with an attached molecule that is able to cleave double-helical DNA e.g. EDTA-Fe(II) (ethylenediaminetraacetic acid-iron complex). The probes where the attached molecule is a label or compound that alters gene expression, are used for specific detection and/or cleavage of double-helical DNA, e.g. for diagnosis, for treatment of disease (particularly caused by viruses, genetic defects or oncogenes), for chromosomal analysis, and for the isolation and mapping of genes. The present sequence represents probe of the invention which is used in an example illustrating how it binds to and cleaves a double stranded fragment of plasmid pDMAGIO given in AAH20315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; Keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding procein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease;
                                                                                                                                                                                                                                                                                                                  New hybridization probe for specific triplex formation with large double helices, useful e.g. for site-specific diagnostic cleavage, contains attached functional residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 3.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                              (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 4B; 20pp; English.
                                                                                                                                         87US-00115922.
90US-00614205.
93US-00152250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF53455 standard; DNA; 15 BP
                                                                                                         98US-00128732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      733 GAGAAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 84.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAAAGAGAAAA 2
C-5"
                                                                                                                                                                                                                                                  Dervan PB, Moser HE;
                                                                                                                                                                                                                                                                                    WPI; 2001-342909/36.
                                     US2001002314-A1.
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                                                                                                         04-AUG-1998;
                                                                                                                                         30-OCT-1987;
16-NOV-1990;
                                                                                                                                                                              12-NOV-1993;
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                                                                     31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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 BXBXSXEEEEEEE
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an skin disorders. The method comprises contacting the skin with an creeptor, IGP binding protein [IGPP]-2 or IGPPP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, rothyyosis, pityriasis, ruba, pilaris, servorthoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, disease, kidney disease, hyperplasia alignancies, other sclerotic diseases, kidney disease, hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scaleroderma; wart; skin cancer; sclerotic disease; hyperancovascular condition; hyperplasia, kidney disease; neobascular condition of the retina; ss.
                                                                                                                                                                                                             Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.5%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 3.8e+02; arive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                       Werther GA, Edmondson SR;
                                                                                                                                                                                                                                                                                                                      Example 8; Page 89; 201pp; English.
                                                                                                (MURD-) MURDOCH CHILDRENS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF53453 standard; DNA; 15 BP.
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                                                         99US-0140345P.
                 21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGF-I oligonucleotide #4413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              734 AGAAACAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.67
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGCAACAGAGCAC 13
                                                                                                                                                                             WPI; 2001-041421/05
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                                                                                                                                                                                                                                                                                  inflammation.
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                                                         21-JUN-1999;
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                                                                                                                                       Wraight CJ,
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99US-0140345P,

21-JUN-1999;

AAZ63819;

RESULT 174 AAZ63819/c

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The present invention describes a dendrimer having branches that terminate with the same polynucleotide (PN) sequence. Also described are: (1) use of a multimeric PN for hybridisation interaction; and (2) an assay for a target PN by hybridisation with an immobilised PN, which comprises the preliminary step of conjugating the target to a dendrimer having reactive terminal groups. The dendrimers comprising PN multimers can be used in hybridisation assays for the detection of target nucleic acids. The use of multimeric PNs allows multiple hybridisation reactions to occur with a resulting increase in the stability of the hybridised components compared to a duplex formed between PN monomers. This increase in stability is characterised by higher melting temperatures and higher temperatures of reassociation exhibited by the multimeric PNs in comparative tests with PN monomers. The present sequence represents a control polymucleotide sequence, which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mod_base= OTHER
/note= "Thymidine has EDTA-FE(II) covalently attached at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New dendrimer compositions, used in hybridization assays for the detection of target nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
                                                                                    Dendrimer; polynucleotide multimer; hybridisation assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 9.8; DB 1; Length 15;
Pred. No. 3.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
                                           Control polynucleotide sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 7; 25pp; English.
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/mod_base= OTHER
'mod_rm'rmidin'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH20313 standard; DNA; 15 BP.
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                                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                        Shchepinov MS, Southern EM;
15-MAR-2000 (first entry)
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Best Local Similarity 84.6
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 AAGAGAAAGAGA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-EDTA-FE(II) probe 7.
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-072636/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
modified base
                                                                                                                                                                    W09961662-A1
                                                                                                                                                                                                                                                        27-MAY-1999;
                                                                                                                                                                                                                                                                                                    27-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2001
                                                                                                                                                                                                                  02-DEC-1999.
                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH20313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the HepatitisC virus (HCV) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the carget the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular carcinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                      Enzymatic nucleic acid, hammerhead ribozyme, virus replication, cleavage, cirrhosis, liver failure, hepatocellular carcinoma, interferon, cancer, autoimmune disease, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                           Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 1866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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Pred. No. 3.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macejak D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 BP; 2 A; 6 C; 2 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blatt L, Mcswiggen JA, Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 71; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0083217P.
98US-0100842P.
99US-00257608.
99US-00274553.
                                                                                    BP.
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84.6%;
                                                                               AAZ63819 standard; RNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ48115 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              732 GGAGAAACAGAAC 744
                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-062023/05
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                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1998;
18-SEP-1998;
25-FEB-1999;
                                                                                                                                                                    28-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                    W09955847-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1999;
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Gaps

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AAZ48115 RESULT 175 AAZ48115/c ID AAZ4811 XX AC AAZ4811 XX 87

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Gaps

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Indels

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Mismatches

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tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from cDNA libraries. The tag sequences can also be used in a method for diagnosing colon or pancreatic cancer in a sample suspected of being neoplastic. The method comprises comparing the level of at least one transcript in a first sample of a tissue to a second sample, where the first sample is a colonic tissue suspected of being neoplastic and the second sample is a normal human colonic tissue. The transcript is identified by a tag selected from AAX30947-11815. The methods of the invention can be used in the diagnosis, prognosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel use of triple helix forming oligonucleotides, useful for in situ detection of double stranded target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; human; chromosome 17 triple-helix forming oligonucleotide; genetic disorder; missing chromosome; aneuploidy; chromosome 21; infectious disease; diagnosis; alpha-satellite region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9.8; DB 1; Length 15;
Pred. No. 3.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 1 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human chromosome alpha-satellite region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Page 13; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX61194 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US023765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    728 GCCAGGAGAACA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGACGAGAACA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fresco JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYPR-) UNIV PRINCETON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-327425/27.
                                                                                                                                                                                                                                                                                                                                   treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9924622-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX61194;
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XXX
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AAX6
AAX6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A method has been developed for killing or inhibiting the growth of bacteria by contacting the bacteria with a peptide nucleic acid (PNA). The PNA is targeted to messenger or ribosomal RNA. The antibacterial composition has bacteriostatic and bacterial properties. The PNA can be used to treat a mammal suffering from a bacterial infection where the PNA is complementary to a region of ribosomal RNA and of mRNA of the bacteriar. Further treatment may include concurrent treatment with an antibiotic. The PNA can also be used as a method of disinfection by selecting an object to be disinfected, contacting the object with PNA (in solution) and rinsing the object with a serile liquid to remove the PNA. The invention provides new ways of tackling bacterial infections which have become resistant to frequently used antibiotics. The present sequence represents a PNA from an example of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b /note= "t is attached to an amidated lysine residue e.g. -t-Lys-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Killing or inhibiting bacterial growth by using a peptide nucleic acid.
                                                                                                                                                                                                                                                              Beta-galactosidase; peptide nucleic acid; PNA; antibacterial;
growth inhibition; antibiotic; bacteria; infection; disinfectant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                             *tag= a
note= "N-acetyl (2-aminoethyl) glycine backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                Beta-galactosidase targeting peptide nucleic acid SEQ ID NO:11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 15 BP; 2 A; 6 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; Page 21; 97pp; English
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0
                                                                                                                                        AAX33140 standard, DNA, 15 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 84.6%;
Conservative
                               731 AGGAGAAACAGAA 743
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                                                                                                                                                                                                     24-JUN-1999 (first entry)
                                                           2 AGGTGAAAAAGAA 14
11; Conservative
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*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS PHARM INC. (NIEL/) NIELSEN P E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Good L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-254325/21.
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es 11, Conserv
                                                                                                                                                                                                                                                                                                                                                                modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nielsen PE,
                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                       AAX33140;
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 Matches
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Matches
                                                                                                          RESULT 173
                                                                                                                           AAX33140/
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15 AGGAGAAAGAGTA 3

Length 15;

Score 9.8; DB 1; Pred. No. 3.8e+02;

44.5%;

Query Match Best Local Similarity

BP; 10 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

86

Hepatitis C virus.

Pavco PA, Macejack D;

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The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV ribozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirthosis, liver failure and/or hepatocellular carcinoma. The HCV infoction in conjunction with one or more condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon. The present sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note: Sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was contained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                           New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
Local Similarity 84.6%; Pred. No. 3.7e+02;
es 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14 BP; 2 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human alpha foetal protein gene oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; triple helix; alpha foetal protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                 Roberts B,
                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 59; 80pp; English.
                                                                                          99US-00274553.
                                                                                                                        99US-00274553
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                                                                                                                                                                                                                                              Blatt L, Mcswiggen JA,
                                                                                                                                                    BLATT L.
MCSWIGGEN J A.
ROBERTS B.
PAVCO P A.
                                                                                                                                                                                                                                                                             WPI; 2002-617759/66
                                                                                                                                                                                (ROBE/) ROBERTS B.
(PAVC/) PAVCO P A.
(MACE/) MACEJACK D.
                             US2002082225-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200277274-A2.
                                                                                          23-MAR-1999;
                                                                                                                        23-MAR-1999;
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                                                           27-JUN-2002
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                                                                                                                                                    BLAT/)
                                                                                                                                                                      (MCSM/)
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                                                                                                                                                                                                                                                     The present invention relates to novel double stranded (ds) DNA sequences which can interact with a third strand to 0 form a stable triple helix. The invention also relates to a method for purifying a ds DNA molecule, comprising contact with a third DNA strand that interacts with a target agequence (TS) in the ds DNA to form a triple helix. The present sequence is an oligomucleotide from human alpha foetal protein gene, used as the ds DNA sequence in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of isolated gene transcripts - useful for developing products for the diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX30947-31815 represent tag sequences of transcripts that are differentially expressed in colorectal cancer, in pancreatic cancer, in both. The tag sequences can be used to identify genes by matching
                                                                                                                                                           or
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                        Purifying double-stranded DNA, useful e.g. for isolating plasmids therapeutic genes, by triple helix formation with oligonuclectide directed to a specific target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tag sequence of a transcript decreased in colorectal cancer.
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44.5%; Score 9.8; DB 1; Length 14;

Best Local Similarity 84.6%; Pred. No. 3.7e+02;

Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14 BP; 9 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; prognosis; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 49; 120pp; English.
                                                                                                                                                                                                                         Claim 16; Page 10; 49pp; French.
               23-MAR-2001; 2001FR-00003953.
23-APR-2001; 2001US-0285272P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX31405 standard; DNA; 15 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   731 AGGAGAAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jogelstein B, Kinzler KW;
                                                             (AVET ) AVENTIS PHARMA SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AGGAGAAGAAGAA 14
                                                                                                                           WPI; 2003-018943/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-070161/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409853319-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX31405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 171
AAX31405/c
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Gaps ;

BP.

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The present sequence represents a polynucleotide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methyloytosine for increased triplex catability. The present sequence is used in the assay of the invention, where it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded DNA test comprises adding a sample containing double-stranded DNA test comprises adding support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting concogenes and Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                               Triplex formation; DNA detection; triple helix; identification; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                              Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify
                                                                                         Triple helix third strand of Hepatitis B virus nucleotides 1810-1823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Substrate for hairpin ribozyme which cleaves HCV at nt. 1863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.5%; Score 9.8; DB 1; Length 14; 84.6%; Pred. No. 3.7e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 14 BP; 0 A; 6 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 19-20; 168pp; English.
                                                                                                                                                                                                                                                                             (PROF-) PROFILE DIAGNOSTIC SCI INC.
             AAX14799/c
ID AAX14799 standard; DNA; 14 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ64722 standard; RNA; 14 BP
                                                                                                                                                                                                                                                       92US-00968436.
                                                                                                                                                                                                                                 93US-00173489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 AGGAGAAGCAGGA 1
                                                                                                                                                                                                                                                                                                    Wang C;
                                                                                                                            oncogene; virus; ss.
                                                                                                                                                                                                                                                                                                                         WPI; 1999-130384/11.
                                                                                                                                                             Hepatitis B virus.
                                                                                                                                                                                                                                 22-DEC-1993;
                                                                                                                                                                                                                                                        29-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2000
                                                                   24-MAR-1999
                                                                                                                                                                                    JS5861244-A.
                                                                                                                                                                                                                                                                                                    Hepburn AG,
                                                                                                                                                                                                          19-JAN-1999
                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                Assay of stranded
                                                                                                                                                                                                                                                                                                                                                                                    bacteria.
                                              AAX14799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ64722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 168
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ID AAZ6.
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AC AAZ6.
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DT 28-M
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DE Subs'
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The present sequence represents the preferred target sequence of an erzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the Hepattiis C virus (HCV) RNA sequence at the base position given in the Gescriptor line. The HCV sequence was screened for optimal ribozyme cleaves the the HCV sequence was screened for optimal ribozyme trayer such contained potential continued proceedings of the mine of the meant of the secondary folding structures and contained potential cribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatoticis C virus (HCV) infection, e.g. cirrhosss, liver failure and hepatocellular carcinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune contains and cancer.
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Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage; cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer; autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic nucleic acid, RNA cleavage; Hepatitis C virus infection; HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide; liver failure; hepatocellular carcinoma; HCV infection; drug therapy; type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; oonsensus interferon; hepatotropic; antiinflammatory; substrate; hairpin ribozyme; HP ribozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel ribozymes for the treatment of diseases and conditions related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.5%; Score 9.8; DB 1; Length 14; 84.6%; Pred. No. 3.7e+02; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macejak D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14 BP; 2 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 95; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABX01559/c
ID ABX01559 standard; RNA; 14 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0083217P.
98US-0100842P.
99US-00257608.
99US-00274553.
                                                                                                                                                                                                                                                                                                                                                                 99WO-US009027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                732 GGAGAACAGAAC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-2002 (first entry)
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 GGTGAAACAGTAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-062023/05
                                                                                                                                                   Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                 26-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-1998;
25-FEB-1999;
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                                                                                                                                                                                                                                                                                           04-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 169
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Length 14;

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Gaps .,

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transforming growth factor beta-1 (TGF beta-1). The oligonucleotides transforming growth factor beta-1 (TGF beta-1). The oligonucleotides exemplify the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that contain 8-30 nucleotides which contain at most 8 nucleotides that consecutive nucleotides able to form three H-bonds each to four consecutive orytosines, do not contain two sequences of three consecutive cytosines, and the ratio between residues able to form two H-bonds each consecutive nucleotides each able to form three H-bonds to three consecutive nucleotides are used to modulate expression of genes, particularly colligonucleotides are used to modulate expression of genes, particularly proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system
beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate analogues. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta-1; TGF beta-1; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in
                                                                                                             Score 9.8; DB 1; Length 14; Pred. No. 3.7e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           TGF-beta-1 antisense oligonucleotide TGF-betal-30.
                                                                           Sequence 14 BP; 7 A; 2 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14 BP; 5 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Fig 3b; 286pp; English.
                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brysch W;
                                                                                                             Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97EP-00101531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97EP-00101531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor modulate, gene expression,
                                                                                                                                                                                                                                                                                                                            AAV48481 standard; DNA; 14
                                                                                                                                                                                          728 GCCAGGAGAACA 740
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                    GCAAGGAGAAGCA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlingensiepen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP856579-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-AUG-1998
                                                                                                                                                                                                                                                                                                                                                              AAV48481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triplex formation, DNA detection, triple helix, identification, bacteria, oncogene, virus, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a polynucleotide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methylcytosine for increased triplex stability. The present sequence is used in the assay of the invention, where it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded DNA test sequences to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic sequences based on triplex formation from double analyte - and hybrid of anchor and reporter sequences, with released if triplex formation occurs, used e.g. to identify
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Priple helix third strand of Hepatitis B virus nucleotides 274-287.
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   Score 9.8; DB 1; Length 14 Pred. No. 3.7e+02; 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Col 19-20; 168pp; English
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                                                                                                                                                                                                                                                                                                                                                              BP.
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      44.5%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                           AAX14811 standard; DNA; 14
                                                                                                                                 729 CCAGGAGAACAG 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
Query Match
Best Local Similarity 84.6<sup>5</sup>
Matches 11, Conservative
                                                                                                                                                                                              ccardadadcad 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-130384/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS5861244-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAX14811;
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                                                                                                                                                                                                                                                                                             RESULT 166
AAX14811/C
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analysing genomic DNA of individuals which react with restriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 60; 74pp; English.
                                                  Example; Page 13; 46pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ78477 standard; DNA; 14 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                              1 GACAAACAGAGCA 13
                                                                                                                                                                                                                                                                                  11; Conservative
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Best Local Similarity
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Bogdahn U;
                                                                                                                                                                               correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
27-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                   fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ78477;
                                                                                                                                                                                                                                                                                Matches
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   ##X8X000000X8
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                                                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting the hypervariable regions of DNA for diagnosing hereditary illnesses and tumours - by hybridising labelled polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HVR; human, animal; forensic science; paternity testing; diagnosis; animal breeding; hereditary diseases; tumours; allele; loss; chromosomal regions; tumour region identification; ss.
                                                                                                                                                                 ligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 28052; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 13 BP; 10 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypervariable region detection probe 14C5.
                                                                                                  Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ40599 standard; DNA; 14 BP
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   06-APR-2001; 2001WO-IB000713
                                    07-APR-2000; 2000DE-01019173
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(first entry)
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                    Set of oligonucleotides,
                                                                                                  Piepenbrock C,
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                                                                                                                                   WPI; 2001-657177/75.
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                                                                     (EPIG-) EPIGENOMICS
                                                                                                                                                                                                    methylation status
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10-AUG-1993
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RESULT 163 AAQ40599

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The sequence is that of a polymucleotide probe which may be used in the detection of new hypervariable regions (HVR) in a DNA sequence. HVR represent a fingerprint useful in e.g. forensic science, paternity testing, animal breeding, etc. The probe may be used as part of a method for the efficient detection in humans or other animals, without the use of mini-satellites or primary enrichment. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transforming growth factor beta; TGF-beta; antisense; treatment; tumour; anglogenesis; breat tumour; neurofibroma; glioma; glioblastoma; carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut; immunosuppression; oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
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84.6%; Pred. No. 3.7e+02;
ative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14 BP; 8 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS

WPI; 2001-657177/75

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2

Homo sapiens

Oligonucleotide SEQ ID NO 263069 for detecting SNP TSC0063818

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABF82073 fat for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Set of oligonuclectides, useful for diagnosis and cell typing, i designed to detect single-nuclectide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 39735; 29pp + Sequence Listing; German.
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                                                                                                                 ABC39718 standard; DNA; 13
                                                                                                                                                                                  20-FEB-2002 (first entry)
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                              13 AGGAGAAAGAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                ABC39718;
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ABH63092/C
ID ABH630
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C ABH630
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DT 22-FEB
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ABC39718/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 263069; 29pp + Sequence Listing; German
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ABC28035
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ABH63092 standard; DNA; 13

22-FEB-2002 (first entry)

ABH63092;

WPI; 2001-657177/75

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Query Match

44.5%; Score 9.8; DB 1; Length 13;

Best Local Similarity 84.6%; Pred. No. 3.6e+02;

Matches 11; Conservative 0; Mismatches 2; Indels
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methylation status.
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                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .gonuclectides, useful for diagnosis and cell typing, it detect single-nuclectide polymorphisms and cytosine
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44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                         Claim 1; SEQ ID NO 88771; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13 BP; 10 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
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                                                methylation status.
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 3.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                           Seguence 13 BP; 10 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABC52235 standard; DNA; 13 BP.
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Best Local Similarity 84.6'
Matches 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                          vec or oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 232878; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 44.5%; Score 9.8; DB 1; Length 13; 1 Similarity 84.6%; Pred. No. 3.6e+02; 11; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                         Oligonucleotide SEQ ID NO 39736 for detecting SNP TSC0012134.
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Pred. No. 3.6e+02;
0; Mismatches 2; Indels
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84.6%;
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Best Local Similarity 84.69
Matches 11; Conservative
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ABC39719 standard; DNA;
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1D ABH3
XX ABH3
XX ABH3
XX ABH3
XX B Olig
XX SX SNP;
XW SNP;
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XW Cent.
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Gaps

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Sequence 13 BP; 8 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABE99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                              Oligonucleotide SEQ ID NO 52251 for detecting SNP TSC0014524.
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     Length 13;
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                                      Indels
44.5%; Score 9.8; DB 1; Lv 84.6%; Pred. No. 3.6e+02; ative 0; Mismatches 2;
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                                                                                                                                                                                                      ABC52234 standard; DNA; 13 BP
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                                                                         731 AGGAGAAACAGAA 743
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                                                                                                           1 AGTAGAAATAGAA 13
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Best Local Similarity 84.6
Matches 11; Conservative
                                        Conservative
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                          ABC52234;
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1 AGGAGAAAGAAA 13

RESULT 155 ABC39719 Berlin K;

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This invention describes novel oligonucleotide primars or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
                                                                                                                                                              Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 263070; 29pp + Sequence Listing; German.
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1 Similarity 84.6%;
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                       (EPIG-) EPIGENOMICS AG.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 84.6
Matches 11; Conservative
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Gaps

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Score 9.8; DB 1; Length 13; Pred. No. 3.6e+02; 0; Mismatches 2; Indels

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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734 AGAAACAGAACAC 746
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ABH32900 standard; DNA; 13
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                                           RESULT 149
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                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                Score 9.8; DB 1; Length 13;
Pred. No. 3.6e+02;
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44.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                        Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 U; 0 Other;
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Matches 11; Conservative (
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but type int/pub/published_pct_sequences
                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                     Oligonucleotide SEQ ID NO 232877 for detecting SNP TSC0056815.
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The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK22770 represent human colon and pancreatic cancer SAGE tags of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection, HCV ribozyme, HCV expression, HCV replication, cirrhosis, virucide, liver failure, hepatocoellular carcinoma, HCV infection, drug therapy, type I interferon; interferon alpha, interferon beta; cytostatic, interferon gamma; consensus interferon, hepatotropic; antiinflammatory, substrate; hammerhead ribozyme, HH ribozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus substrate #717 for HCV hammerhead ribozyme #717.
                                                                                                                                                                                                               New human nucleic acid containing specific SAGE tags, useful as diagnostic markers for cancer, also derived probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.5%; Score 10; DB 1; Length 15; 100.0%; Pred. No. 3.6e+02; tive 0; Mismatches 0; Indels
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                                                                                            Zhou W;
                                                                                            Zhang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roberts B,
                                                                                                                                                                                                                                                                                                    Disclosure; Col 52; 161pp; English.
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                                                                                        Kinzler KW,
                             (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX00935 standard; RNA; 15
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es 10; Conservative
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MCSWIGGEN J A.
                                                                                                                                                       WPI; 2002-153821/20.
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PAVCO P A.
MACEJACK D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-617759/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002082225-A1.
                                                                                        Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-1999;
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(MACE/)
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Claim 1; Page 42; 80pp; English

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Gaps

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The present invention relates to enzymatic nucleic acids which specifically volave RNA derived from Hepatitis C virus (HCV). The specifically volave RNA derived from Hepatitis C virus (HCV). The nazymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV incomplete accomplete to treat circhosis, liver failure and/or hepatocellular carcinoma. The HCV infection in conjunction with one or more condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon, especially confection in conjunction with one or more sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note: Some of the sequence data for this patent did not form part of the chained in electronic format directly from the USPTO web site at sequence complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The coligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF89999, ABH00010-ABH99989 and ABI00010-ABI82073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide SEQ ID NO 28051 for detecting SNP TSC0007919.
                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 45.5%; Score 10; DB 1; Length 15; Local Similarity 100.0%; Pred. No. 3.6e+02; No. 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 0 A; 6 C; 4 G; 0 T; 5 U; 0 Other;
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RESULT 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to single mucleotide polymorphisms in the gene encoding the human v-fos FBJ murine osteosarcoma viral oncogene homologue (FDS) polypeptide. A method for haplotyping the FOS gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the Ryb haplotype pairs can be sesigned to specific genotypes. An association between a trait and a haplotype or haplotype pair in a population exhibiting the trait with the FOS gene can be identified by comparing the frequency of the haplotype or haplotype pair. FOS and its associated with the haplotype or haplotype 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                             Human, v-fos FBJ murine osteosarcoma viral oncogene homologue; FOS; cytostatic; gene therapy; single nucleotide polymorphism; haplotyping; haplotype pair; developmental bone disorder; cancer; tumour; ss; primer; chromosome 14q21-q31; sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel genetic variants of V-Fos FBJ Murine Osteosarcoma Viral Oncogene Homolog (FOS) isogenes, useful for improving efficiency and reliability in drug development for treating developmental bone disorders.
                                                Human FOS gene allele-specific oligonucleotide sequencing primer #19.
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                                                                                                                                                                                                                                                                                                                                                                             Lee HH;
                                                                                                                                                                                                                                                                                                                                                                             Kliem SE, Koshy B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 14; 73pp; English.
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The invention comprises the DNA and amino acid sequence of the human lipase, endothelial (LIPG) isogene. Specifically, the invention relates to the discovery of 20 novel polymorphic sites within the LIPG gene. The LIPG coding sequence and protein are useful for screening drugs that can be used to treat atherosclerosis and other cardiovascular disorders. The LIPG coding sequence can also be used to haplotype and genotype the LIPG gene of an individual. The DNA sequences ABL91822 - ABL91881 represent LIPG gene allele specific oligonucleotide primers
                                                          Human, ss, allele specific oligonucleotide; primer; single nucleotide polymorphism; SNP; lipase endothelial isogene; LIPG; drug screening; aheroselerosis; cardiovascular disorder; LIPG the haplotyping; LIPG genotyping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel genetic variants of Lipase, Endothelial isogenes, useful for improving efficiency and reliability in drug development for treating diseases associated with LIPG activity, e.g. atherosclerosis.
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Human LIPG gene allele specific oligonucleotide primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kliem SE, Messer C;
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                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-2001; 2001WO-US026639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENA-) GENAISSANCE PHARM INC
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Gaps

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Indels

Pred. No. 3.6e+02; Mismatches 0;

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100.0%;

Best Local Similarity 100. Matches 10; Conservative

728 GCCAGGAGAA 737

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GCCAGGAGAA

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The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the HepatitisC virus (HCV) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified Ribozymes were synthesised to target these sites and their activities optimised by either varying the target these sites and their activities optimised by either varying the cleavage sites and their activities optimised by either varying the uncleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatotis C virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular carcinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage; cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer; autoimmune disease; ss.
being neoplastic and the second sample is a normal human colonic tissue. The transcript is identified by a tag selected from AAX30947-31815. The methods of the invention can be used in the diagnosis, prognosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ç
                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2516.
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                                                                                                                                                                                                                                        45.5%; Score 10; DB 1; Length 15; 100.0%; Pred. No. 3.6e+02; cive 0; Mismatches 0; Indels
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                                                                                                                                                                        Sequence 15 BP; 6 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blatt L, Mcswiggen JA, Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 73; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ63882 standard; RNA; 15 BP.
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99US-00274553.
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98US-0100842P.
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                             732 GGAGAAACAG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGAACAG 14
                                                                                                           treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
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18-SEP-1998;
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AAZG 3882
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45.5%; Score 10; DB 1; Length 15;

Query Match

Sequence 15 BP; 0 A; 6 C; 4 G; 0 T; 5 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genotyping human small inducible cytokine Al-I-309, homologous to mous
Tca-3 gene of individual, involves determining identity of nucleotide
pair at specific polymorphic sites for two copies of the gene.
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                                                                                                                                                                    Human, single nucleotide polymorphism; SNP; SCYA1; chromosome 17; small inducible cytokine Al-1-309; haplotyping; genetyping; gene; atherosclerosis; human immunodeficiency virus; HIV infection; allele-specific oligonucleotide; ASO; primer; ss.
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                                                                                                                                     ASO primer #11 to detect human SCYA1 gene polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephens JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 BP; 6 A; 4 C; 4 G; 0 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sausker EA,
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                                    BP
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                                                                                                                                                                                                                                                                                                                                                             16-APR-2001; 2001WO-US012305.
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                                  AAS14448 standard; DNA; 15
                                                                                                     (first entry)
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                                                                                                   23-APR-2002
                                                                                                                                                                                                                                                           Homo sapiens
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                                                                    AAS14448;
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RESULT 142
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                  AAS14448
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastroin estinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99889, ABF0010-ABE99889 and ABI0010-ABE9980 and ABI0010-ABE9073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
target; substrate; catalyst; modulation; expression; Raf gene; delivery;
screening; identification; synthesis; deprotection; purification; cancer;
inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human B-raf target sequence nucleotide position 388.
                                                                                                                                                                                            Sequence 13 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 1 Other;
                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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97US-0049002P.
97US-0056808P.
97US-0061321P.
97US-0061324P.
97US-006486EP.
97US-0068212P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                       736 AAACAGAACACC 747
                                                                                                                                                                                                                                                                                                                     13 RAACAAAACACC 2
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05-NOV-1997;
19-DEC-1997;
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09-JUN-1997
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02-OCT-1997
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Matches
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Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenceis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.

A method has been developed for the identification of a nucleic acid capable of modulating a process in a biological system. The method

Claim 179; Page 174; 259pp; English.

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comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising caradom sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with care used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic acide and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 repersent NACs that can be used in the control of the Raf gene activity. AAV90922 to AAV93877 repersesion of a Raf gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX30947-31815 represent tag sequences of transcripts that are differentially expressed in colorectal cancer, in pancreatic cancer, or in both. The tag sequences can be used to identify genes by matching the tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from cDNA libraries. The tag sequences can also be used in a method for diagnosing colon or pancreatic cancer in a sample suspected of being neoplastic. The method comprises comparing the level of at least one transcript in a first sample of a tissue to a second sample, where the first sample is a colonic tissue suspected of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of isolated gene transcripts - useful for developing products for diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tag sequence; colorectal cancer; pancreatic cancer; colon cancer; diagnosis; prognosis; treatment; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lag sequence of a transcript decreased in colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%; Score 10; DB 1; Length 14; llarity 100.0%; Pred. No. 3.5e+02; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
----- 10; Conserve
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schultz1-727.rng

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form mar of the printed specification, but was obtained in electronic format from WIPO at
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 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 264229; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%; Score 10; DB 1; Length 13; 83.3%; Pred. No. 3.4e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                          Berlin K;
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                                                                                                                                                      06-APR-2001; 2001WO-IB000713.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 83.3
es 10; Conservative
                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 RAACATAACACC 2
                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                         WPI; 2001-657177/75
                                                                                                                                                                                                                                                                                                                                             designed to detect methylation status.
                                                                                   WO200177384-A2
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                                                    Homo sapiens.
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                                                                                                                                                                                                                                                          Olek A,
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ABH64253
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                                                                                                                                                                                                             acid (PRA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diseases and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABF09989, ABF00010-ABF99989 and ABI0010-ABF2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                 oet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide SEQ ID NO 180067 for detecting SNP TSC0044584.
                                                                                                                                                                  Claim 1; SEQ ID NO 264230; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 180067; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.5%; Score 10; DB 1; Length 13; 83.3%; Pred. No. 3.48+02; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 1 Other;
                              Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABF80070 standard; DNA; 13 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 83.3
nes 10; Conservative
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                              Piepenbrock C,
(EPIG-) EPIGENOMICS AG.
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                                                                WPI; 2001-657177/75
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                                olek A,
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ABF80071 standard; DNA; 13
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                                                                                                                                                                                                               Homo sapiens
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                                                                            ABF80071;
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                                                                                                                                                                                                                                                                                                                                                                           olek A,
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                        RESULT 135
ABF80071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis, atopby dermatitis, and, supparently and string skin rosaces, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
response to vaccination and/or therapy, in cancer immunoprophylaxis, immunotherapy and diagnosis, and monitoring of tumor progression or regression, and to produce large quantities of readily purified antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                      Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
                                                                                                       Gaps
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                                                                           45.5%; Score 10; DB 1; Length 11; 100.0%; Pred. No. 3.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.5%; Score 10; DB 1; Length 11; ilarity 100.0%; Pred. No. 3.2e+02; Conservative 0; Mismatches 0; Indels
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                                                   Seguence 11 BP; 5 A; 2 C; 3 G; 0 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 120; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petersohn D, Conradt M, Hofmann K;
                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                              ABV65653 standard; cDNA; 11
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                         10; Conservative
                                                                                                                                   730 CAGGAGAAAC 739
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                                                                                                                                                         CAGGAGAAAC
                                                                                                                                                                                                                                                                                                             Human skin EST 3439
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                                                                            Query Match
Best Local Similarity
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                   RESULT 134
                                                                                                         Matches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prefraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disonders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
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Oligonucleotide SEQ ID NO 180068 for detecting SNP TSC0044584.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 180068; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-APR-2000; 2000DE-01019173.
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The invention comprises the DNA and amino acid sequence of the human lipase, endochelial (LIPG) isogene. Specifically, the invention relates to the discovery of 20 novel polymorphic sites within the LIPG gene. The LIPG coding sequence and protein are useful for screening drugs that can be used to treat atherosclerosis and other cardiovascular disorders. The LIPG coding sequence can also be used to haplotype and genotype the LIPG gene of an individual. The DNA sequences ABL91862 - ABL91901 represent
                                                 Novel genetic variants of Lipase, Endothelial isogenes, useful for improving efficiency and reliability in drug development for treating diseases associated with LIPG activity, e.g. atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPG gene primer extension oligonucleotides
                                                                                                                                                                      Claim 18; Page 14; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF28124 standard; RNA; 11 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to modified human thymic stromal lymphopoietin (TSLP) protein and polymucleotide sequences. TSLP protein is useful for stimulating lymphocyte proliferation of lymphopoiess, or inducing STATS. TSLP DNA is useful for producing a furin-resistant polypeptide having at thest one functional human TSLP activity. The invention is useful in the manufacture of a medicament for stimulating lymphocyte proliferation, for promoting lymphocyte proliferation, for promoting lymphopoiesis, or for inducing phosphorylation of STATS. It is also useful as a vaccine for treating ALDS, autoimmune diseases (e.g. transplant rejection), or bacterial or viral infections. The present sequence is human TSLP furin cleavage site peptide encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1) ss; primer; extension oligonucleotide;
le nucleotide polymorphism; SNP; lipase endothelial isogene; LIPG;
screening; atherosclerosis; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 New modified human thymic stromal lymphopoietin (TSLP) protein and polymucleotide, useful for stimulating lymphocyte proliferation of lymphopoiesis, particularly as a vaccine for treating e.g. AIDS or autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 BP; 10 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
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Pred. No. 3.3e+02;
0; Mismatches 3;
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LIPG haplotyping; LIPG genotyping.
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                                                                                                               23-JUL-2002; 2002WO-US023475
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Local Similarity 80.0%;
les 12; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                      Van Ness KP,
                                                                                                                                                                                                                              (IMMV) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                             WPI; 2003-393470/37.
P-PSDB; AAE37156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single nucleotide
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                                                       24-APR-2003
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                                                                                                                                                                                                                                                                                      Lyman SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL91866;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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ABL91866/C
XX
AC ABL9.
DT 11-JJ
XX Human
XX Hu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing recombinant replicable vesiculovirus, useful as vaccines for treating or preventing microbial infections, comprises culturing a cell containing a nucleic acid for the expression of vesiculovirus antigenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invetion relates to producing a recombinant replicable vesiculovirus. The method involves culturing a cell containing a first recombinant nucleic acid that can be transcribed to produce an RNA comprising a vesiculovirus antigenomic (+) RNA containing the vesiculovirus promoter for replication and a ribozyme sequence immediately downstream the antigenomic (+) RNA. The method is useful for producing recombinant replicable vesiculoviruses, which can be used as vaccines for the treatment or prevention of infections by a pathogenic microorganism. The recombinant replicable vesiculoviruses are useful in diagnosing and monitoring progression of infectious disorders, including
                                       Gaps
                                       ;
0
Query Match 45.5%; Score 10; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                      Vesiculovirus; vaccine; infection; cancer; ss
                                                                                                                                                                                                                                                                                                                     Vesicular stomatitis virus gene junction #1.
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99US-00274553
                                                 99US-00274553
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                            Mcswiggen JA,
                                                                                   BLATT L.
MCSWIGGEN J A.
ROBERTS B.
PAVCO P A.
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                                                                                                                                                                                                                          WPI; 2002-617759/66.
                                                                                                                                                       MACEJACK D
                23-MAR-1999;
                                                 23-MAR-1999;
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                                                                                 (BLAT/) 1 (MCSW/) 1 (ROBE/) 1 (PAVC/) 1 (MACE/) 1
                                                                                                                                                                                          Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhaed (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV ribozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat crithosis, liver failure and/or replication of hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more condition associated with HCV infection in conjunction with one or more condition associated with HCV infection in conjunction with one or more context of sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note: sequence capte for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPPO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                            New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection, HCV ribozyme; HCV expression, HCV replication, cirrhosis, virucide, liver failure, hepatocellular carcinoma, HCV infection, drug therapy, type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon; hepatotropic; antiinflammatory; substrate; hammerhead ribozyme; HH ribozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus substrate #716 for HCV hammerhead ribozyme #716.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.4%; Score 10.2; DB 1; Length 15; 80.0%; Pred. No. 3.3e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                            Pavco PA, Macejack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 0 A; 5 C; 2 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                               Roberts B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 42; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВЪ
                                                 99US-00274553
                                                                                      99US-00274553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 80.0 ses 12; Conservative
                                                                                                                                                                                                                            Blatt L, Mcswiggen JA,
                                                                                                                      BLATT L.
MCSWIGGEN J A.
ROBERTS B.
PAVCO P A.
                                                                                                                                                                                                                                                               WPI; 2002-617759/66
                                                                                                                                                                          (PAVC/) PAVCO P A. (MACE/) MACEJACK D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus
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                                                   23-MAR-1999;
                                                                                      23-MAR-1999;
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                  27-JUN-2002
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                                                                                                                        (BLAT/)
                                                                                                                                       (MCSW/)
(ROBE/)
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ABX00934/c

Matches

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The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a harmerhead (HH) or hairpin of enzymatic nucleic acid or ribozyme is in a harmerhead (HH) or hairpin of the substrate sequences defined in the specification. The HCV concluding the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or replication of hopatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more condition associated with HCV infection in conjunction with one or more condition associated with HCV infection in conjunction with one or more acondition associated with HCV infection in conjunction. The present sequence represents a substrate for a HCV harmerhead (HH) ribozyme. Note: Some of the sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thymic stromal lymphopoietin; TSLP; lymphopoiesis; STATS; antibacterial; furin-resistant protein; lymphocyte; vaccine; AIDS; autoimmune disease; transplant rejection; infection; immunosuppressive; immunostimulant;
                                                                                                                                                                                    New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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/note= "CDS does not include start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
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Macejack D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TSLP furin cleavage site peptide encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 0 A; 6 C; 2 G; 0 T; 7 U; 0 Other;
     Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seqdata.uspto.gov/psipsDIDEntry.html
          Roberts B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 42; 80pp; English.
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schultz1-727.rng

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Page

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WO9955847-A2,
                                                   26-APR-1999;
                          04-NOV-1999
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Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage; cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer; autoimmune disease; ss. Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection. Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2513. Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Claim 1; Page 73; 123pp; English 98US-0083217P. 98US-0100842P. 99US-00257608. 99US-00274553. 99WO-US009027 (RIBO-) RIBOZYME PHARM INC. WPI; 2000-062023/05. Hepatitis C virus 27-APR-1998; 18-SEP-1998; 25-FEB-1999; 23-MAR-1999;

Macejak D;

The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the Hepatitis C virus (HCV) RNA sequence at the base position given in the describtor line. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatities C virus (HCV) infection, e.g. cirthosis, liver failure and hepatocellular carcinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune Sequence 15 BP; 0 A; 5 C; 2 G; 0 T; 8 U; 0 Other; diseases, and cancer Query Match

.; 0 46.4%; Score 10.2; DB 1; Length 15; 80.0%; Pred. No. 3.3e+02; tive 0; Mismatches 3; Indels 12, Conservative Best Local Similarity Matches 12, Conserv

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Gaps

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729 CCAGGAGAACAGAA 743 15 CCAGGAGAAGGAAAA à

AAF49128 standard; DNA; 15 (first entry) IGF-I oligonucleotide #88. 30-MAR-2001 AAF49128;

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Antisense therapy, antiproliferative, antiinflammatory, antipsoriatic, cytostatic, dermatological; cardiant; virucide, ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFB3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea, ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense alignouclectide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFB]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, of inflammation and/or other disorders. The present sequence is an inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense oligonuclectides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, robar, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or Gaps ; 0 46.4%; Score 10.2; DB 1; Length 15; 80.0%; Pred. No. 3.3e+02; 3; Indels hyperneovascular condition, hyperplasia, kidney disease, neovascular condition of the retina, ss. Sequence 15 BP; 0 A; 5 C; 4 G; 6 T; 0 U; 0 Other; . 0; Mismatches Edmondson SR; (MURD-) MURDOCH CHILDRENS RES INST. Example 8; Page 61; 201pp; English. 99US-0140345P. 21-JJN-2000; 2000WO-AU000693 733 GAGAACAGAACACC 747 GAGAAACAGGAGCCC 1 Wraight CJ, Werther GA, 12; Conservative WPI; 2001-041421/05. Similarity WO200078341-A1. inflammation Homo sapiens 21-JUN-1999; 38-DEC-2000. Local RESULT 129 ABX00933/c ઠ q

Bnzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection, HCV ribozyme, HCV expression, HCV replication, cirrhosis, virucide; liver failure, hepatocellular carcinoma, HCV infection, drug therapy, type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma, consensus interferon, hepatotropic; antiinflammatory; substrate; hammerhead ribozyme; HH ribozyme; ss. Hepatitis C virus substrate #715 for HCV hammerhead ribozyme #715. (first entry) 23-DEC-2002

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ABX00933 standard; RNA; 15

ABX00933;

Hepatitis C virus.

US2002082225-A1

AAZ63881 standard; RNA; 15 BP.

RESULT 126

AAZ63881/

(first entry)

28-MAR-2000

AAZ63881;

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The sequences given in AAQ74218-34 are primers which were used in the extraction of viral RNA and cDNA synthesis of genes from type A and type B influenza virus RNA. The first strand of cDNA from type A and type B influenza virus RNA. The first strand of cDNA from thype A genes was maplified using a primer which is complementary to a conserved region located at the 3' terminus of the viral RNA for all A strain genes. A separate set of primers was required for amplification of genes from B/Panama/45/90 as it does not have common sequences at each end of viral RNA. The amplifies sequences were inserted into the expression plasmid VIJns is an expression vector which expression plasmid VIJns is an expression of an antigenic influenza virus genes, capable of inducing the expression of an antigenic influenza virus gene product which induces a specific immune response upon introduction of the DNA construct into animal tissue in vivo and resultant uptake of the DNA construct by cells which express the encoded influenza gene. These vectors act as polymucleotide vaccines, which induces neutralising antibodies against human influenza virus. The encoded influenza virus cantibodies against human influenza virus. The encoded influenza virus cart as polymucleotide vaccines, which induces meutralising antibodies against human influenza virus. The encoded influenza virus gene encodes nucleoprotein, hemaglutinin, polymerase, matrix or nonstructural human influenza virus gene products. The virus gene is coperably linked to one or more control sequences for incorporation in the control of the products of th
                                                                                                                                                                                                                                        Influenza virus; antigen; specific; immune response; nucleoprotein; hemagglutinin; polymerase; matrix protein; non-structural protein; human; vaccine; PCR; primer; polymerase chain reaction; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide vaccine comprising influenza virus genes - for vaccination against more than one strain of influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JJ, Dwarki VJ, Liu MA, Montgomery DL, Parker SE;
1, Ulmer JB;
                                                                                                                                                                                       Influenza virus strain B/Panama/45/90 NS and HA gene primer.
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46.4%; Score 10.2; DB 1; Length 15;

Best Local Similarity 80.0%; Pred. No. 3.3e+02;

Matches 12; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Page 47; 171pp; English.
AAQ74220 standard; cDNA; 15 BP.
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93US-00089985
                                                                                                       (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-317017/39.
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08-JUL-1993;
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Shiver JW,
                                                                                                       25-MAR-2003
02-JUN-1995
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The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves can the pate position given in the descriptor line. The HVV sequence at the base position given in the descriptor line. The HVV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified Ribozymes were synthesised to target these sites and their activities optimised by either varying the target these sites and their activities optimised by either varying the carget these sites and their activities optimised by either varying the carget the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and hepatitis curinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                    Enzymatic nucleic acid, hammerhead ribozyme, virus replication, cleavage,
cirrhosis, liver failure, hepatocellular carcinoma, interferon, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                    Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.4%; Score 10.2; DB 1; Length 15; 80.0%; Pred. No. 3.38+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 BP; 0 A; 6 C; 2 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 73; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ63880 standard; RNA; 15 BP
                                                                                                                                                                                                                                                                                                                      99WO-US009027.
                                                                                                                                                                                                                                                                                                                                                                       98US-0100842P.
                                                                                                                                                                                                                                                                                                                                                                                                           99US-00274553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           728 GCCAGGAGAAACAGA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                             (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 GCCAGGAGAAGGAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 80.0
les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcswiggen JA,
                                                                                                                                                                        autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-062023/05.
                                                                                                                                                                                                          Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                      26-APR-1999;
                                                                                                                                                                                                                                                W09955847-A2
                                                                                                                                                                                                                                                                                                                                                                       18-SEP-1998;
25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-1999;
                                                                                                                                                                                                                                                                                  04-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Length 16; 1; Indels

Sequence 16 BP; 2 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

ch 47.3%; Score 10.4; DB 1; Similarity 91.7%; Pred. No. 3.2e+02; 11; Conservative 0; Mismatches 1;

728 GCCAGGAGAAC 739

The present sequence is a probe used in a method for monitoring antihepatitis B virus (HBV) drug resistance in a patient by genetic detection of any one of mutations L528M, M552V/I and/or V/L/M551 in HBV DNA polymerase in a biological sample from the patient. The method is useful in the field of genetic detection of anti-HBV drug resistance during HBV therapy. The method is rapid, reliable and precise

Claim 2; Page 9; 64pp; English.

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAS56729-AAS56968 represent DNA encoding BRCA-1 regulators, ribozyme target recognition RNA sequences, DNA fragments encoding the RNA and primers used in the methods of the invention. Hybridisation of ribozymes to their targets results in cleavage of the RNA target. The ribozymes can be used to cleave regulators of the tumour suppressor BRCA-1, resulting in upregulation or downregulation of BRCA-1 in a cell. The mRNA targets include those encoding the BRCA-1 regulator BR1, inhibitor CHLR2, AF6. BR2 and BR3. Regulation of BRCA-1 is useful for treating and diagnosing cancer and other proliferative disorders. The severity of an incleance of cancer can be lessened by regulating tumour proliferation through modulation of BRCA-1. The sequences of the invention are useful in the development of anti-cancer drugs
                                                                                                                                                                                                                                  Novel polypeptides that are the regulators of BRCA-1, useful for treating cancer and diagnosing the presence of neoplastic cells in biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monitoring anti-HBV drug resistance by genetic detection of mutations in DNA polymerase of HBV in patient's sample, involves hybridizing the polymucleic acids of the sample with a probe and detecting the hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 47.3%; Score 10.4; DB 1; Length 16; Local Similarity 91.7%; Pred. No. 3.2e+02; les 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HBV DNA polymerase gene L528M mutation probe HBPr274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16 BP; 7 A; 4 C; 3 G; 0 T; 2 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 26, 97pp, English.
                                                                                                                     Wong-Staal F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Geyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              뭠.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF56037 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation detection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    736 AAACAGAACACC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AAAGAGAACACC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stuyver L, Maertens G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-138370/14.
                                                                                                                  Beger C, Barber J,
                               (IMMU-) IMMUSOL INC
                                                                                                                                                                       WPI; 2001-611503/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus
                                                          BEGE/) BEGER C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200104358-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                             sample,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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IID AAF5
IID AAF5
AAC AAF5
XXX AAF5
XXX ABF5
XXX HBV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for predicting the likelihood of a patient suffering an onset of chronic obstructive pulmonary disease (COPD) exacerbation. The method comprises assaying for the presence of human rhinovirus using a fluorogenic real time PCR assay. The present sequence is a PCR primer for human rhinovirus, used to illustrate the method of the invention. This sequence is complementary to the antisense RNA at position 169 to 184 in the 5' non-coding region of RV1b. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Predicting the likelihood of a patient suffering an onset of chronic obstructive pulmonary disease exacerbation by assaying for a virus, particularly a picornavirus allows management of the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                           PCR; primer; chronic obstructive pulmonary disease; COPD; RV1b;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.3%; Score 10.4; DB 1; Length 16; 91.7%; Pred. No. 3.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16 BP; 1 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Ward CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 11; 19pp; English.
                                                                                                                                                                                Human rhinovirus PCR primer #2.
                                                                        ABN83342 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                  28-NOV-2001; 2001EP-00204552.
                                                                                                                                                                                                                                                                                                                                                                 30-NOV-2000; 2000GB-00029270
                                                                                                                                                  (first entry)
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GCCATGAGAAAC 2
                                                                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                         Blair ED, Snowden BW,
                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGAAACAGAA
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                                                                                                                                                                                                                                          Human rhinovirus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                        EP1211326-A2
                                                                                                                                                  12-AUG-2002
                                                                                                                                                                                                                                                                                                     05-JUN-2002.
                                                                                                                                   29-AUG-2003
                                                                                                      ABN83342;
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WO200170982-A2.

27-SEP-2001

Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pck primers AAX01274-75 were used in a RT-PCR to amplify a 180 bp dragment of the 5' untranslated region (UTR) of Picornavirus, which can detected using probe AAX01276. The primers are used in the method of the invention. The specification describes a new method for obtaining cDNA derived from multiple RNA respiratory pathogens present in cells from a producing obtained. The method comprises extracting RNA from the cells, producing cDNA by reverse transcribing the RNA using pooled short oligonucleotides of random sequence and PCR amplifying the cDNA by using pathogens. The oligonucleotides specific to two or more RNA respiratory pathogens. The oligonucleotides are useful for obtaining and disgnosing multiple RNA pathogen infections, especially single-stranded RNA viruses which cause pneumonia, common cold, exercise induced bronchoconstriction (EIB) and asthma
                                                                                  RNA respiratory pathogen; common cold; multiple RNA pathogen infection; single-stranded RNA virus; picoromavirus; parainfluenza; respiratory syncytial virus; pneumonia; EIB; asthma; exercise induced bronchoconstriction; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection and diagnosis of multiple RNA respiratory pathogens - using pooled random sequenced oligonuclectides as primers for reverse transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                               PCR primer 1 used to amplify a 380 bp 5' UTR fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16 BP; 1 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Target validation ribozyme TV30 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 12; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                              (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                         98CA-02231271
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             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                  Dakhama A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-071226/07.
                                                                                                                                                                                         Picornaviridae
                                                                                                                                                                                                                                                                                                         05-MAR-1998;
                                                                                                                                                                                                                                  CA2231271-A.
                                                                                                                                                                                                                                                                    06-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                  Hegele RG,
                                                                                                                                                                              Synthetic
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Best Local S:
Matches 11)
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Sequences AAS56729-AAS56968 represent DNA encoding BRCA-1 regulators, ribozyme target recognition RNA sequences, DNA fragments encoding the RNA and primers used in the methods of the invention. Hybridsation of ribozymes to their targets results in cleavage of the RNA target. The ribozymes can be used to cleave regulators of the tumour suppressor BRCA-1, resulting in upregulation or downregulation of BRCA-1 in a cell. The mRNA targets include those encoding the BRCA-1 regulator BR1, inhibitor dominant negative 4 (ID4), breast basic conserved protein 1 (BBC1), CHLR2, AF6, BR2 and BR3. Regulation of BRCA-1 is useful for treating and diagnosing cancer and other proliferative disorders. The severity of an incidence of cancer can be lessened by regulating tumour proliferation through modulation of BRCA-1 sequences of the invention are useful in the development of anti-cancer drugs
                                                                                                                                                                                                                                                                                                                  Novel polypeptides that are the regulators of BRCA-1, useful for treating cancer and diagnosing the presence of neoplastic cells in biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, BRCA-1 regulator, ribozyme, BR1, RNA target recognition, probe, cytostatic, RNA cleavage, tumour suppressor; PCR primer, CHLR2, AF6, BR2, inhibitor dominant negative 4, breast basic conserved protein 1, BBC1; BR3; ID4; cancer, proliferative disorder, tumour proliferation; ss.
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47.3%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16 BP; 7 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BR2 protein ribozyme sequence tag RNA #3.
                                                                                                                                                                                                                                                Barber J, Wong-Staal F;
                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 65; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS56768 standard; RNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US009559.
                                                                                                                       23-MAR-2001; 2001WO-US009559
                                                                                                                                                         23-MAR-2000; 2000US-00536058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-00536058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       736 AAACAGAACACC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AAAGAGAACACC 16
                                                                                                                                                                                           (IMMU-) IMMUSOL INC
                                                                                                                                                                                                                                                                                    WPI; 2001-611503/70
                                                                                                                                                                                                            (BEGE/) BEGER C
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                                                                                                                                                                                                                                                Beger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS56768;
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The present invention relates to nucleic acid molecules which modulate the gravites is, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as harmer-head ribozymes, DNAzymes, anceives, zinzymes, amberzymes, and G-cleaver ribozymes, Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene carcinoma. The present sequence represents a substrate for one of the HBV enzymatic nucleic acid sequences disclosed in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus infection.
 degenerative, disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Morrissey D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 BP; 1 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.3%; Score 10.4; DB 1; 91.7%; Pred. No. 3.1e+02; cive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 214; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX03274 standard; DNA; 16 BP.
                                                                                                                                                                                 26-MAR-2001; 2001US-00817879.
08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-0337055P.
                                                                                                                                                       26-MAR-2002; 2002WO-US009187
                                                                                                                                                                                                                                                                          RIBOZYME PHARM INC.
BLATT L.
MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      728 GCCAGGAGAAAC 739
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Draper K, Roberts E;
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                                                               Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                   ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                        LEE P.
DRAPER K.
                                                                                                                                                                                                                                                                                                                                                        PAVCO P.
                                                                                            WO200281494-A1.
                                                                                                                          17-CCT-2002.
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Best Local S
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(BLAT/)
(MACE/)
(MCSW/)
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(PAVC/)
(LEEP/)
(DRAP/)
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AAX03274/C
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AC AAX032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer SAGE tags of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecule, Hepatitis C virus, HCV; Hepatitis B virus, HBV; RNA stability; RNA expression, RNA synthesis, antisense; enzymatic nucleic acid, hammerhead ribozyme; DNAzyme; inozyme; zinzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                              Human, colon cancer, colorectal cancer, pancreatic cancer, SAGB tag, serial analysis of gene expression; diagnostic, prognostic, probe, cancer marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human nucleic acid containing specific SAGE tags, useful as diagnostic markers for cancer, also derived probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vogelstein B, Kinzler KW, Zhang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 22; 161pp; English.
                                                                                                                                                                                 Human colon cancer SAGE tag #132.
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ilarity 91.7%;
Conservative (
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                                                                                          ABK32031 standard; DNA; 15
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                                                                                                                                                      (first entry)
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TGCCAGGAGGAA 14
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es 11; Conser
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                                                                                                                                                      23-APR-2002
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                                                                                                                         ABK32031;
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The invention relates to a novel isolated polypeptide comprising a sequence which is a polymorphic variant of a reference sequence for the purinergic receptor P2Y. G-protein coupled, 1 (PSRY1) protein or its fragment. The polymorphic variant comprises one or more variant amino acids selected from valine at a position 34 and glycine at a position for a polymorphic variants are useful in studying the expression and function of P2RY1, in expressing P2RY1 protein for use in screening for candidate drugs to treat diseases related to P2RY1 activity, in studying the effect of the variation on the biological activity of P2RY1, and the binding affinity of candidate drugs targeting P2RY1 for the treatment of disorders related to platelet aggregation. The hablotyping methods are
                                                     The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human dynein, axonemal light polypeptide chain 4 (DNAL4) gene located on chromosome 22q13.1, and methods for haplotyping and/or genotyping the DNAL4 gene. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the DNAL4 gene polymorphisms. The polymorphisms and screened compounds are useful for the treatment of diseases associated with DNAL4 activity, such as neurological disorders. AAS19907-AAS19920 represent ASO probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New purinergic receptor P2Y G-protein coupled 1 (P2RV1) gene polymorphic variants, useful e.g. in studying the expression and function of P2RV1 and screening candidate drugs for treating diseases related to P2RV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant; coagulant; platelet aggregation; haplotyping; drug screening; transgenic animal; human; allele-specific oligonucleotide; ss.
                                                                                                                                                                                                                                                                                         Sequence 15 BP, 1 A, 5 C, 2 G; 6 T, 0 U, 1 Other;
                                                                                                                                                                                                                                                                                                                                 Query Match
47.3%; Score 10.4; DB 1;
Best Local Similarity 78.6%; Pred. No. 3.1e+02;
Matches 11; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P2RY1 gene allele-specific oligonucleotide #38.
                                                                                                                                                                                                                                                   detecting human DNAL4 gene polymorphisms
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                    Claim 16; Page 13; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK09887 standard; DNA; 15 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                        730 CAGGAGAAACAGAA 743
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condition or disease predicted to be associated with P2RYI activity, or specific condition or disease associated with P2RYI activity, or specific condition or disease associated with P2RYI activity. The transgenic animals are useful for studying expression of the P2RYI isogenes in vivo, for in vivo screening and testing of drugs targeted against P2RYI protein, and for testing the efficacy of the P2RYI and compounds for disorders related to platelet aggregation in a biological system. ABK09950-ABK09924 represent human purinersic receptor the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colon and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, colon cancer, colorectal cancer, pancreatic cancer, SAGE tag, serial analysis of gene expression, diagnostic, prognostic, probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human nucleic acid containing specific SAGE tags, useful as diagnostic markers for cancer, also derived probes.
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                                                                                                                                                                                                                                      47.3%; Score 10.4; DB 1; Length 15; 78.6%; Pred. No. 3.16+02; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human colorectal and pancreatic cancer SAGE tag #133.
                                                                                                                                                                                                         Sequence 15 BP; 0 A; 5 C; 3 G; 6 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vogelstein B, Kinzler KW, Zhang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Col 93; 161pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK32766 standard; DNA; 15
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Best Local Similarity 78.65
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                               14 RGGGGACACAGAAC 1
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer marker; ss
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 117
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Length 15; Indels 727 TGCCAGGAGAAA 738

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The invention relates to a novel human 6-phosphofructo-2-kinase/ fructose -2,6-biphosphatase 2 (PFKBE2) isogene. The PFKFB2 of the invention has yetostatic and antidiabetic activity. The polymoleotides may have a use in gene therapy. The identified candidate agents targeting PFKFB2, are useful for treating cancer and diabetes. The methods of the invention are useful for improving the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with PFKFB2 activity. The present sequence represents a allele specific oligonucleotide (ASO) probe used in the invention to detect PFKFB2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genotyping human dynein, axonemal light polypeptide chain 4 gene of individual, useful for determining haplotype of individual, comprises determining identity of nucleotide pair at specific polymorphic sites for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, single nucleotide polymorphism; SNP; DNAL4; chromosome 22q13.1;
dynein axonemal light polypeptide chain 4; haplotyping; genotyping;
neuroprotective; neurological disorder; allele-specific oligonucleotide;
                                                                                                                                                                                                  New 6-phosphofruoto-2-kinase/fructose-2,6-bisphosphatase 2 (PFKFB2) gene variants, for improving efficiency and reliability in the development of drugs for treating diseases associated with PFKFB2 activity e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASO probe #7 to detect human DNAL4 gene polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 6 A; 4 C; 3 G; 1 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                        Claim 16; Page 13; 95pp; English
                                                                              (GENA-) GENAISSANCE PHARM INC.
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                                       07-JUN-2000; 2000US-0209935P.
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07-JUN-2001; 2001WO-US018458.
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                                                                                                                                                               WPI; 2002-566434/60.
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                                                                                                                        Kazemi A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymorphisms
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Best Local S
                                                                                                                      Duda A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel polymucleotide sequence which is a polymorphic variant of a reference sequence for the cofilin 1 (nonmuscle) (CFL1) gene or its fragment, or a polymorphic variant of a reference sequence for a CFL1 DNA or its fragment. The polymucleotide of the invention may have a use in gene therapy, and in antisense gene therapy. The polymucleotide is useful for studying the expression and function of CFL1 and expressing CFL1 protein for use in screening function of CFL1 and expressing CFL1 protein for use in screening polymorphism and haplotype data are useful for validating whether CFL1 is a suitable target for drugs to treat immunological disorders, screening for such drugs and reducing bias in clinical trials of such drugs. The present sequence represents one of a set of allele-specific oligomucleotide (ASO) PCR primer used in the invention to detect
                                                                                                                                                                                                                                                                                                                                                                                                                             Novel genetic variants of human cofilin 1, CFL1 gene for studying expression, function of the gene and expressing CFL1 protein useful in identifying drugs to treat immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; PFKFB2; cytostatic; antidiabetic; gene therapy; cancer; diabetes; ss; ASO; allele specific oligonucleotide; probe; polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                     Human, cofilin 1, CFL1, gene therapy, antisense gene therapy, immunological disorder; ASO; allele-specific oligonuclectide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.3%; Score 10.4; DB 1; Length 15; 78.6%; Pred. No. 3.1e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                   Sausker EA;
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                                                                                                                                                                                                                                                                                                                                                   Koshy B,
                                                                                                                                                                                                                                                                                                                                                   Kliem SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 13; 84pp; English
Human CFL1 ASO PCR primer #20.
                                                                                                                                                                                                                                                                                                         (GENA-) GENAISSANCE PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV99770 standard; DNA; 15
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-566437/60.
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                                                                                                    Homo sapiens.
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Gaps .

Score 10.4, DB 1; Length 15; Pred. No. 3.1e+02; 1; Mismatches 2; Indels

47.38; 78.68;

Koshy B;

Choi JY,

AAS18254 standard; DNA; 15 BP

AAS18254;

727 TGCCAGGAGAA 738

TGCCAGGAGGAA 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
sample suspected of being neoplastic. The method comprises comparing the level of at least one transcript in a first sample of a tissue to a second sample, where the first sample is a colonic tissue suspected of being neoplastic and the second sample is a normal human colonic tissue. The transcript is identified by a tag selected from AAX30947-31315. The methods of the invention can be used in the diagnosis, prognosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of isolated gene transcripts - useful for developing products for diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcript tag sequence increased in pancreatic and colorectal cancer.
                                                                                                                                                                                                                       Gaps
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Local Similarity 91.7%; Pred. No. 3.1e+02;
les 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                             47.3%; Score 10.4; DB 1; Length 15; ilarity 91.7%; Pred. No. 3.1e+02; Conservative 0; Mismatches 1; Indels
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                                                                                                                                              Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 80; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                                                                                                   AAX31812 standard; DNA; 15
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                                                                                                                                                                                                                                                        727 TGCCAGGAGAAA 738
                                                                                                                                                                                                                                                                                            TGCCAGGAGGAA 14
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                                                                                                             treatment of cancer
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treatment of cancer
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es 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide having polymorphic variant of IMP2 dehydrogenase gene, useful for studying expression of the gene in vivo, and for testing efficacy of therapeutic agents for cancer in biological
                                                                                                        Human; single nucleotide polymorphism; SNP; IMPDH2; chromosome 3p21.2; IMP dehydrogenase 2; haplotyping; genotyping; cancer; cytostatic; allele-specific oligonucleotide; ASO; primer; ss.
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                                                                             ASO primer #1 to detect IMPDH2 gene polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                       Stephens JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 BP; 1 A; 3 C; 2 G; 8 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                         Choi JY, Koshy B, Lee HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 13; 70pp; English.
                                                                                                                                                                                                                                                                                                                                        (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ88673 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                          11-APR-2000; 2000US-0196248P.
                                                                                                                                                                                                                                                                         11-APR-2001; 2001WO-US011851
                                              (first entry)
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Best Local Similarity 91.7%
Marches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene polymorphisms
                                                                                                                                                                                                           WO200177363-A2.
                                                                                                                                                                              Homo sapiens
                                               25-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          system
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ID ABQE
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AC ABQE
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DT 23-6
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Gaps

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The present sequence represents a preferred target sequence for an enzymatic nucleotide acid (i.e. a ribozyme) which cleaves relA mRNA at the nucleotide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NF-kappaB and is implicated specifically in the induction of inflammatory responses. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit relA expression, making them potentially useful for treating rheumatoid arthritis, restenosis and asthma as well as for increasing tolerance to transplanted tissues. The potential immunosuppressive properties of a ribozyme that cleaves relA mRNA means that uses are limited to local delivery, acute indications or ex vivo treatment. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 15 BP; 2 A; 6 C; 1 G; 0 T; 6 U; 0 Other;

Gaps . 0 Length 15; 1; Indels Score 10.4; DB 1; Pred. No. 3.1e+02; 0; Mismatches 1; 47.3%; 91.7%; 11; Conservative Query Match Best Local Similarity Matches 11; Conserv

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731 AGGAGAAACAGA 742

13 AGGGGAAACAGA

AAT50236 standard; RNA; 15

AAT50236;

07-MAR-1997 (first entry)

Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage; neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy; reverse cholesterol transport; high density lipoprotein; therapy; CETP; familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia; peripheral vascular disease, hyperbecalipoproteinaemia; RCT; inhibitor; angioplastic restenosis; low density lipoprotein; diabetes; HDL; rabbit; Rabbit CETP HH ribozyme target sequence #797.

Oryctolagus cuniculus.

WO9620279-A1

95WO-US016000 11-DEC-1995; 94US-00363240 23-DEC-1994;

(RIBO-) RIBOZYME PHARM INC. (WARN) WARNER LAMBERT CO.

Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, WPI; 1996-321852/32.

Pape M;

New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial hypercholesterolaemia.

Claim 4; Page 41; 72pp; English.

AAT50138-T50359 represent target sequences for the rabbit cholesterol ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT50360-T50546). CETP is a 74 kD glycoprotein that facilitates neutral lipid

AAX30947-31815 represent tag sequences of transcripts that are differentially expressed in colorectal cancer, in pancreatic cancer, or in both. The tag sequences can be used to identify genes by matching the tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from cDNA libraries. The tag sequences can also be used in a method for diagnosing colon or pancreatic cancer in a

Claim 2; Page 30; 120pp; English.

transfer between plasma lipoproteins. The numbering of the targets refers to the position of the cleavage site in full length CETP. The ribozyme then binds to 5 nucleotides either side of this site. The ribozymes are able to cleave mRNA from the gene encoding CETP, thereby blocking synthesis and/or expression of the mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway can be inhibited (or eliminated) thereby preventing the reduction in size density of the high density lipoproteins (HDL), prolonging HDL half life, and therefore increasing HDL levels. The ribozymes can be used to treat conditions associated with abnormal levels of CETP, specifically atherosclerosis, familial hyperbetalipoproteinaemia, peripheral vascular disease, dyslipidaemia, hyperbetalipoproteinaemia, hyposlphalipoproteinaemia, wascular complications of diabetes, transplant, atherectomy and low density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels). The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH ribozymes con also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH ribozymes con also be used the CETP gene, they have low non-specific ó Use of isolated gene transcripts - useful for developing products for the diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer. Gaps Tag sequence; colorectal cancer; pancreatic cancer; colon cancer; diagnosis; prognosis; treatment; ss. 0 Tag sequence of a transcript increased in colorectal cancer. Length 15; 1; Indels Sequence 15 BP; 1 A; 4 C; 3 G; 0 T; 7 U; 0 Other; Score 10.4; DB 1; Pred. No. 3.1e+02; 0; Mismatches 1; AAX31078 standard; DNA; 15 BP. 97US-0047352P. 47.3%; 91.7%; (UYJO) UNIV JOHNS HOPKINS. (first entry) Jogelstein B, Kinzler KW; 732 GGAGAAACAGAA 743 11; Conservative GGAGAACCAGAA 1 WPI; 1999-070161/06. Query Match Best Local Similarity 20-MAY-1998; Homo sapiens 409853319-A2 21-MAY-1997; 21-MAY-1999 26-NOV-1998. AAX31078; activity Matches AAX31078 ઠ

AAT54806,

(first entry)

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Rod opsin hairpin ribozyme target oligonucleotide SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                Sequence 14 BP; 1 A; 4 C; 2 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                       exemplification of the present invention
                                                                                                                                                     Claim 1; Page 64; 115pp; English.
                                                                                          01-MAY-2001; 2001US-00847601
                                                                                 01-MAY-2002; 2002WO-US013679
                                                                                                   UYFL ) UNIV FLORIDA
                                                                                                                     WPI; 2003-111880/10.
                                                              WO200288320-A2
                                                      Homo sapiens
             09-APR-2003
                                                                        07-NOV-2002
                                                                                                            Lewin AS,
    ABZ72778;
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Best Local Similarity 91.7%; Matches 11; Conservative

Query Match

731 AGGAGAAACAGA 742 || ||||||||| 14 AGCAGAAACAGA 3

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Grant MB

Shaw LC,

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Mcswiggen JA;
ler D, Thompson JD;
                                                                                                                                                                                                   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribozymes having modified bases and methods for producing them - for use
                                                                                                                                                             Mouse relA hammerhead ribozyme target sequence (nt. position 94)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in inhibiting disease related genes.
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Usman N, Wincott FE,
BP.
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94US-00245736.
94US-00271280.
94US-00291932.
94US-00291433.
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94US-00300000.
94US-00311486.
94US-00311349.
94US-00314397.
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94US-00319492.
94US-00321993.
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94US-00337608.
94US-00345516.
94US-00357577.
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94US-00222795
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AATS4806 standard; RNA; 15
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                                                                                          (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stinchcomb DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9523225-A2
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                                                                                          25-MAR-2003
07-APR-1997
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Modak A,
Tracz D,
                                             AAT54806;
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17-AUG-19
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The present invention describes a recombinant adeno-associated virus (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a first tibozyme that specifically cleaves an mRNA encoding a protein, copypeptide, or peptide selected from the group of rod opsin, iNOS, calpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V, (b) a corrector comprising a polynucleotide encoding the ribozyme, where the polynucleotide encoding the ribozyme, where the polynucleotide operably positioned downstream of at least a first or promoter that directs expression of the polynucleotide in a selected comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide; or (e) a comprising the ribozyme or the polynucleotide; or (e) a comprising the ribozyme or the polynucleotide. Also described is a method comprising the ribozyme or the polynucleotide. Also described is a method comprising the ribozyme, and for a time effective to specifically cleave the mRNA in the cell. (I) can be used for treating a disease or retinal compathy or (dasertinal dasers) and conderention of the mammalian eye, such as a retinal disease or retinal cystumention. (I) is also useful for manifacturing a medicament for treating the diseases mentioned above, including autosomal dominant cretinities or a blood-retinal barrier dysfunction. (I) can also be useful for treating the diseases mentioned above, including autosomal dominant cretinities or a blood-retinal barrier dysfunction. (I) can also be useful for treating the disease mentioned above, including autosomal dominant cretinities or a blood-retinal barrier dysfunction of the encoding of compatible of the disease of the 
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                                                                 Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target; ophthalmological; gene therapy; eye; retinal dysfunction; AAV; diabetic retinopathy; mecular degeneration; autosomal dominant retinitis; blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A recombinant adeno-associated virus-vectored ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Length 14;

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Transforming growth factor beta; TGF-beta; antisense; treatment; tumour; angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma; carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut; immunosuppression; oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analogues. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlingensiepen
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                                                                                                                      Length 13;
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                                                                                                                                              1; Indels
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                                                                                           Sequence 13 BP; 7 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                   Score 10.4; DB 1;
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating immunosuppression, tumours, etc.
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                                                                                                                                                                                                                                                                      BP.
                                                                                                                   47.3%;
91.7%;
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(first entry)
                                                                                                         Query Match
Best Local Similarity 91...
These 11; Conservative
                                                                                                                                                                          736 AAACAGAACACC 747
                                                                                                                                                                                                  2 AAACACAACACC 13
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Bogdahn U;
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27-JUN-1995
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Seguence 14 BP; 6 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a universal molecular Turing machine comprising a circular DNA molecule, having sites representing information storage of the Turing machine, having sites representing information storage of the Turing machine, having sites representing information (Inv) restriction site also inside the circular DNA molecule, and adjacent to the Inv restriction site; a current symbol, encoded on the circular DNA molecule at a distance from the state restriction site; a sequence of intervening nucleotides between the state restriction site and the current symbol; a set of the asymmetric restriction as each of asymmetric restriction asymmetry as to the current symbol; a set of asymmetric restriction and not of the current symbol; a set of transition oligonucleotides, which are inserted into the dircular DNA molecule as additional symbols to encode changes to the information storage caused by operation of the Turing machine. The Turing machine is a model of computation. The universal molecular Turing machine is capable of simulating any Turing machine is a model of simulating any Turing machine is a simulating and molecular machine is capable of simulating machine is a simulating and molecular machine is capable of simulating machine in the simulating machine is capable of simulating machine is capable of simulating machine is capable of simulating machine in the simulat
                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecular Turing machine; circular DNA molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Universal molecular Turing machine - based on circular DNA molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               machine and hence any algorithm. AAV70176 to AAV70206 represent oligonuclectides used to exemplify the present invention
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              Score 10.4; DB 1; Length 1
Pred. No. 3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO:4 from Figure 14 of US5843661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 14; 90pp; English.
                                                                                                                                                                                                                                                                                                             AAV70179 standard; DNA; 14 BP.
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Ouery Match
Best Local Similarity 91.78
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Universal DNA based
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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ABZ72778/C
ID ABZ727
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WO200177384-A2

18-OCT-2001

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disponsis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                              i.s
                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.3%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 2.9e+02; cive 0; Mismatches 1; Indels
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                                                                                                                                                                            Claim 1; SEQ ID NO 173165; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABF73169 standard; DNA; 13 BP.
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Best Local Similarity 91.77
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABF82073 data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ^ Match 47.3%; Score 10.4; DB 1; Length 13; Local Similarity 91.7%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 240241; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                             Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABF73168 standard; DNA; 13 BP.
                                                                                                                                          06-APR-2001; 2001WO-IB000713.
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Query Match Best Loca Matches

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18-OCT-2001

Homo sapiens

ABF73168/C

ID ABF731

AC ABF73

AX AC ABF73

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